

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:15:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971288.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_SRR2971288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971288.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:15:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971288.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,888,820
Mapped reads	5,869,283 / 85.2%
Unmapped reads	1,019,537 / 14.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	279,577 / 4.06%
Duplication rate	3.7%
Clipped reads	520,956 / 7.56%

2.2. ACGT Content

Number/percentage of A's	67,557,115 / 29.16%
Number/percentage of C's	46,857,408 / 20.23%
Number/percentage of T's	69,180,437 / 29.86%
Number/percentage of G's	48,057,733 / 20.74%
Number/percentage of N's	13,265 / 0.01%
GC Percentage	40.97%

2.3. Coverage

Mean	0.0748
Standard Deviation	0.6227

2.4. Mapping Quality

Mean Mapping Quality	41.27
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2.5. Mismatches and indels

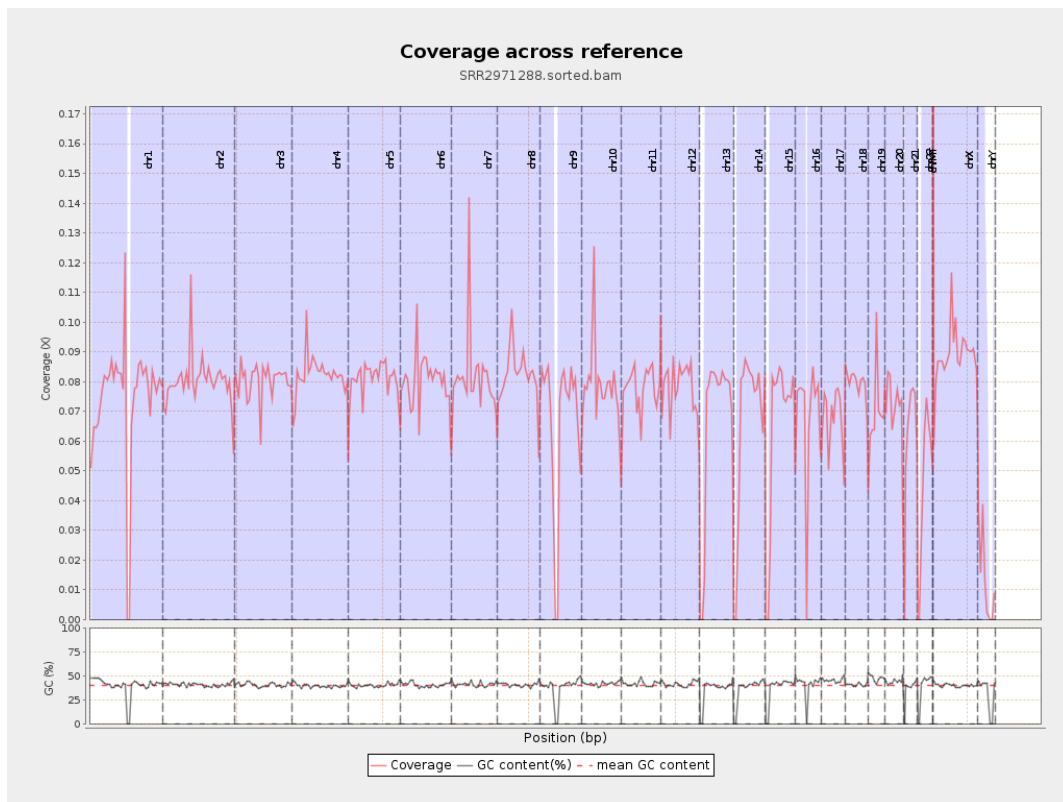
General error rate	0.29%
Mismatches	663,698
Insertions	7,484
Mapped reads with at least one insertion	0.13%
Deletions	19,294
Mapped reads with at least one deletion	0.33%
Homopolymer indels	40.91%

2.6. Chromosome stats

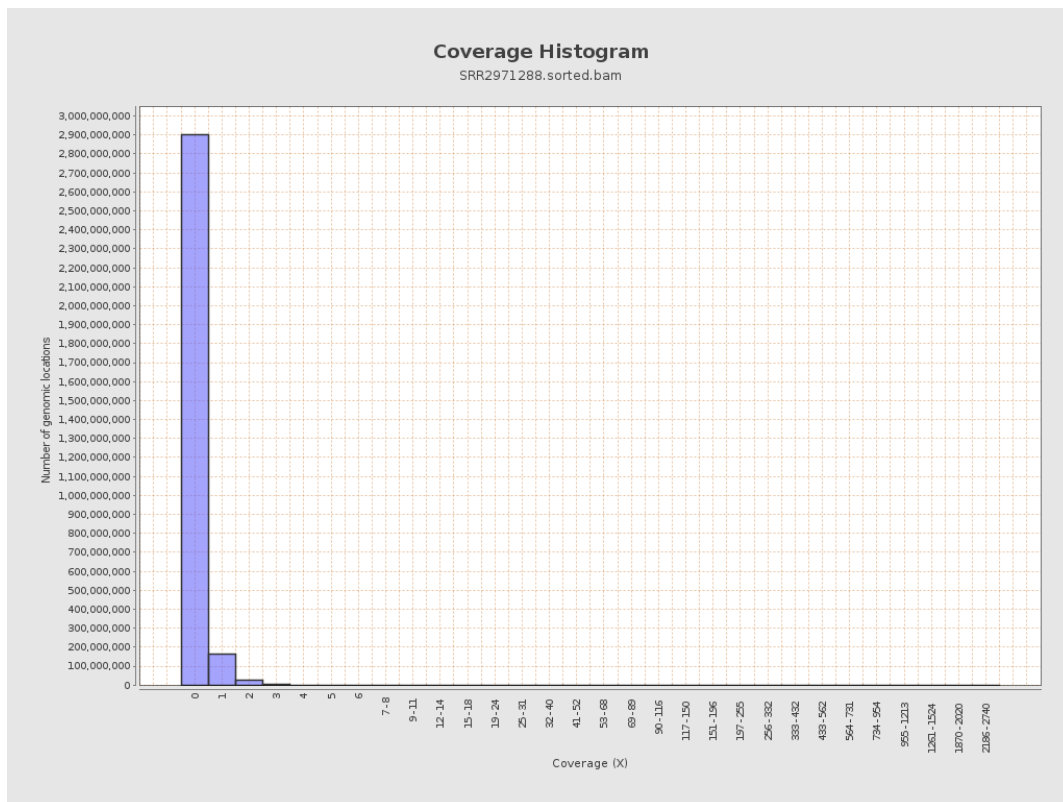
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18461800	0.0741	1.1217
chr2	243199373	19509221	0.0802	0.4897
chr3	198022430	15906604	0.0803	0.3271
chr4	191154276	15750836	0.0824	0.3608
chr5	180915260	14587999	0.0806	0.3356
chr6	171115067	13804056	0.0807	0.4315
chr7	159138663	12942592	0.0813	0.8746
chr8	146364022	12032982	0.0822	1.3746

chr9	141213431	9463623	0.067	0.4778
chr10	135534747	10686892	0.0788	0.526
chr11	135006516	10471466	0.0776	0.4316
chr12	133851895	10433855	0.078	0.3327
chr13	115169878	7606687	0.066	0.294
chr14	107349540	7148219	0.0666	0.3757
chr15	102531392	6499391	0.0634	0.2886
chr16	90354753	6021238	0.0666	0.3399
chr17	81195210	5521992	0.068	0.3189
chr18	78077248	6234852	0.0799	0.8771
chr19	59128983	4147692	0.0701	1.0497
chr20	63025520	4558102	0.0723	0.3283
chr21	48129895	2946807	0.0612	0.336
chr22	51304566	2349839	0.0458	0.2476
chrMT	16571	11077	0.6685	1.0309
chrX	155270560	13796453	0.0889	0.4129
chrY	59373566	795787	0.0134	0.2038

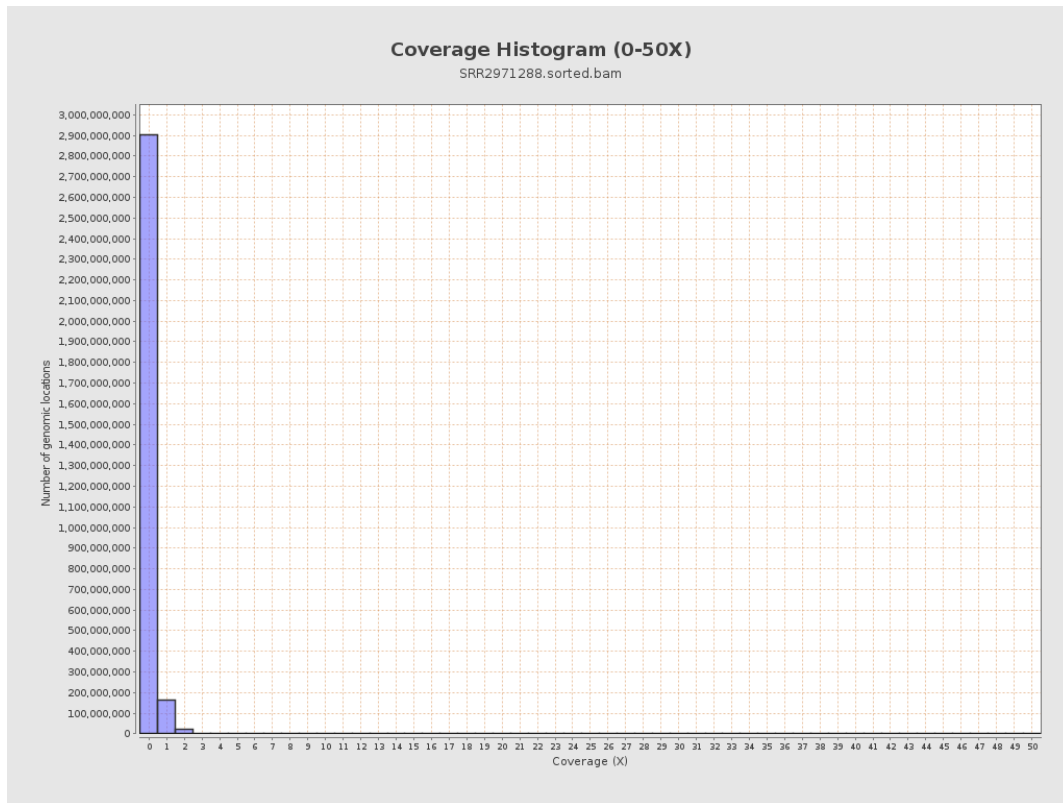
3. Results : Coverage across reference



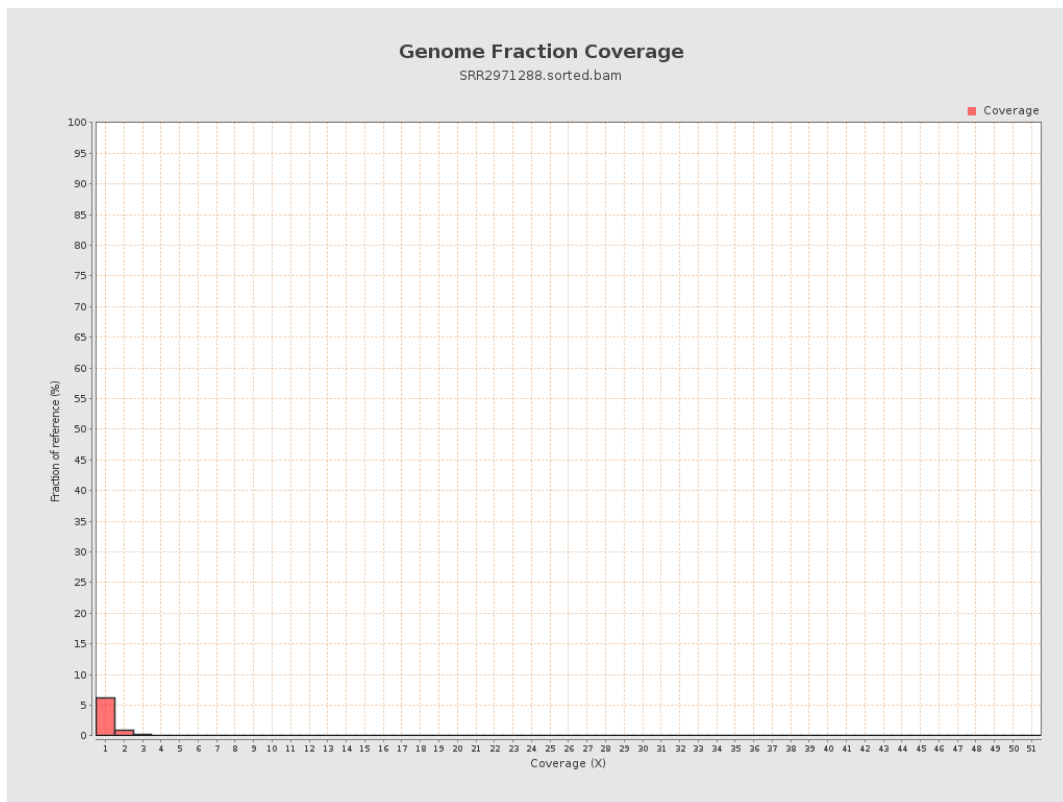
4. Results : Coverage Histogram



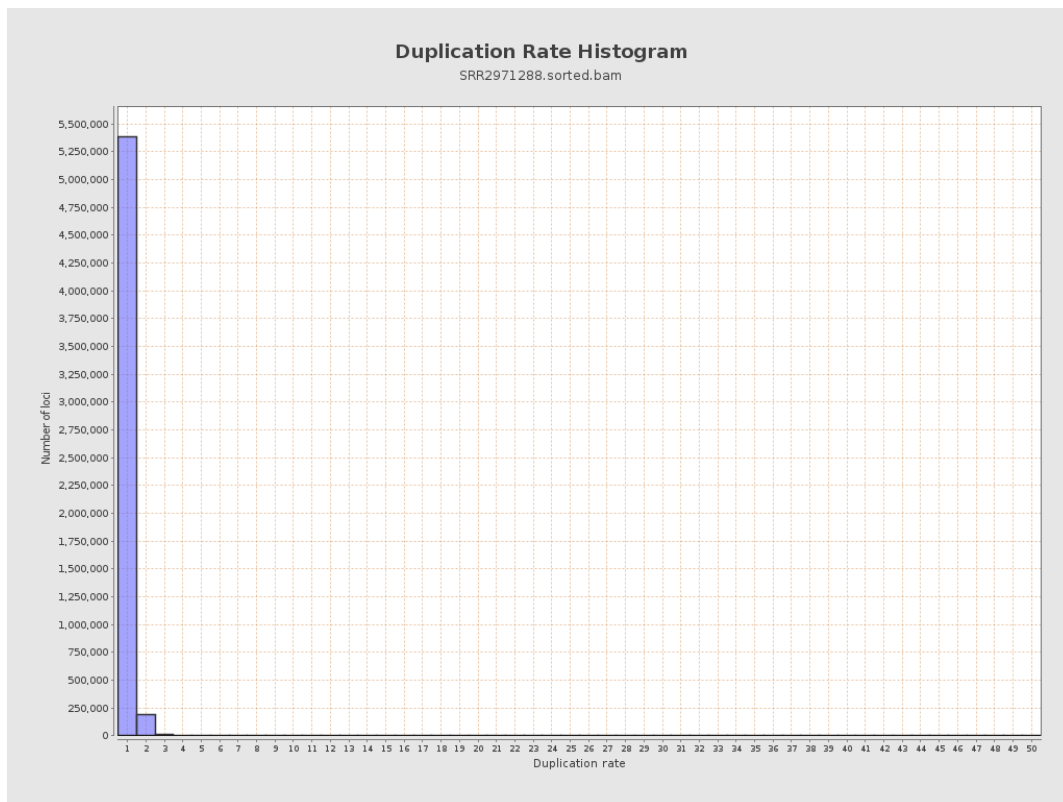
5. Results : Coverage Histogram (0-50X)



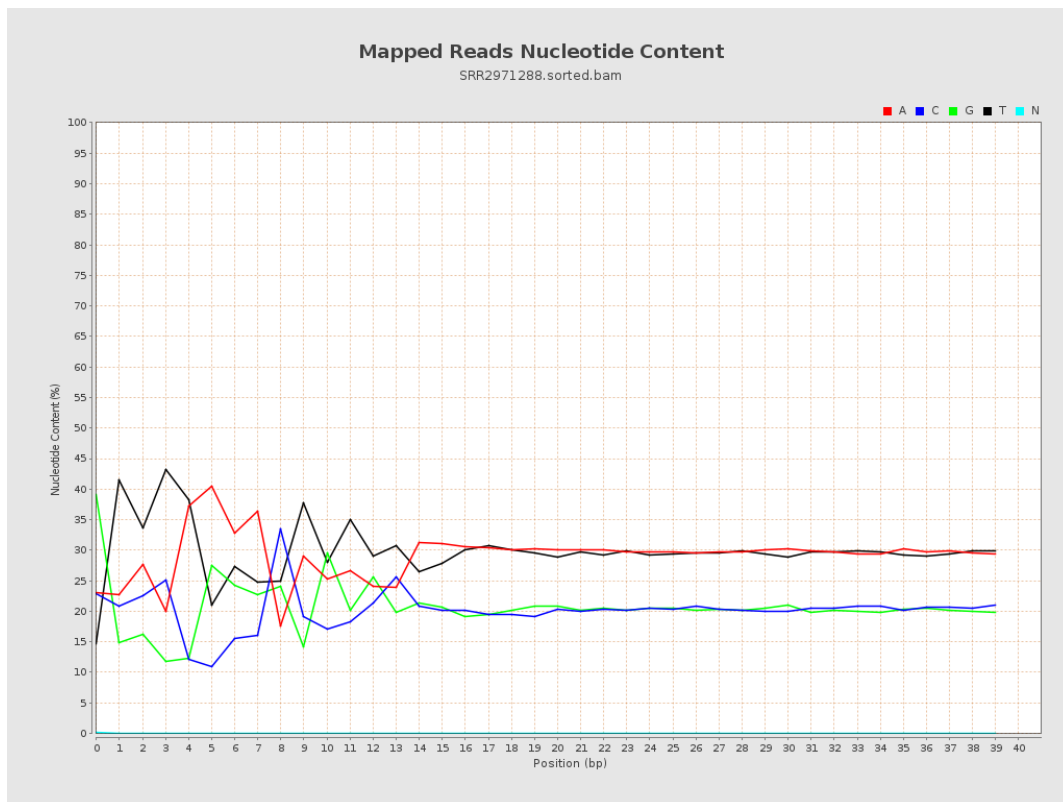
6. Results : Genome Fraction Coverage



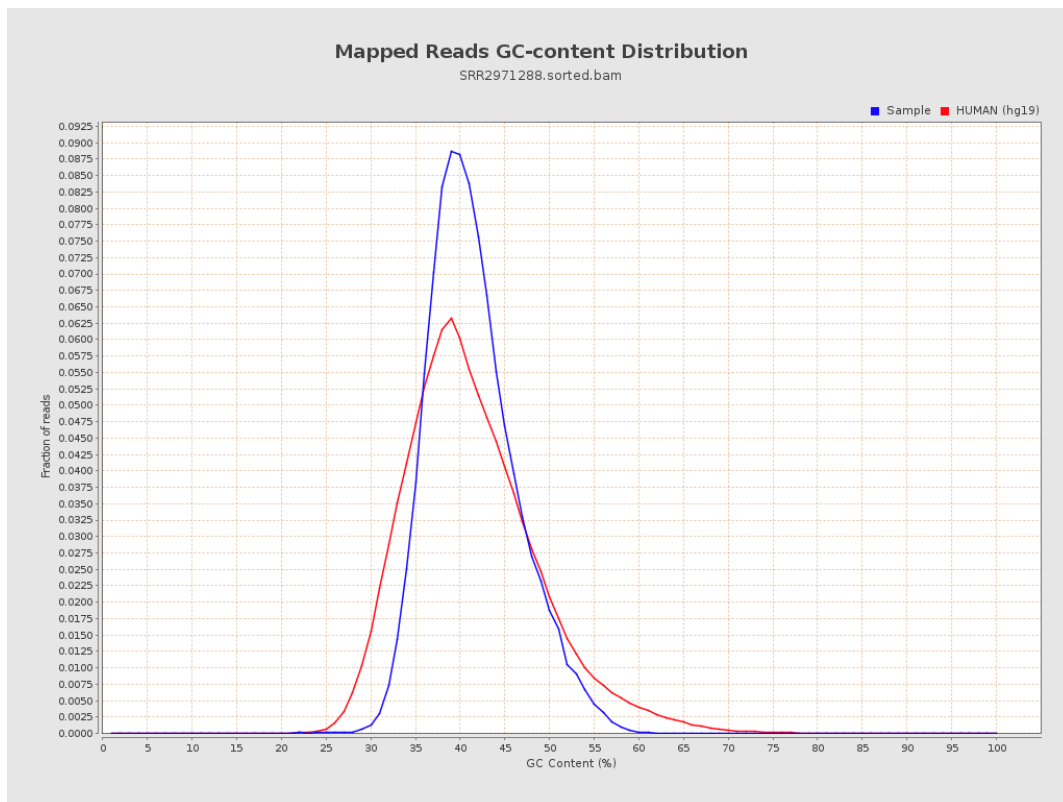
7. Results : Duplication Rate Histogram



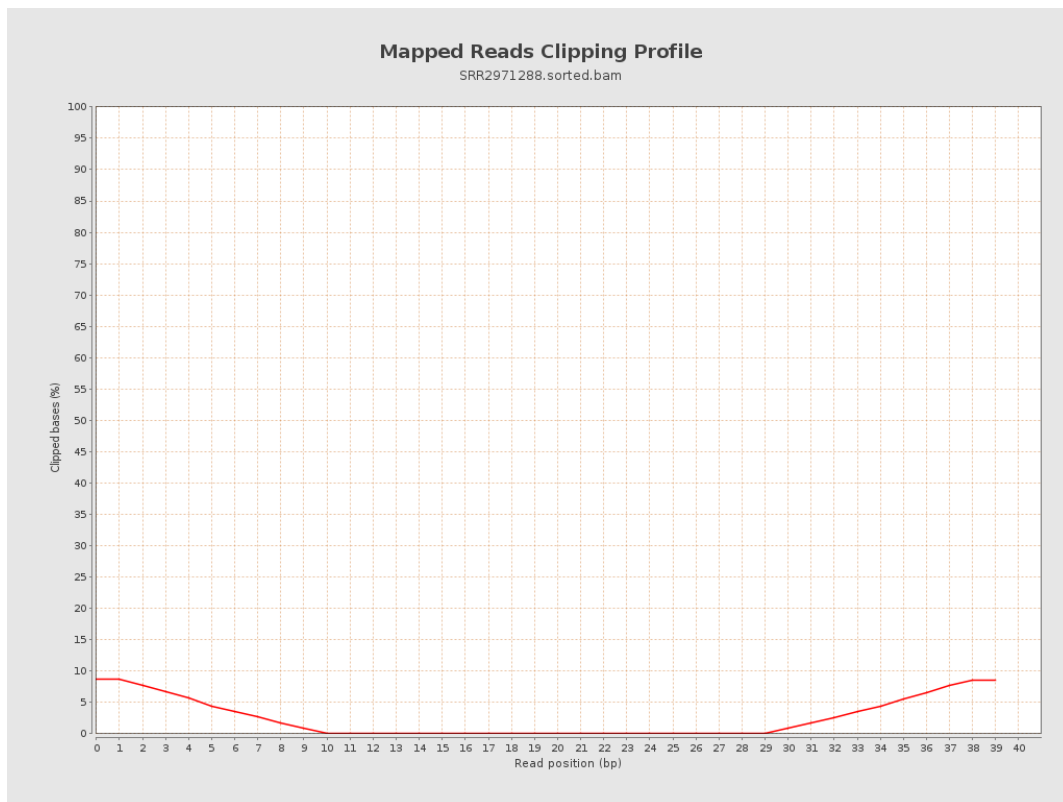
8. Results : Mapped Reads Nucleotide Content



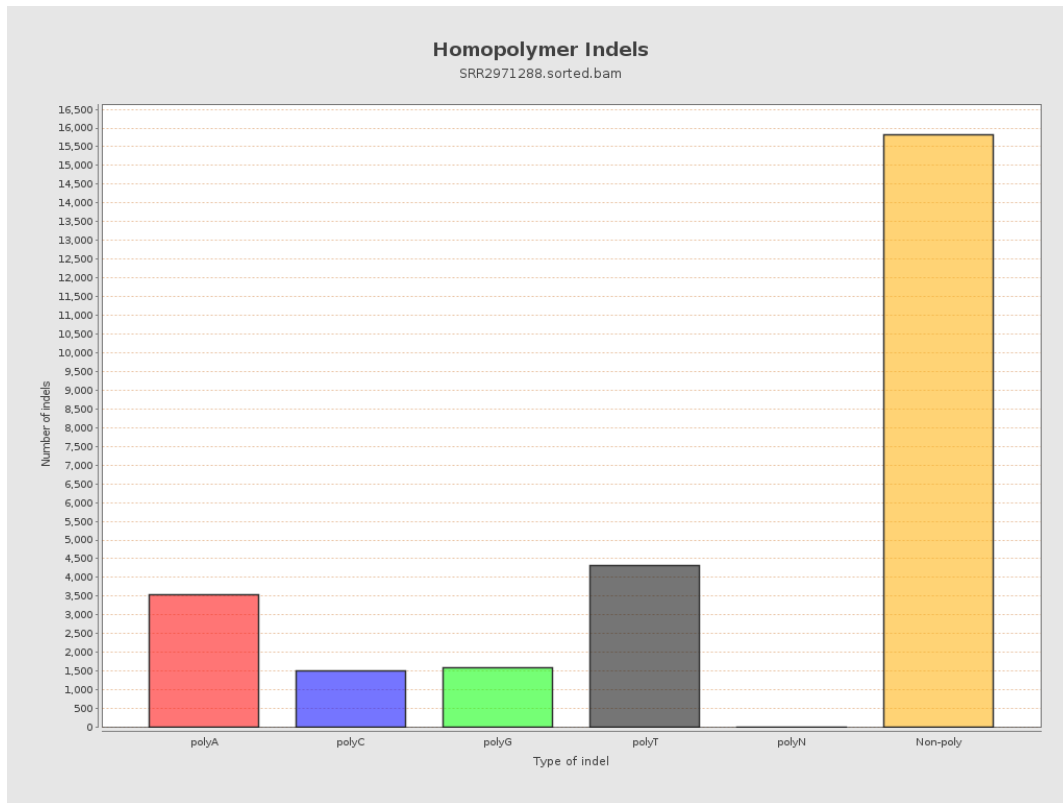
9. Results : Mapped Reads GC-content Distribution



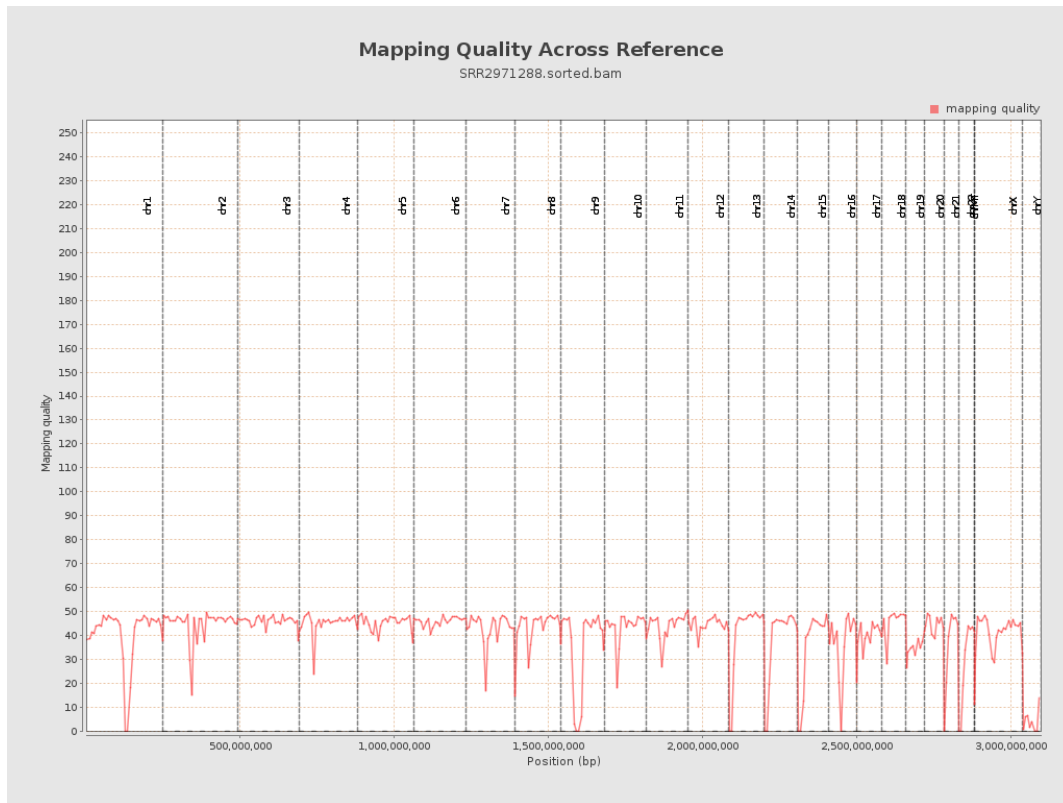
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

