

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:06:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971287.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_SRR2971287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971287.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:06:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971287.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,680,103
Mapped reads	9,218,688 / 86.32%
Unmapped reads	1,461,415 / 13.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	880,994 / 8.25%
Duplication rate	6.28%
Clipped reads	1,057,060 / 9.9%

2.2. ACGT Content

Number/percentage of A's	101,745,450 / 28.06%
Number/percentage of C's	77,098,885 / 21.26%
Number/percentage of T's	105,021,534 / 28.96%
Number/percentage of G's	78,784,061 / 21.72%
Number/percentage of N's	2,642 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.1172
Standard Deviation	1.8765

2.4. Mapping Quality

Mean Mapping Quality	31.26
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2.5. Mismatches and indels

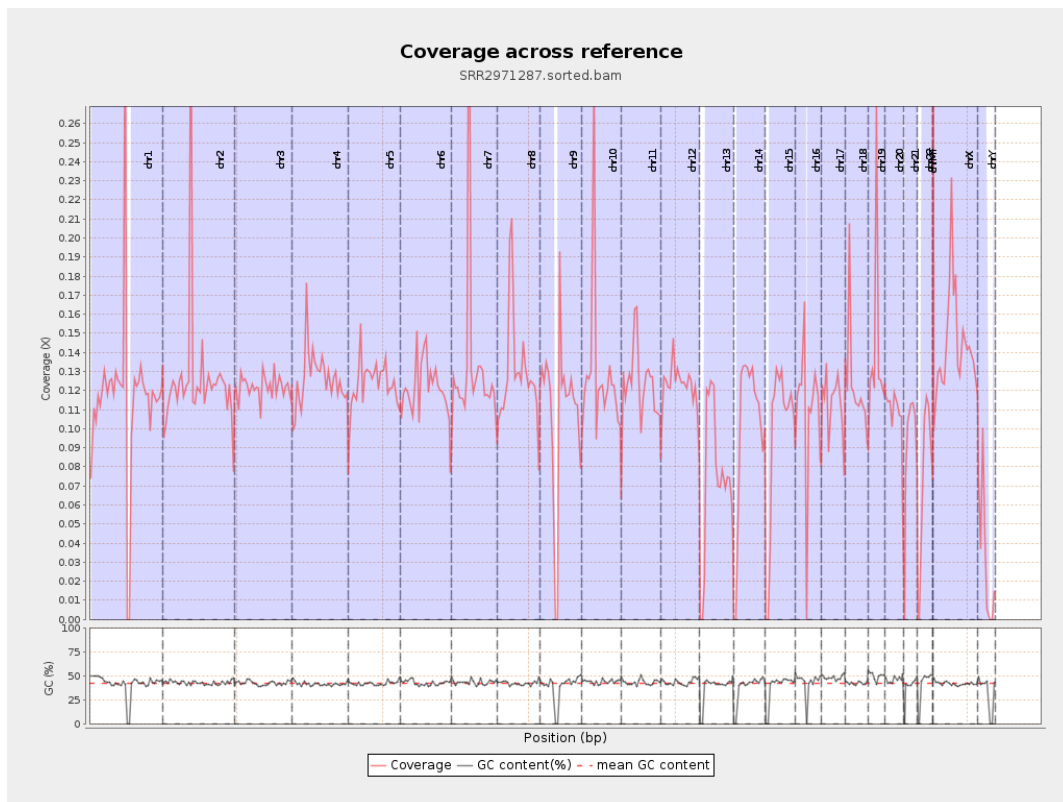
General error rate	0.4%
Mismatches	1,415,497
Insertions	15,312
Mapped reads with at least one insertion	0.17%
Deletions	28,707
Mapped reads with at least one deletion	0.31%
Homopolymer indels	36.62%

2.6. Chromosome stats

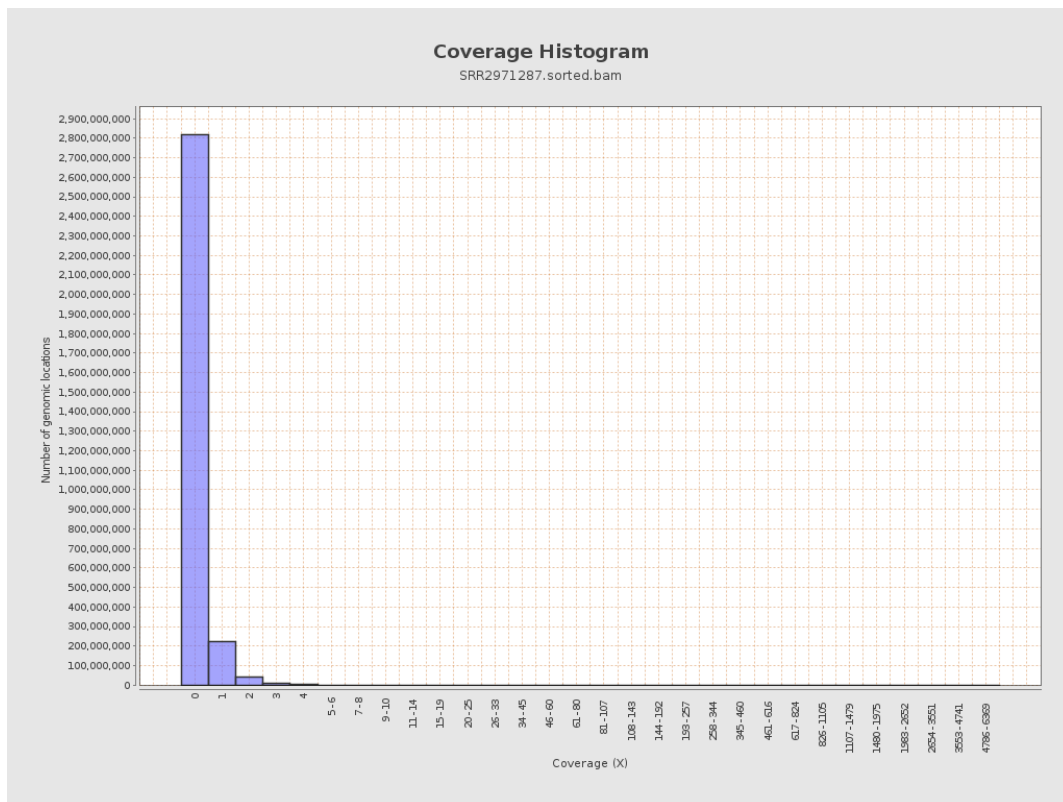
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29119707	0.1168	4.2538
chr2	243199373	30690825	0.1262	1.5839
chr3	198022430	24131357	0.1219	0.4624
chr4	191154276	24166706	0.1264	0.5394
chr5	180915260	22341202	0.1235	0.5693
chr6	171115067	20812142	0.1216	0.5513
chr7	159138663	21201640	0.1332	2.6697
chr8	146364022	18917242	0.1292	2.8121

chr9	141213431	15346870	0.1087	1.606
chr10	135534747	17292820	0.1276	1.4263
chr11	135006516	16688495	0.1236	1.1811
chr12	133851895	16434072	0.1228	0.6229
chr13	115169878	8495827	0.0738	0.3272
chr14	107349540	10907613	0.1016	0.9133
chr15	102531392	9736278	0.095	0.3963
chr16	90354753	9735624	0.1077	0.721
chr17	81195210	9326090	0.1149	0.6167
chr18	78077248	9698808	0.1242	3.5401
chr19	59128983	8407102	0.1422	4.143
chr20	63025520	6848565	0.1087	0.6127
chr21	48129895	4358709	0.0906	0.6796
chr22	51304566	3798544	0.074	0.3391
chrMT	16571	15940	0.9619	1.3481
chrX	155270560	22270914	0.1434	0.9792
chrY	59373566	1944147	0.0327	0.3998

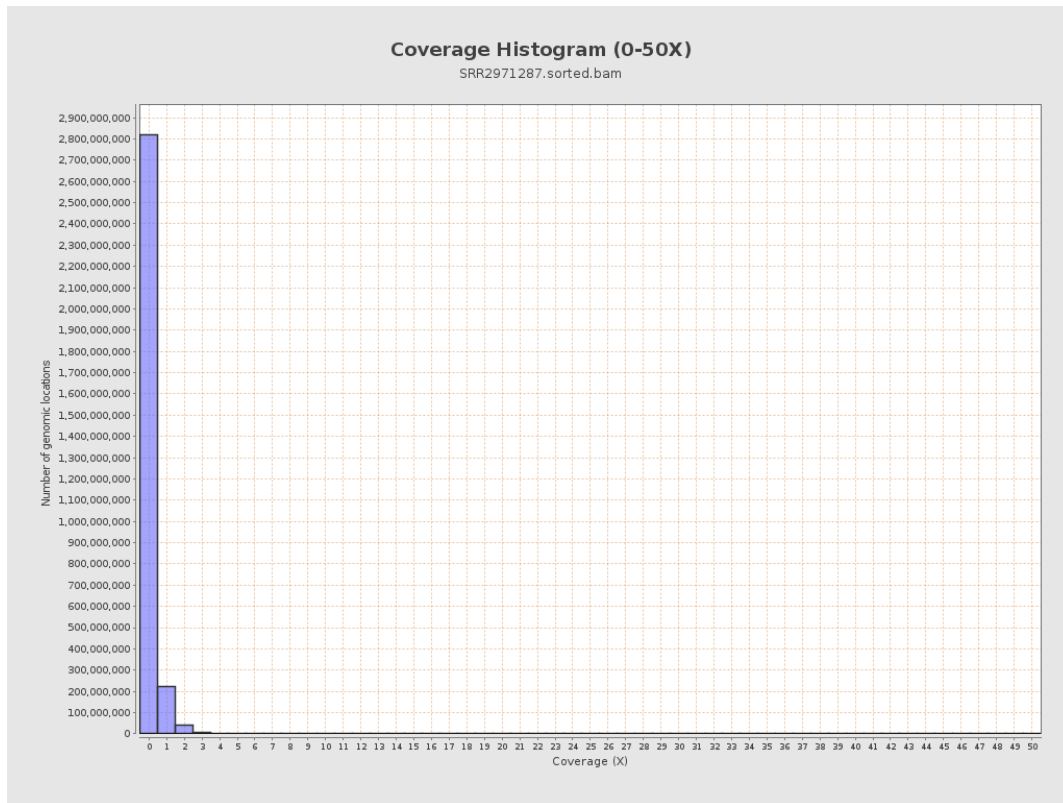
3. Results : Coverage across reference



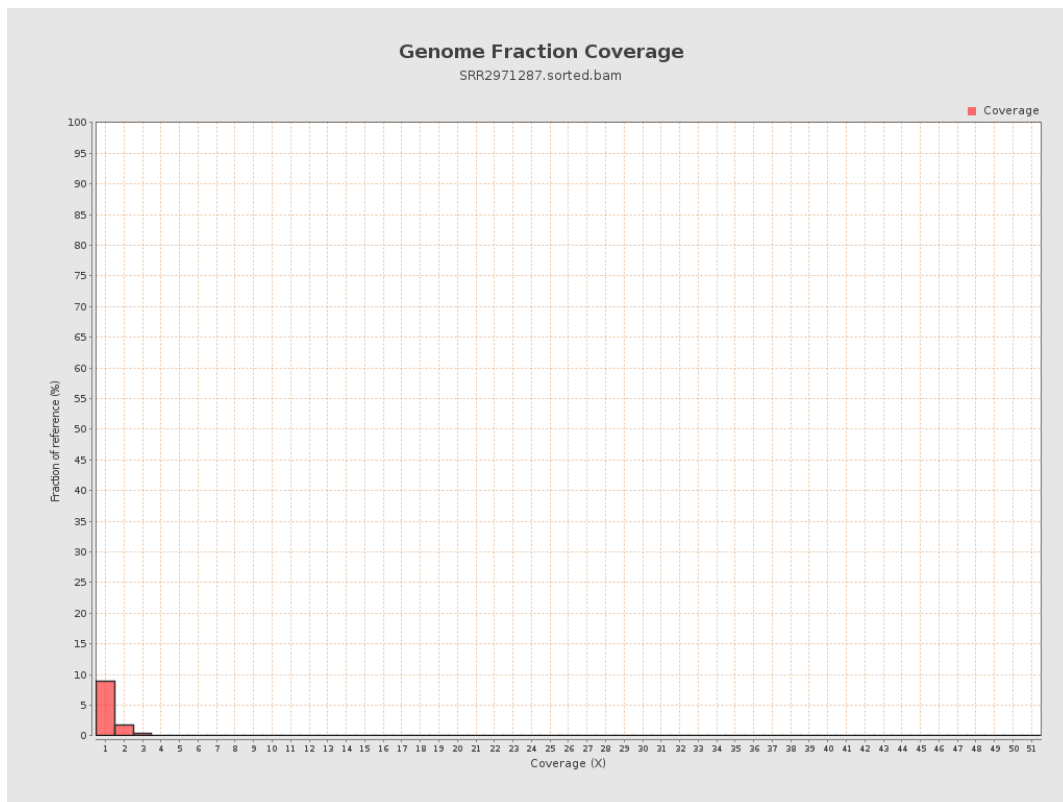
4. Results : Coverage Histogram



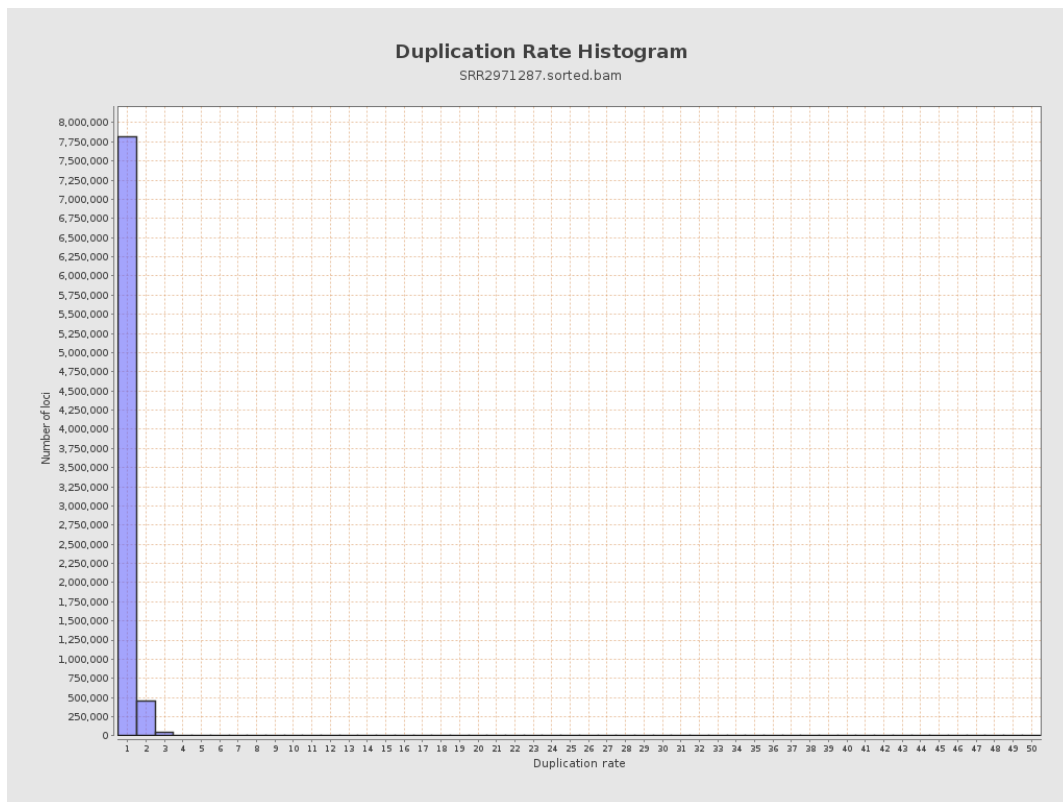
5. Results : Coverage Histogram (0-50X)



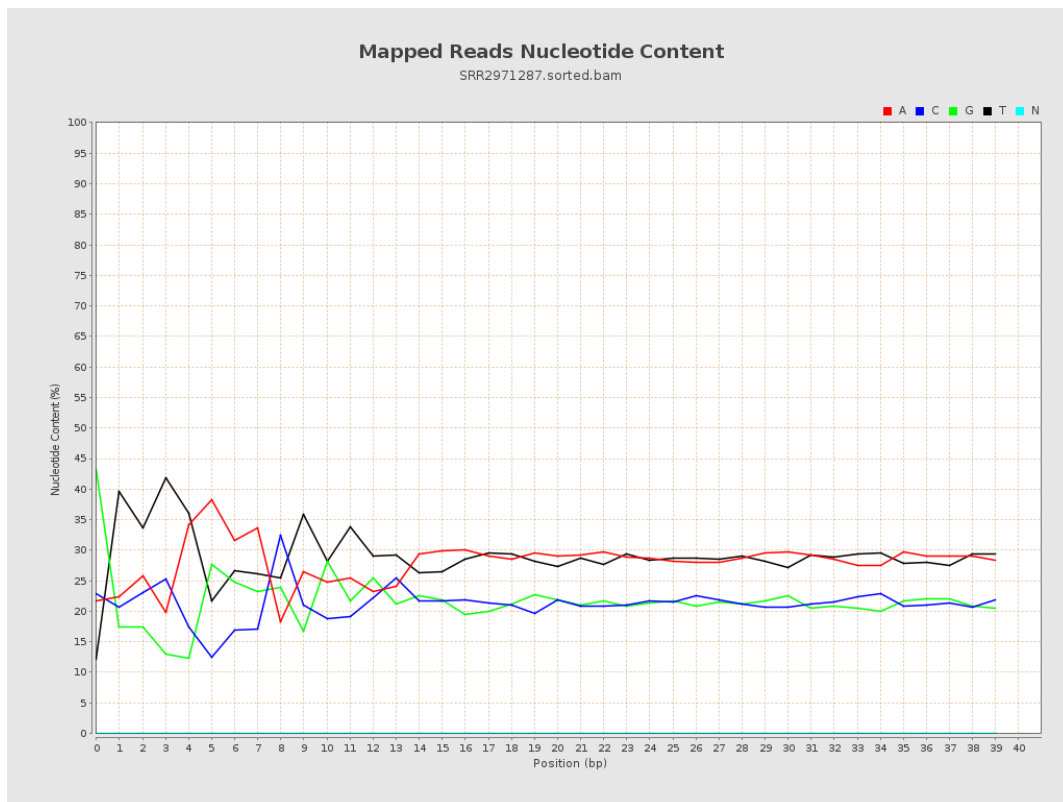
6. Results : Genome Fraction Coverage



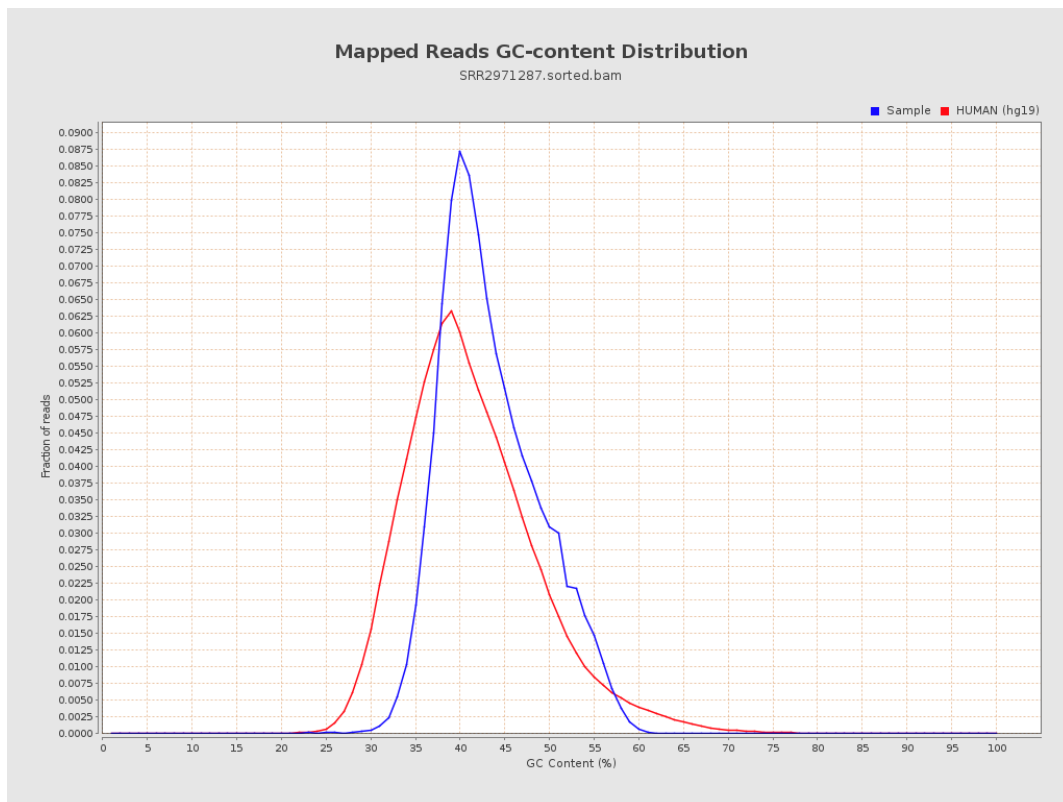
7. Results : Duplication Rate Histogram



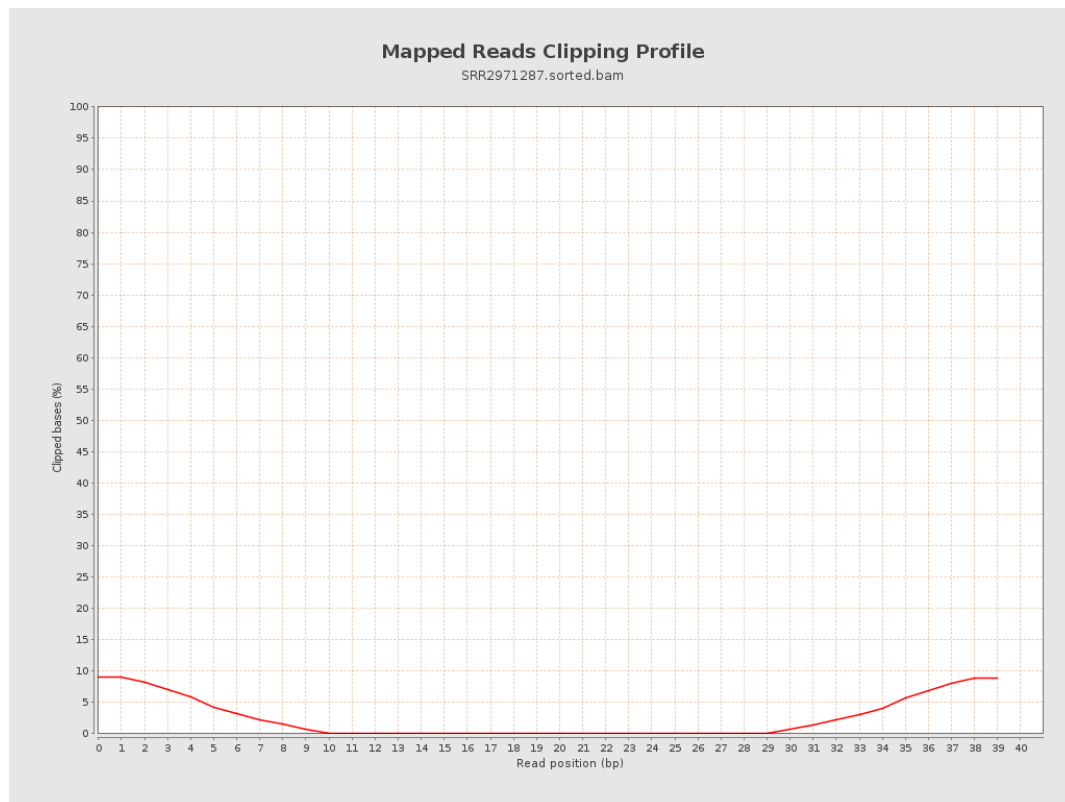
8. Results : Mapped Reads Nucleotide Content



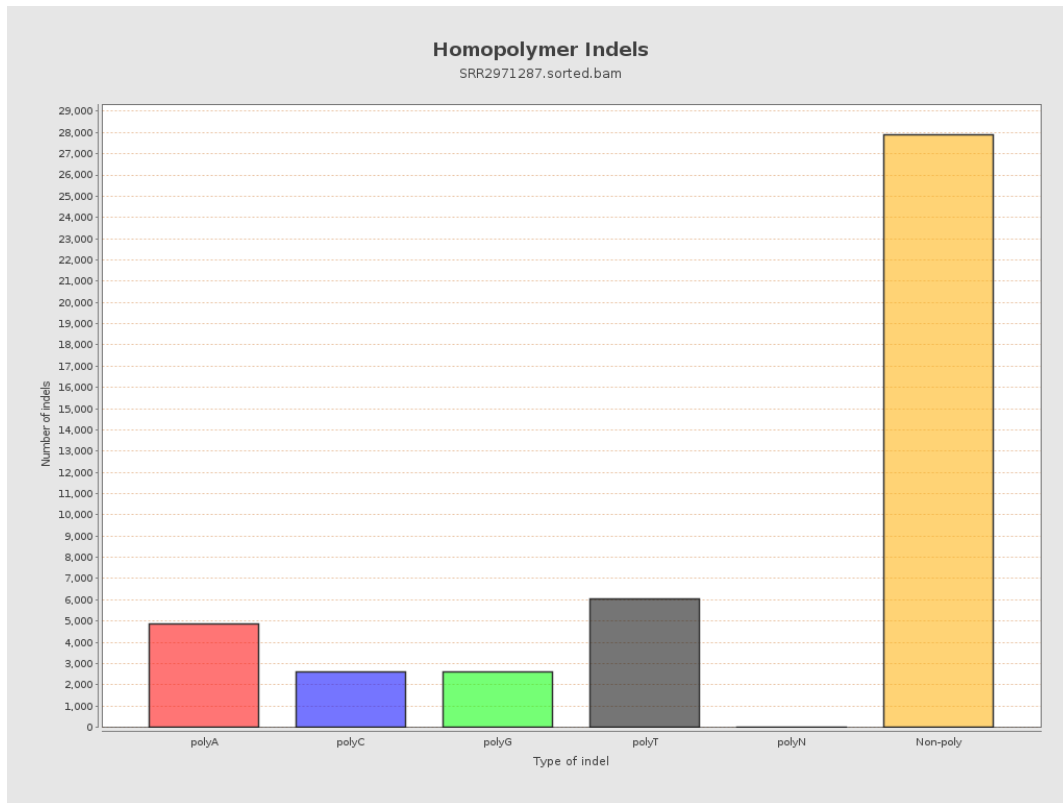
9. Results : Mapped Reads GC-content Distribution



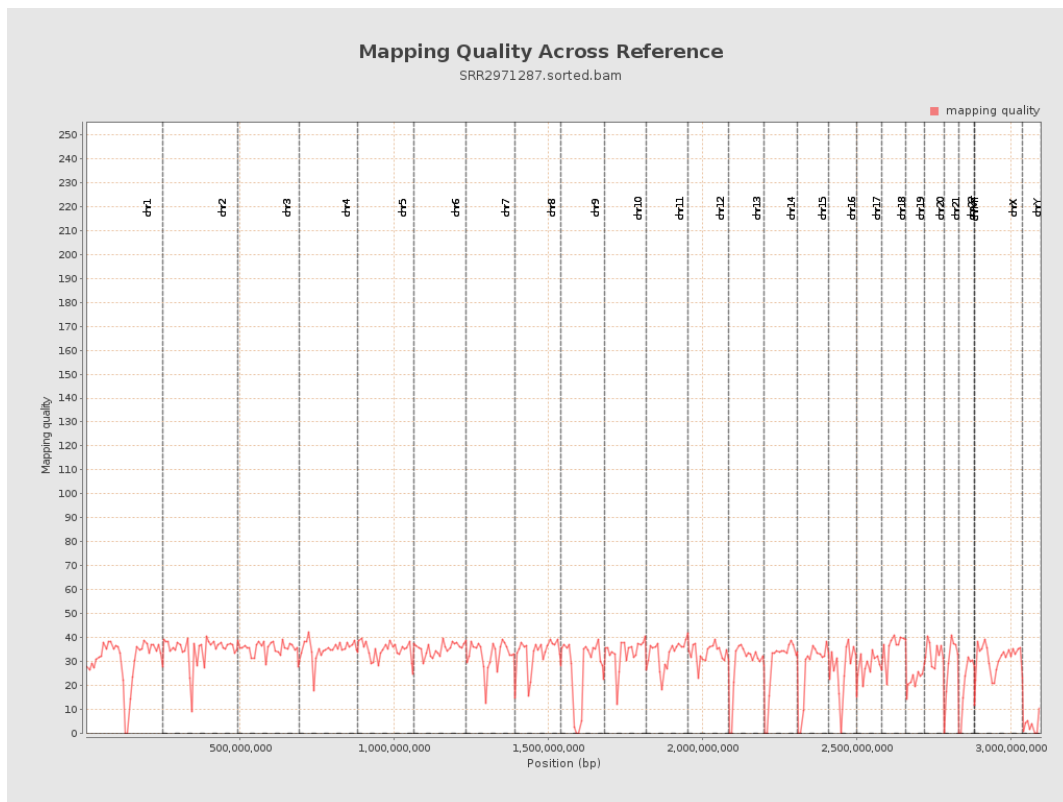
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

