

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:32:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971290.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_SRR2971290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971290.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:32:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,297,328
Mapped reads	8,696,685 / 84.46%
Unmapped reads	1,600,643 / 15.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	532,923 / 5.18%
Duplication rate	4.68%
Clipped reads	824,314 / 8.01%

2.2. ACGT Content

Number/percentage of A's	101,035,967 / 29.45%
Number/percentage of C's	68,897,619 / 20.08%
Number/percentage of T's	102,773,375 / 29.96%
Number/percentage of G's	70,307,912 / 20.5%
Number/percentage of N's	16,530 / 0%
GC Percentage	40.58%

2.3. Coverage

Mean	0.1108
Standard Deviation	0.9923

2.4. Mapping Quality

Mean Mapping Quality	41.14
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2.5. Mismatches and indels

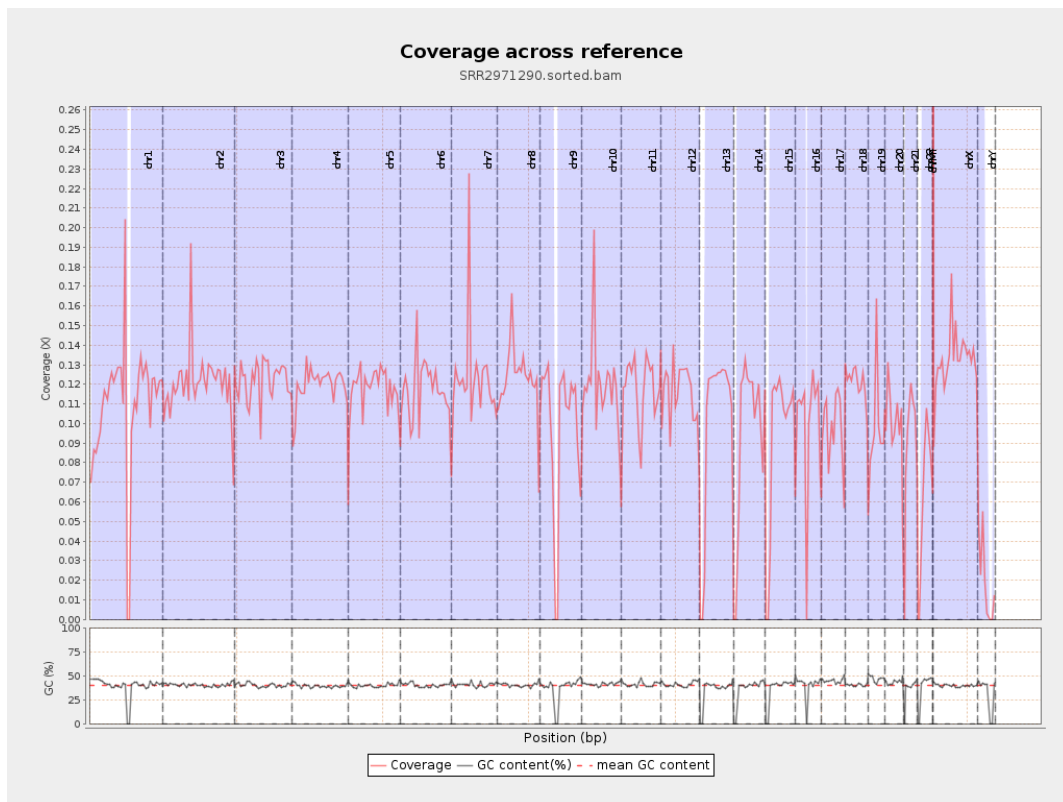
General error rate	0.3%
Mismatches	1,005,787
Insertions	12,053
Mapped reads with at least one insertion	0.14%
Deletions	27,784
Mapped reads with at least one deletion	0.32%
Homopolymer indels	40.57%

2.6. Chromosome stats

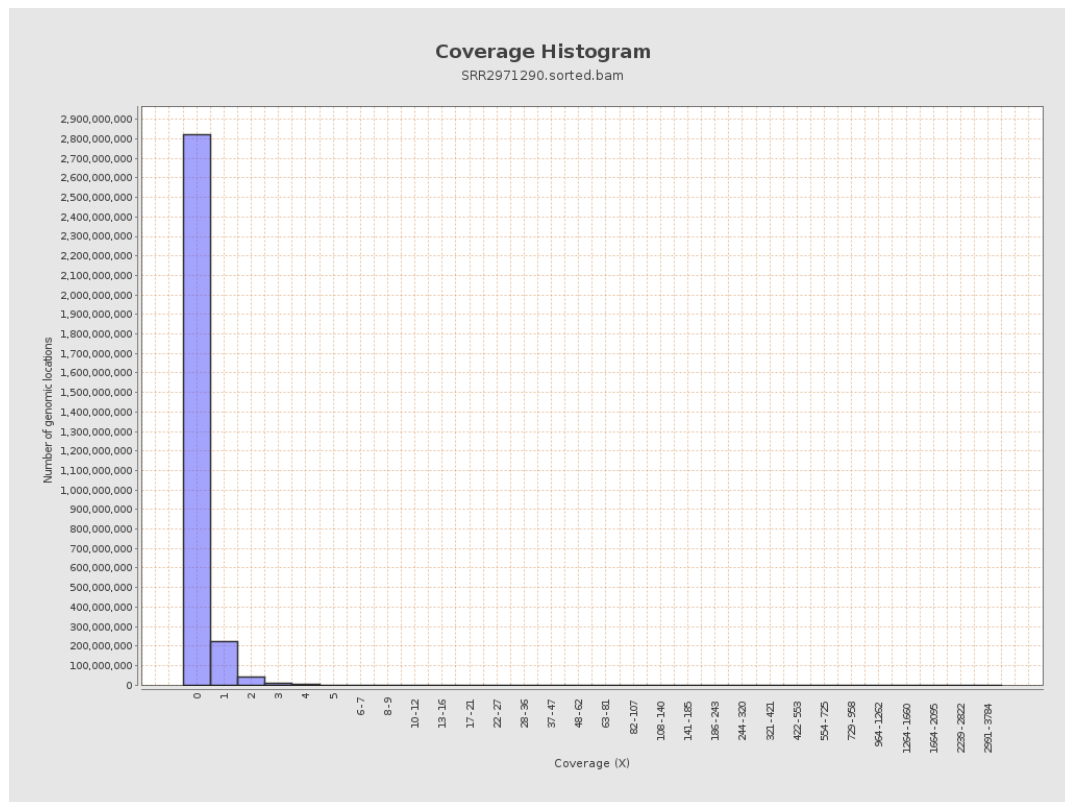
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27158546	0.109	2.0642
chr2	243199373	29352338	0.1207	0.7592
chr3	198022430	24199335	0.1222	0.4224
chr4	191154276	22887554	0.1197	0.4415
chr5	180915260	21292077	0.1177	0.4284
chr6	171115067	20151664	0.1178	0.6119
chr7	159138663	19482411	0.1224	1.4077
chr8	146364022	18017710	0.1231	1.9094

chr9	141213431	13931493	0.0987	0.7527
chr10	135534747	16219869	0.1197	0.8403
chr11	135006516	15815703	0.1171	0.6507
chr12	133851895	15481212	0.1157	0.4439
chr13	115169878	11596559	0.1007	0.3721
chr14	107349540	10209862	0.0951	0.5503
chr15	102531392	9382507	0.0915	0.3604
chr16	90354753	8808847	0.0975	0.4766
chr17	81195210	8012071	0.0987	0.424
chr18	78077248	9482561	0.1215	1.4874
chr19	59128983	5840827	0.0988	1.9051
chr20	63025520	6441293	0.1022	0.416
chr21	48129895	4313062	0.0896	0.4472
chr22	51304566	3302601	0.0644	0.3052
chrMT	16571	19832	1.1968	1.4688
chrX	155270560	20538376	0.1323	0.5894
chrY	59373566	1127746	0.019	0.2461

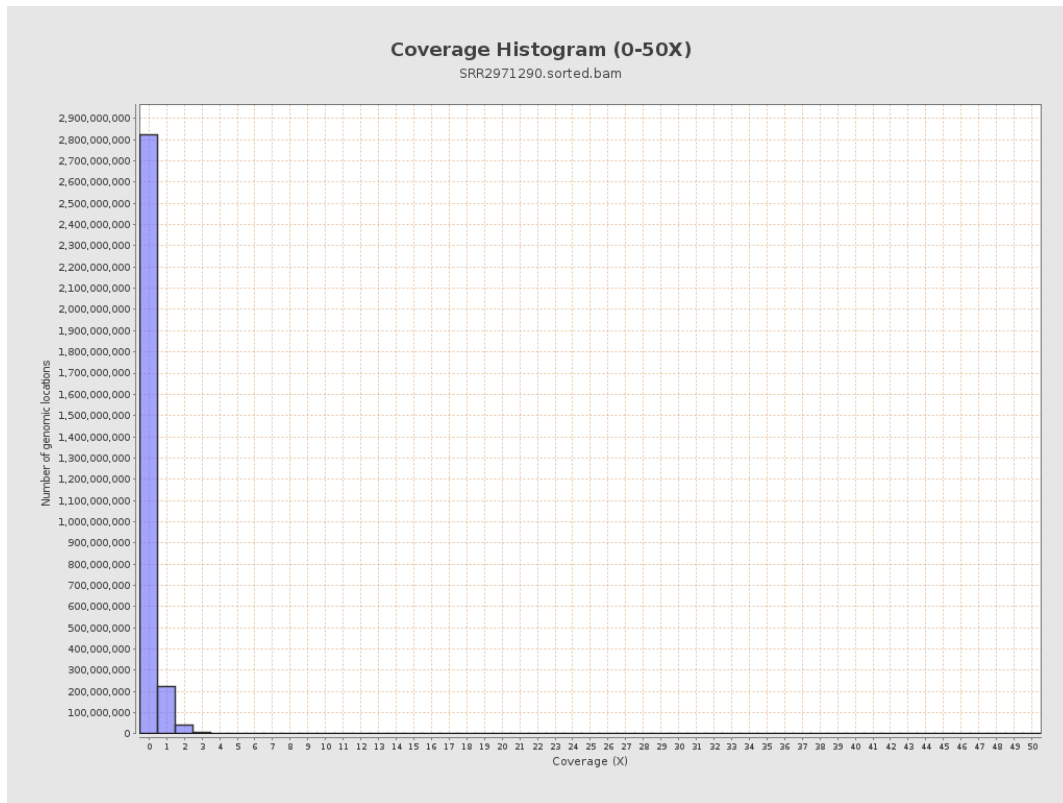
3. Results : Coverage across reference



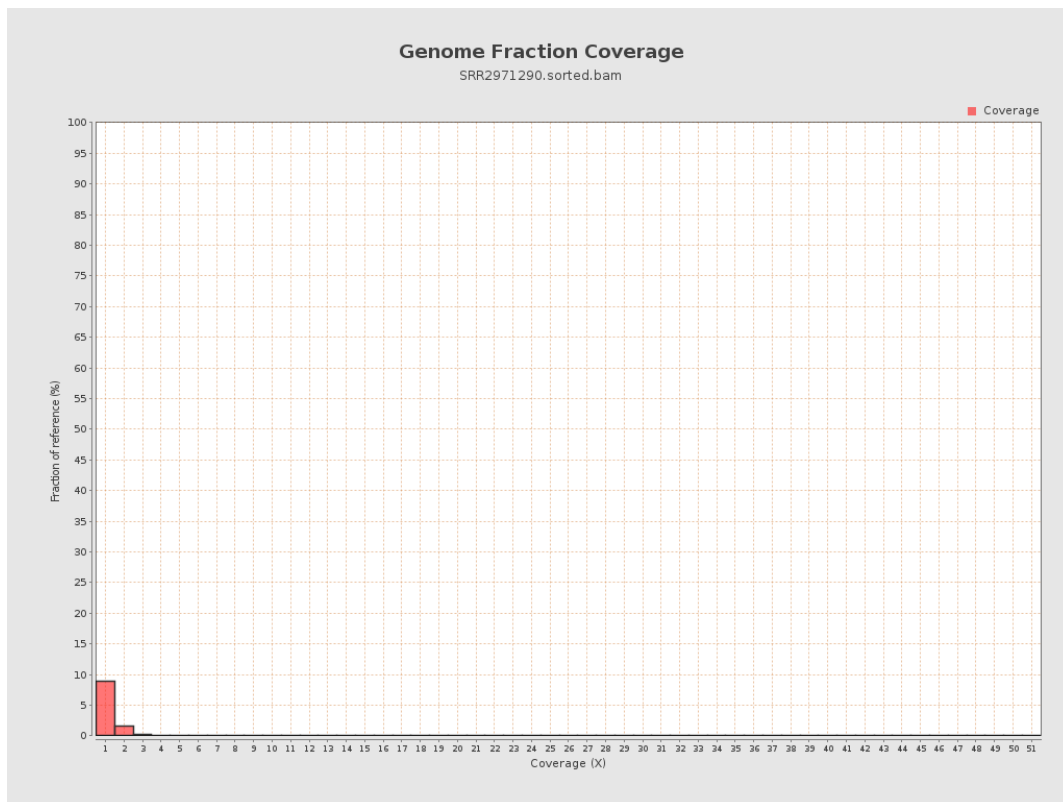
4. Results : Coverage Histogram



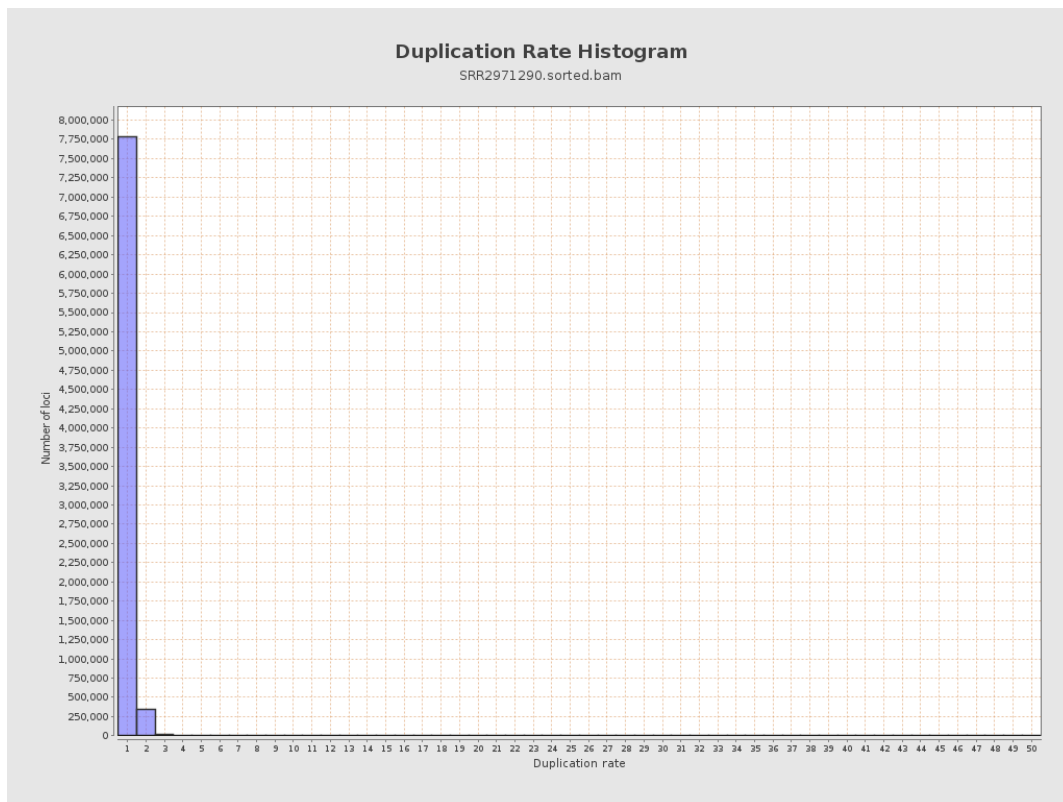
5. Results : Coverage Histogram (0-50X)



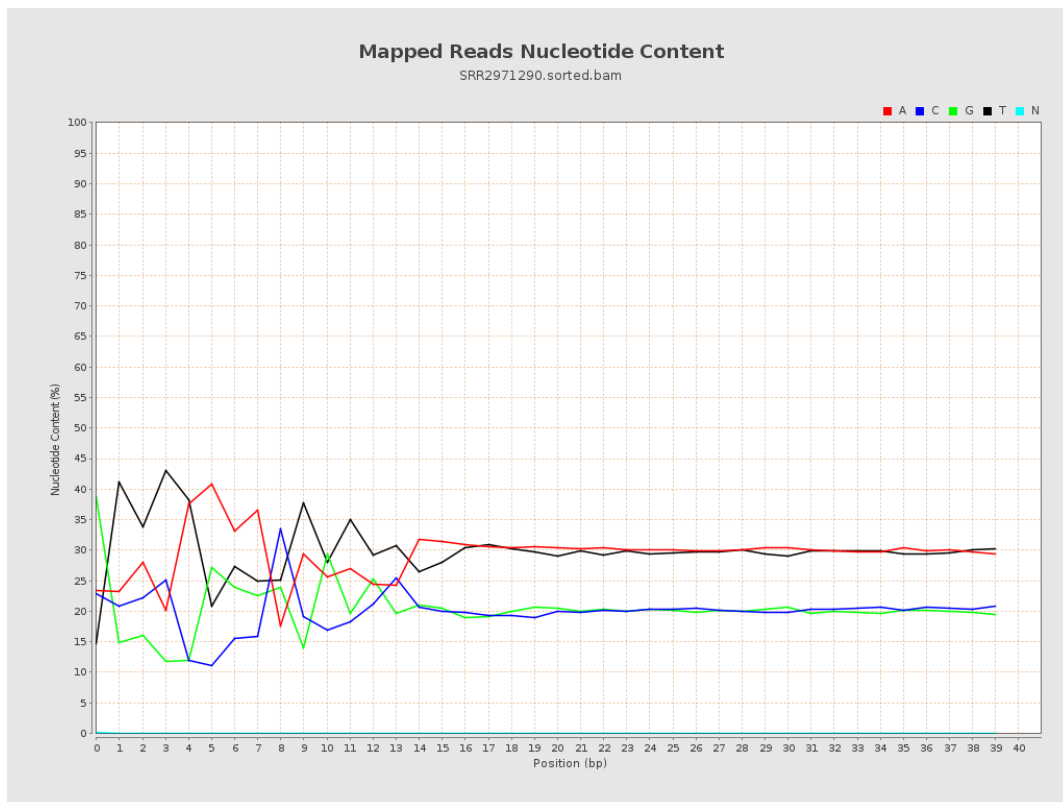
6. Results : Genome Fraction Coverage



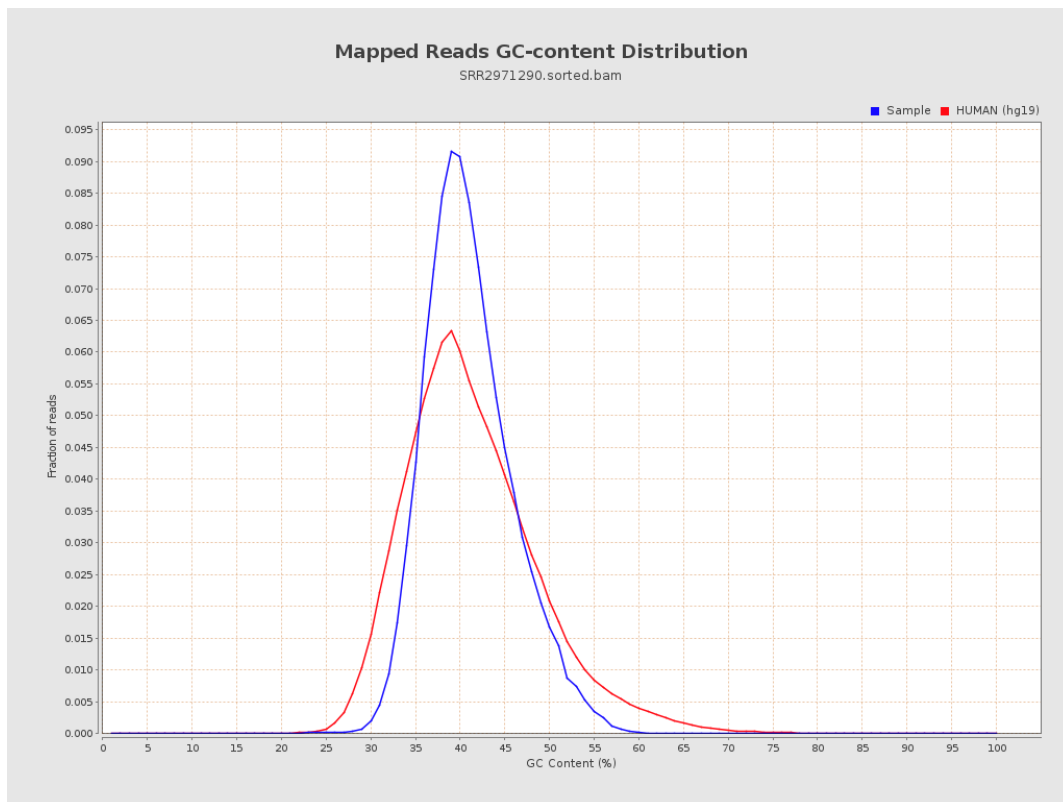
7. Results : Duplication Rate Histogram



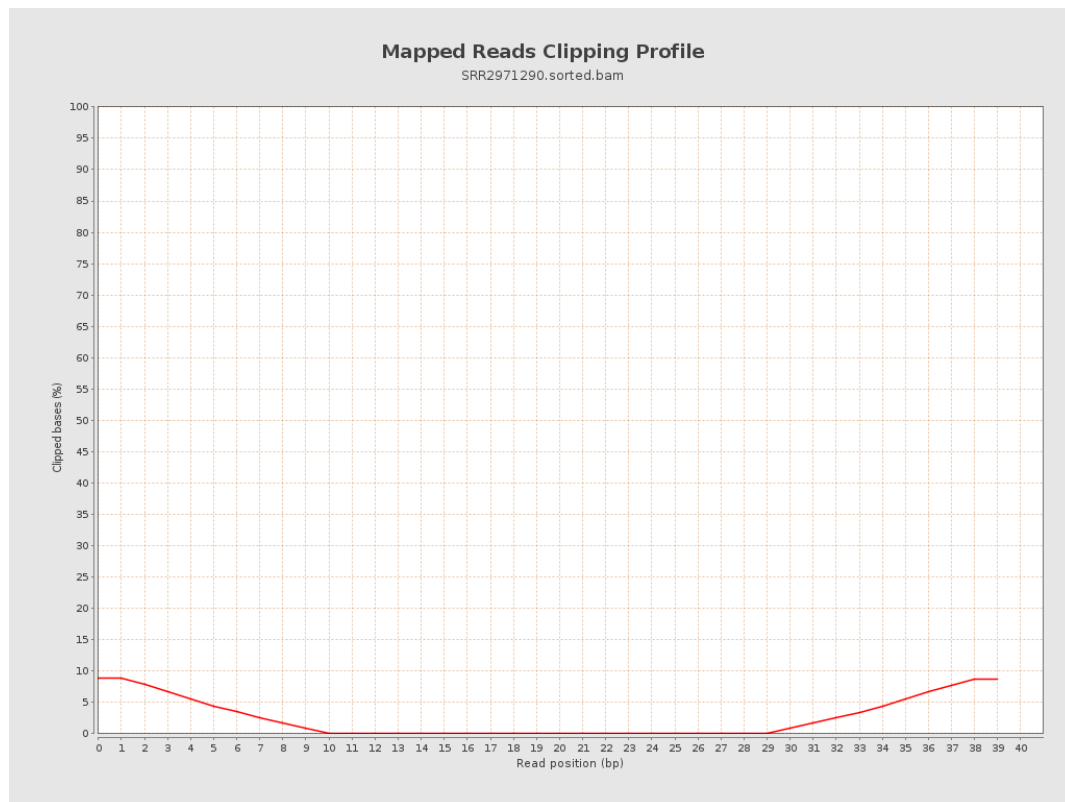
8. Results : Mapped Reads Nucleotide Content



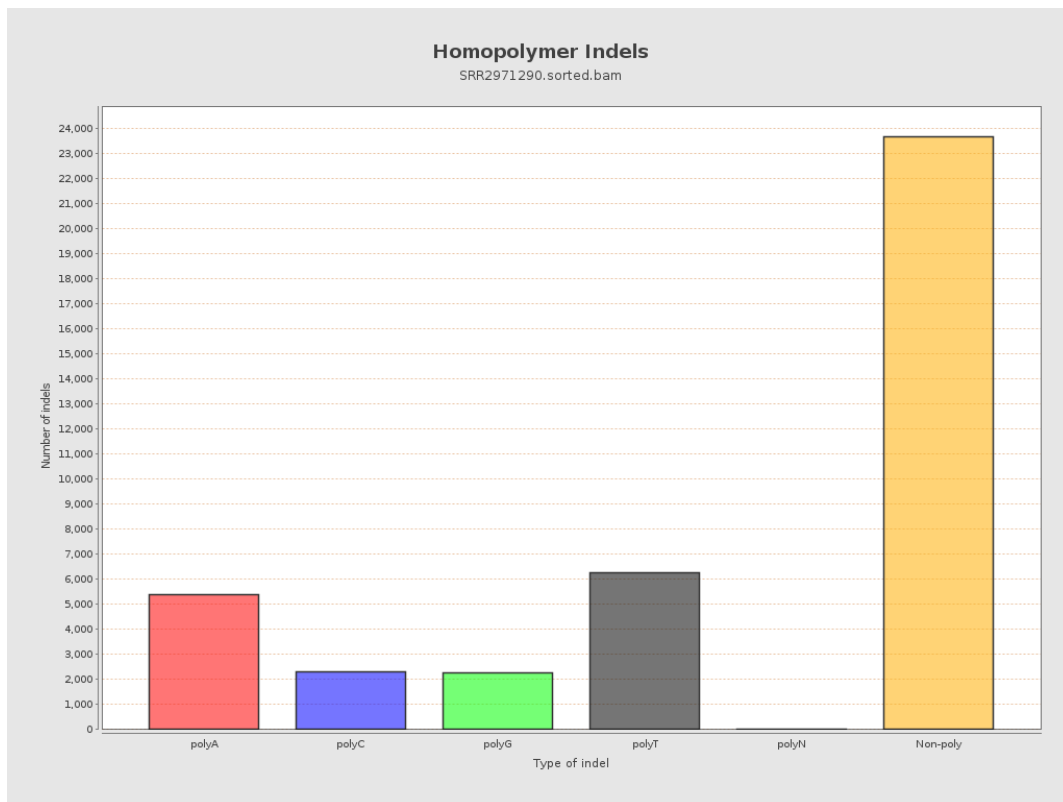
9. Results : Mapped Reads GC-content Distribution



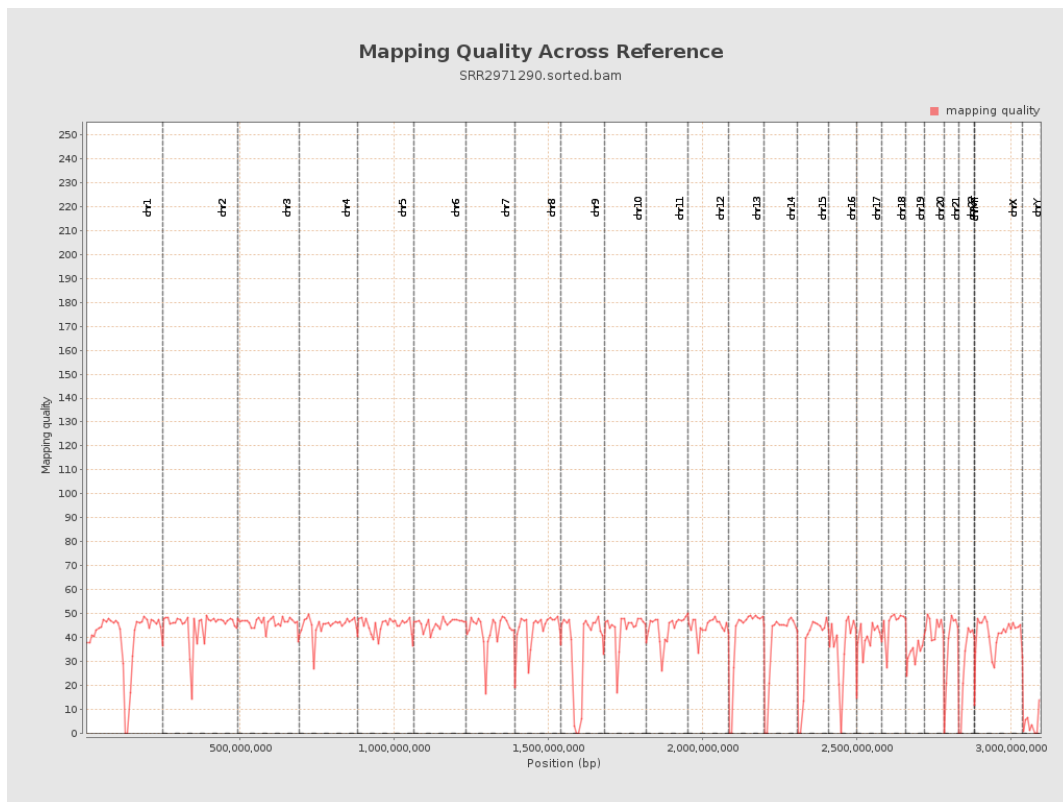
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

