

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:32:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971278.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_SRR2971278 /home/luna/Desktop/database/homo_hsa/hsa.fa SRR2971278.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:32:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971278.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,180,827
Mapped reads	8,953,822 / 73.51%
Unmapped reads	3,227,005 / 26.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	845,708 / 6.94%
Duplication rate	8.44%
Clipped reads	674,471 / 5.54%

2.2. ACGT Content

Number/percentage of A's	101,741,595 / 28.74%
Number/percentage of C's	73,462,014 / 20.75%
Number/percentage of T's	103,434,987 / 29.22%
Number/percentage of G's	75,311,879 / 21.28%
Number/percentage of N's	2,991 / 0%
GC Percentage	42.03%

2.3. Coverage

Mean	0.1143
Standard Deviation	0.9579

2.4. Mapping Quality

Mean Mapping Quality	44.24
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2.5. Mismatches and indels

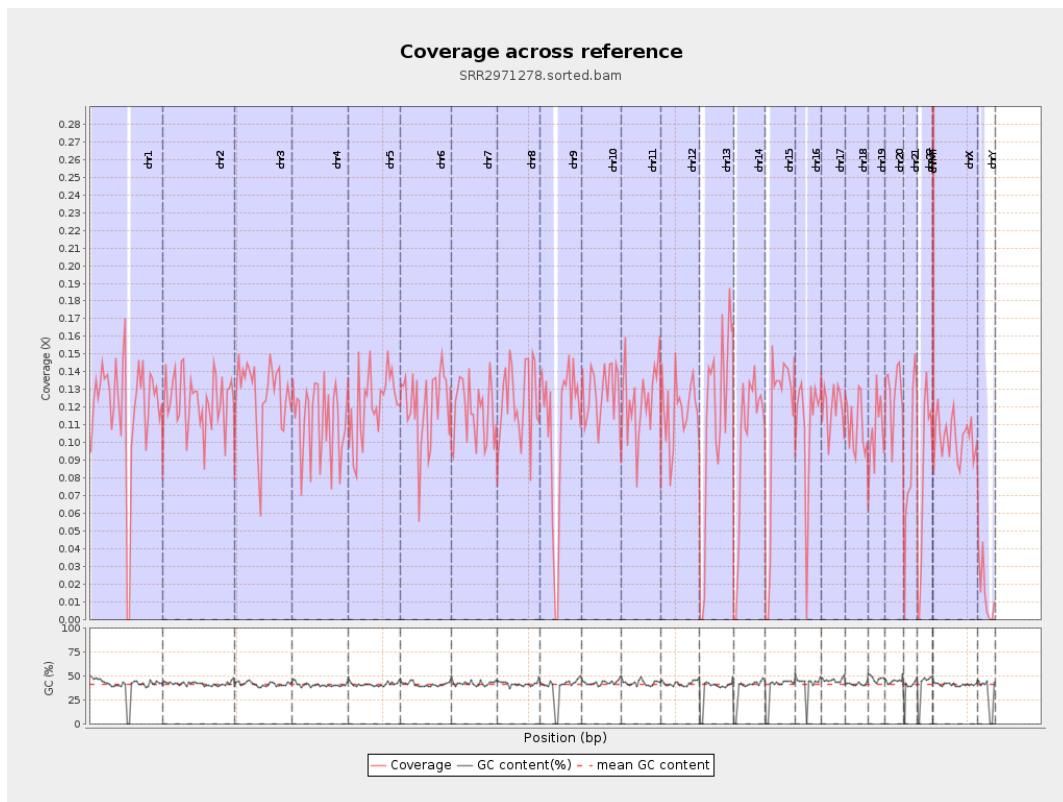
General error rate	0.25%
Mismatches	861,231
Insertions	10,719
Mapped reads with at least one insertion	0.12%
Deletions	26,674
Mapped reads with at least one deletion	0.3%
Homopolymer indels	41.26%

2.6. Chromosome stats

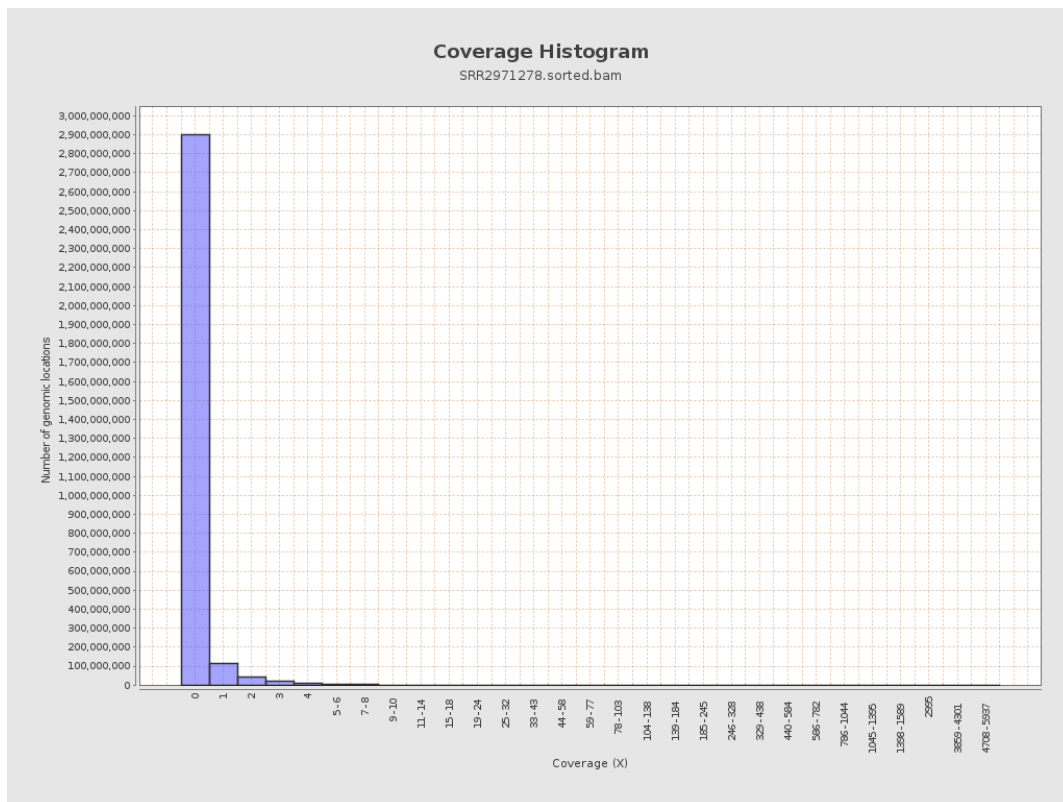
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29810757	0.1196	1.3925
chr2	243199373	30114542	0.1238	0.6334
chr3	198022430	24931354	0.1259	0.5777
chr4	191154276	21470946	0.1123	0.5638
chr5	180915260	22020122	0.1217	0.5729
chr6	171115067	20731110	0.1212	0.5934
chr7	159138663	18665031	0.1173	0.9879
chr8	146364022	18067472	0.1234	2.915

chr9	141213431	15208960	0.1077	0.611
chr10	135534747	17293153	0.1276	0.6993
chr11	135006516	16747804	0.1241	0.687
chr12	133851895	15991018	0.1195	0.5739
chr13	115169878	12915969	0.1121	0.5509
chr14	107349540	10874101	0.1013	0.5509
chr15	102531392	11206432	0.1093	0.5302
chr16	90354753	9777743	0.1082	0.5509
chr17	81195210	9729680	0.1198	0.5819
chr18	78077248	8527672	0.1092	0.8749
chr19	59128983	6295360	0.1065	1.1371
chr20	63025520	8089505	0.1284	0.5973
chr21	48129895	4395415	0.0913	0.5275
chr22	51304566	4233972	0.0825	0.4802
chrMT	16571	43890	2.6486	3.7522
chrX	155270560	15955261	0.1028	0.5488
chrY	59373566	890661	0.015	0.2647

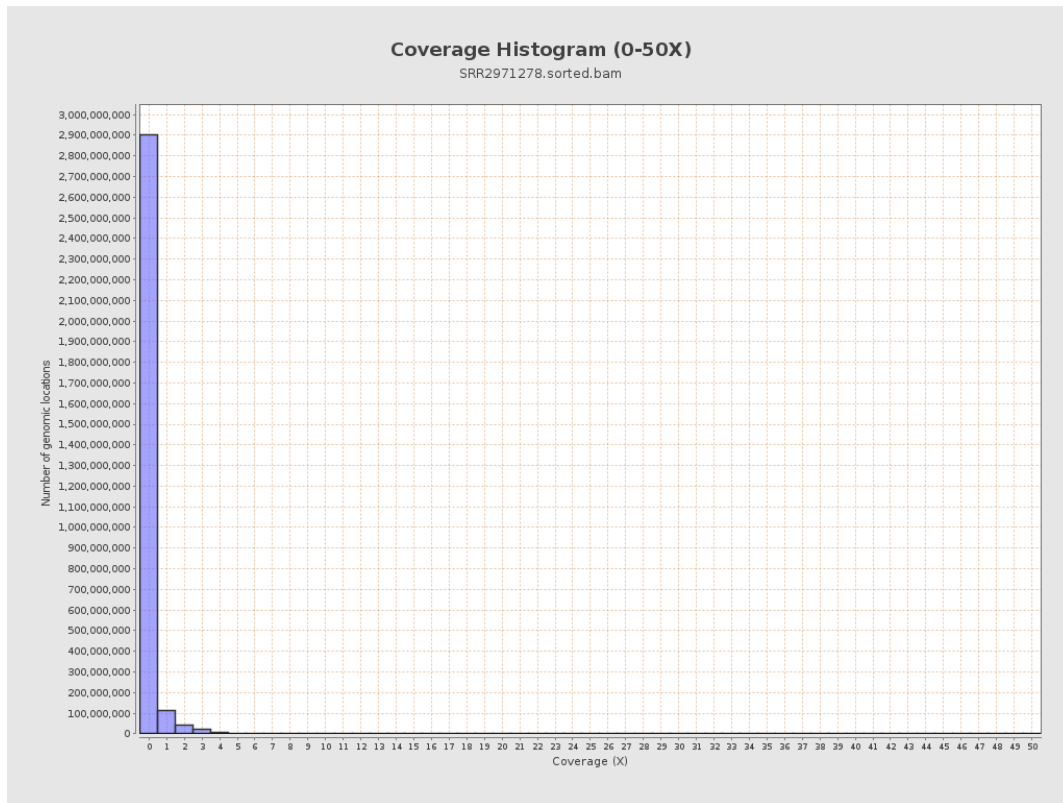
3. Results : Coverage across reference



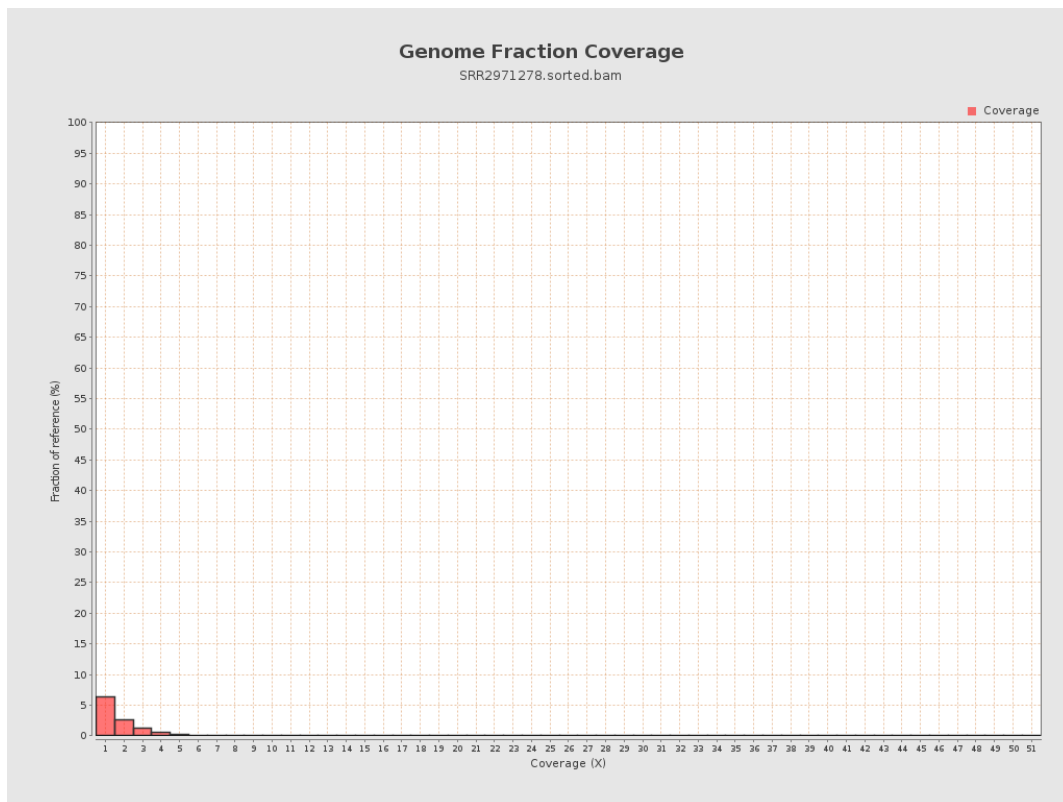
4. Results : Coverage Histogram



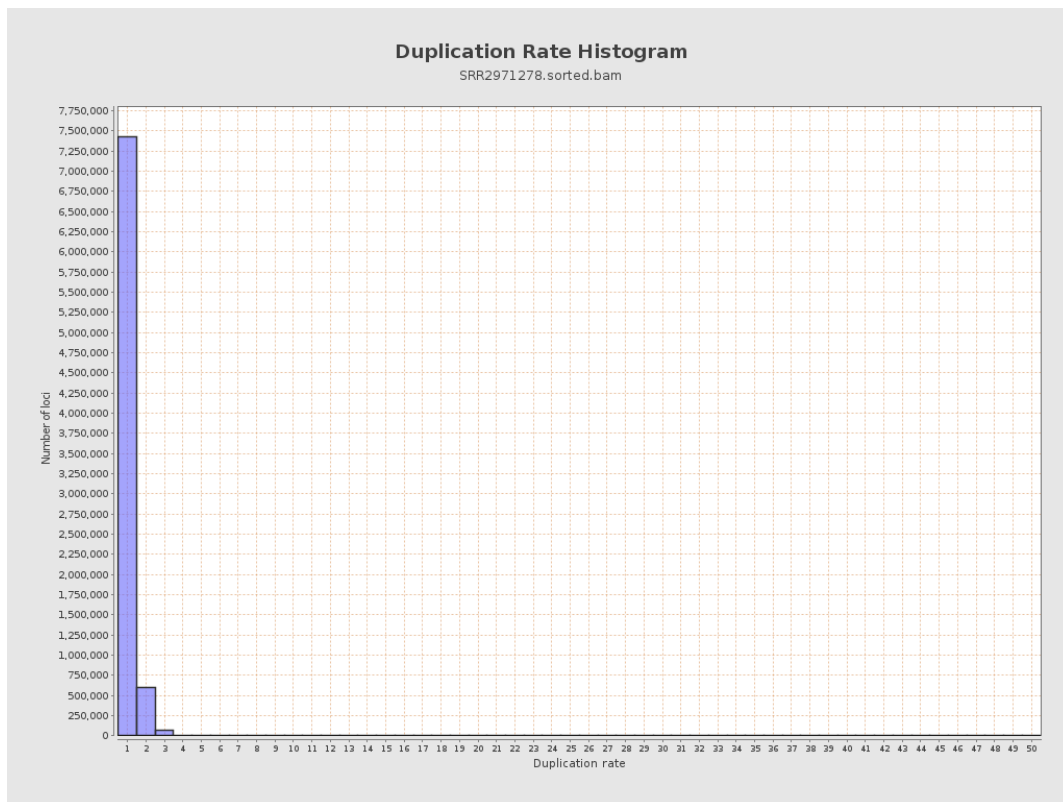
5. Results : Coverage Histogram (0-50X)



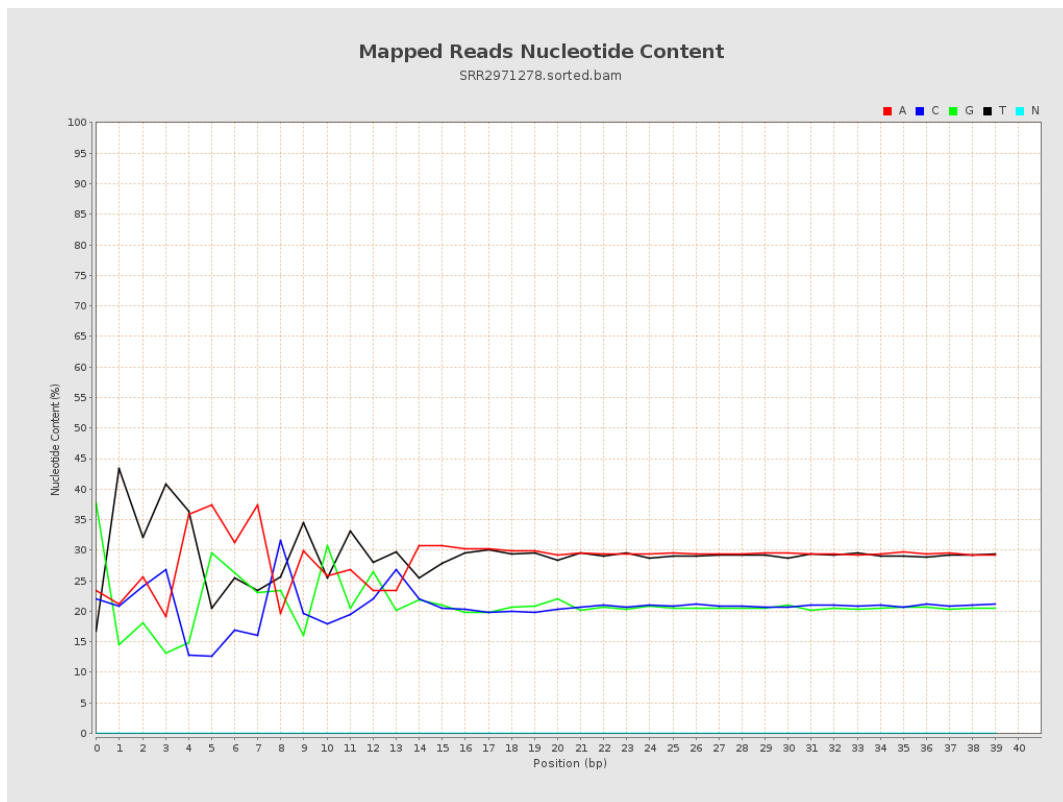
6. Results : Genome Fraction Coverage



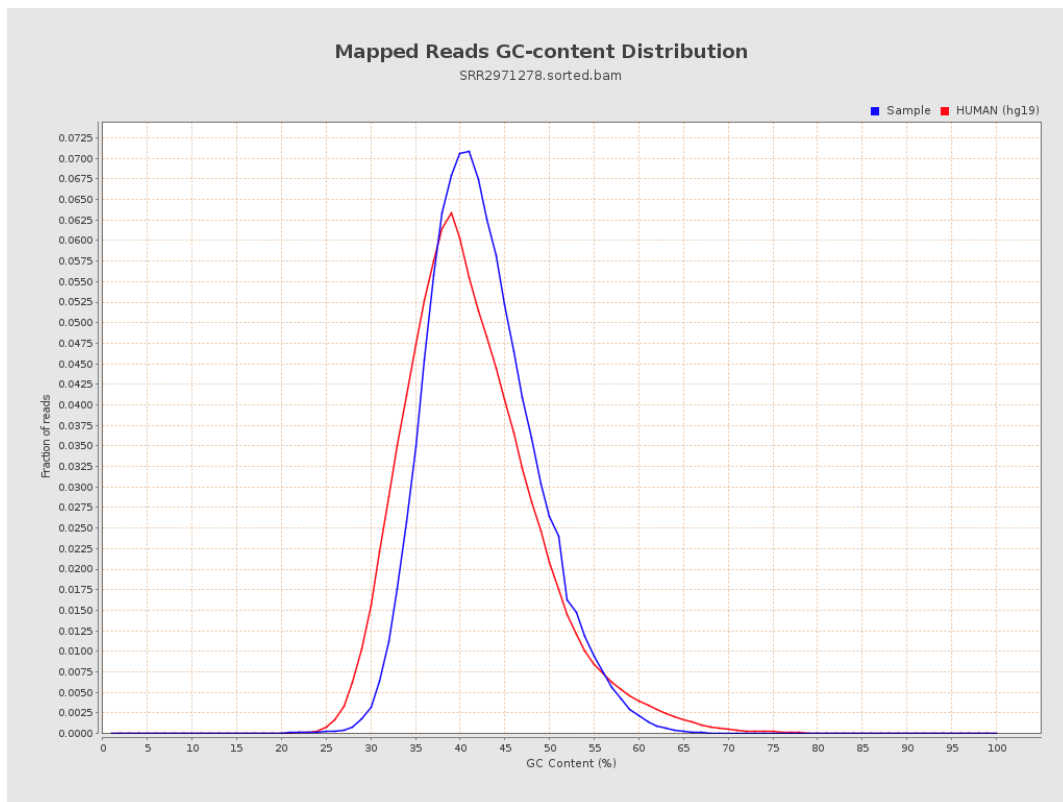
7. Results : Duplication Rate Histogram



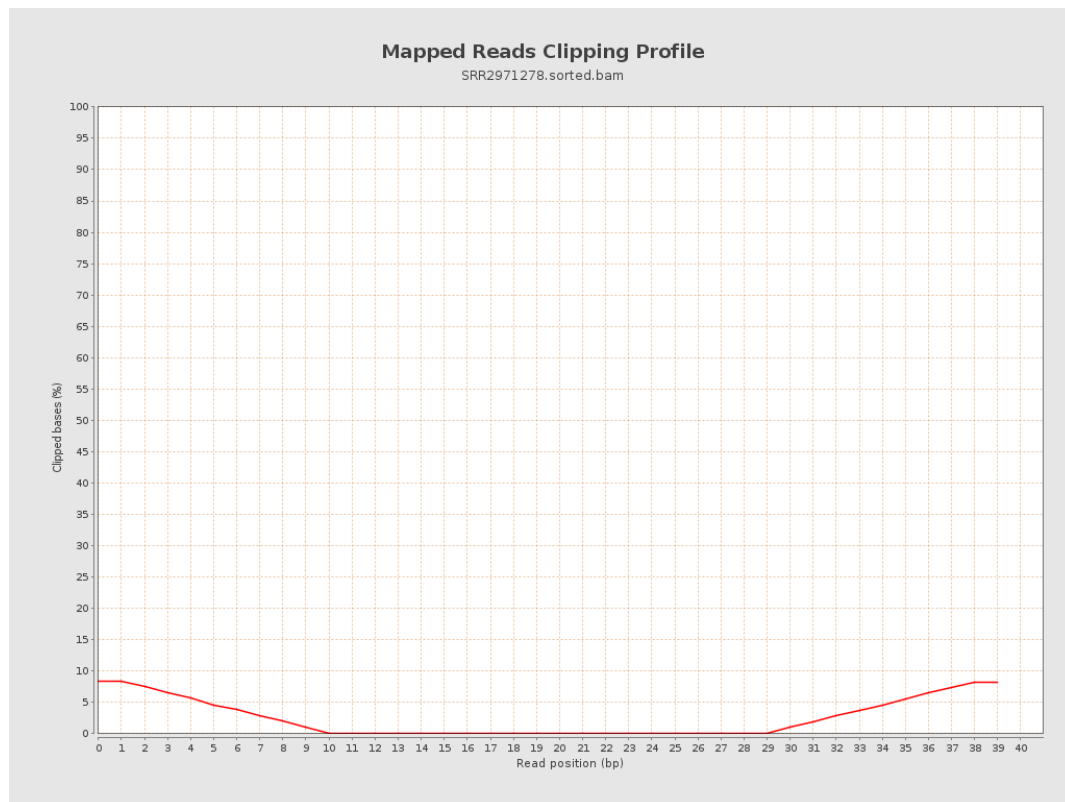
8. Results : Mapped Reads Nucleotide Content



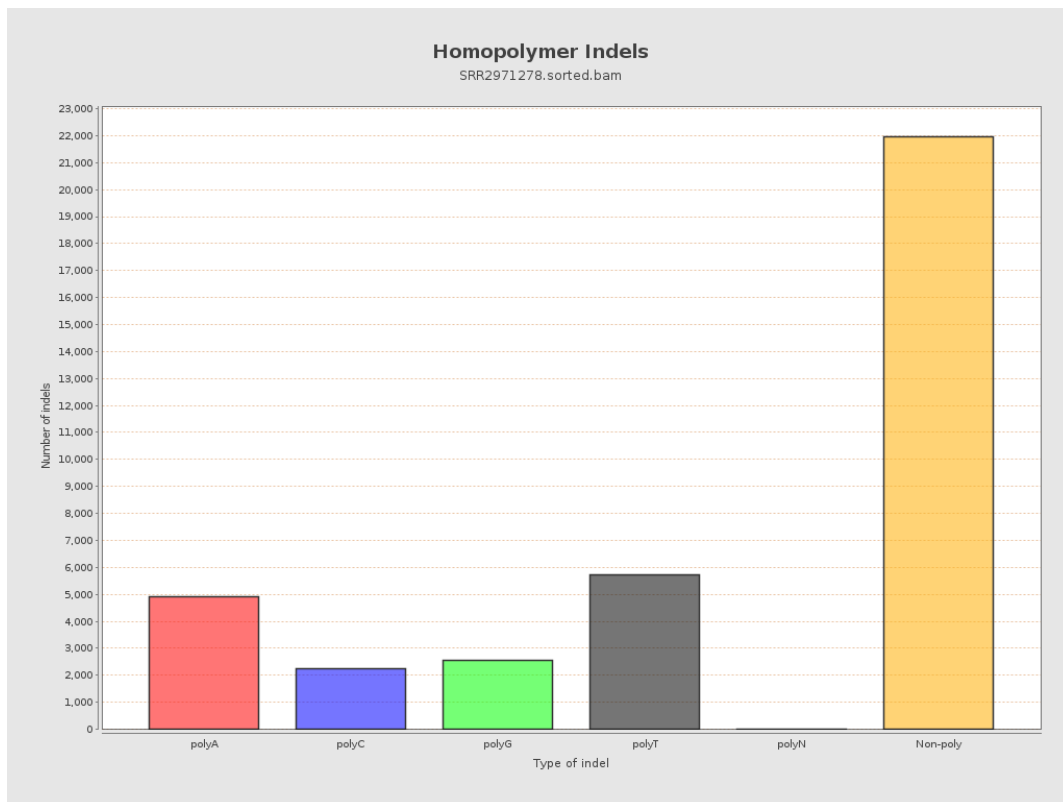
9. Results : Mapped Reads GC-content Distribution



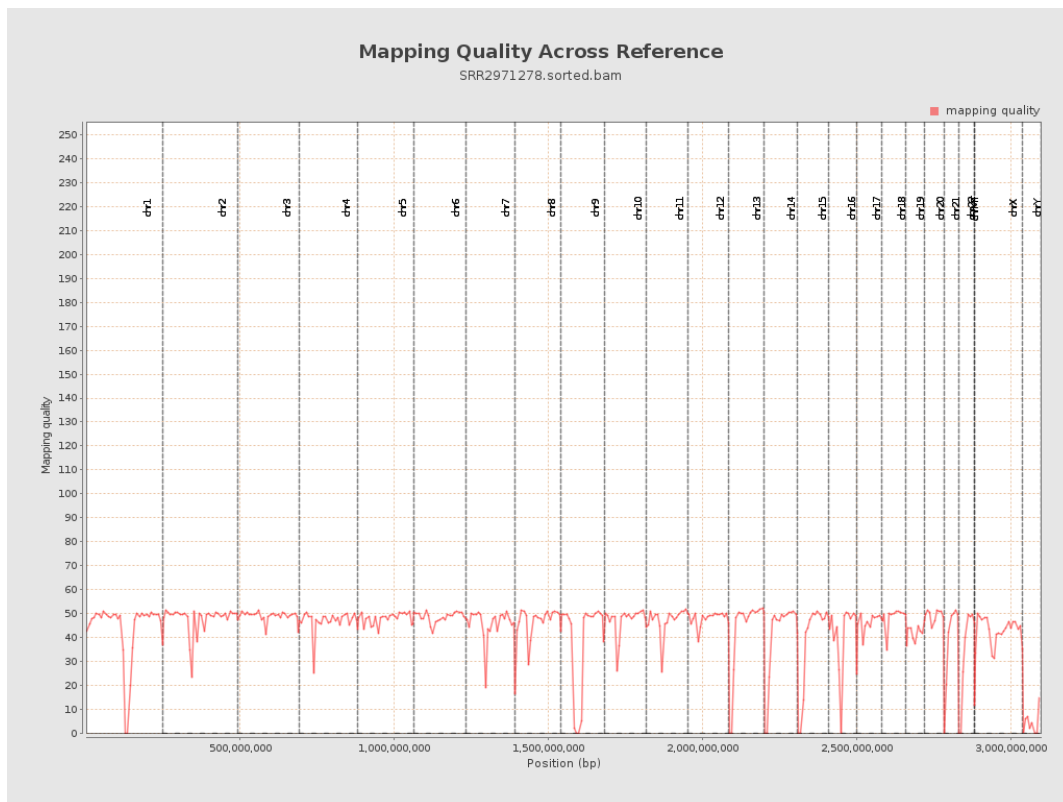
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

