Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:00:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003999.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_SRR6003999 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003999.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:00:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003999.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,449,033
Mapped reads	3,150,053 / 91.33%
Unmapped reads	298,980 / 8.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,101 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	127,512 / 3.7%
Duplication rate	2.81%
Clipped reads	1,511,095 / 43.81%

2.2. ACGT Content

Number/percentage of A's	55,694,254 / 26.84%
Number/percentage of C's	40,117,005 / 19.34%
Number/percentage of T's	62,834,868 / 30.29%
Number/percentage of G's	48,784,951 / 23.51%
Number/percentage of N's	41,406 / 0.02%
GC Percentage	42.85%

2.3. Coverage

Mean	0.067

Standard Deviation	0.579

2.4. Mapping Quality

Mean Mapping Quality	43.22

2.5. Mismatches and indels

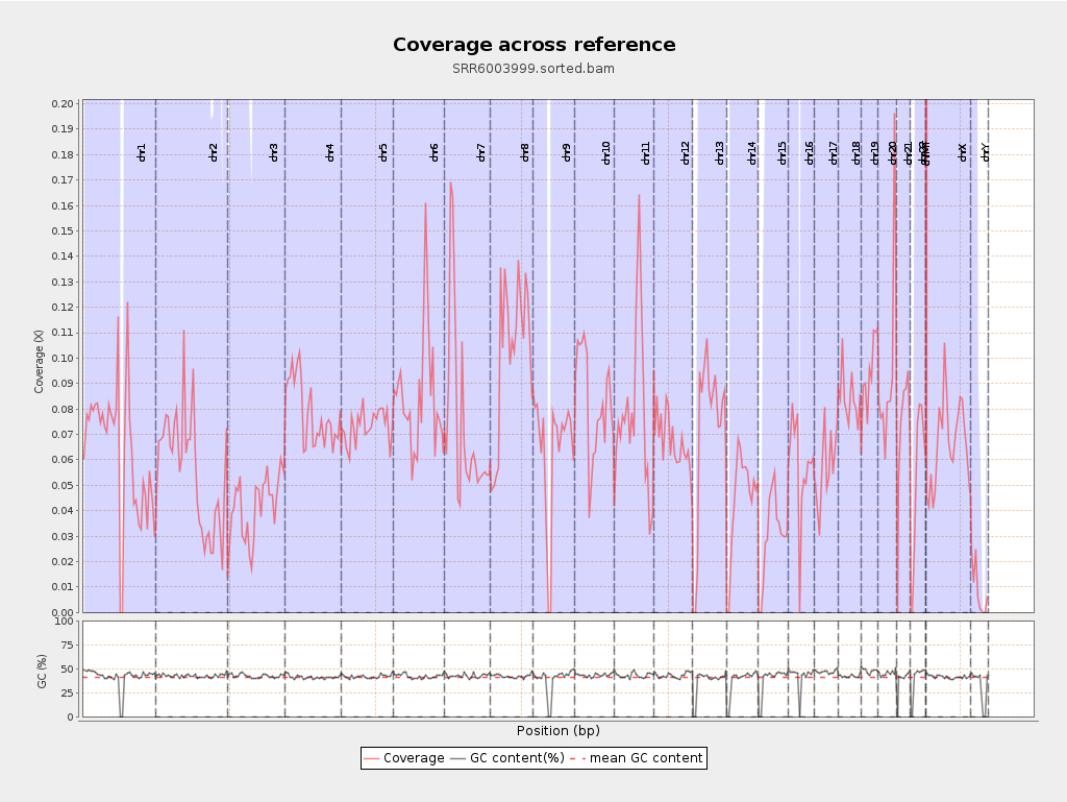
General error rate	0.83%
Mismatches	1,692,418
Insertions	16,704
Mapped reads with at least one insertion	0.52%
Deletions	52,228
Mapped reads with at least one deletion	1.64%
Homopolymer indels	45.69%

2.6. Chromosome stats

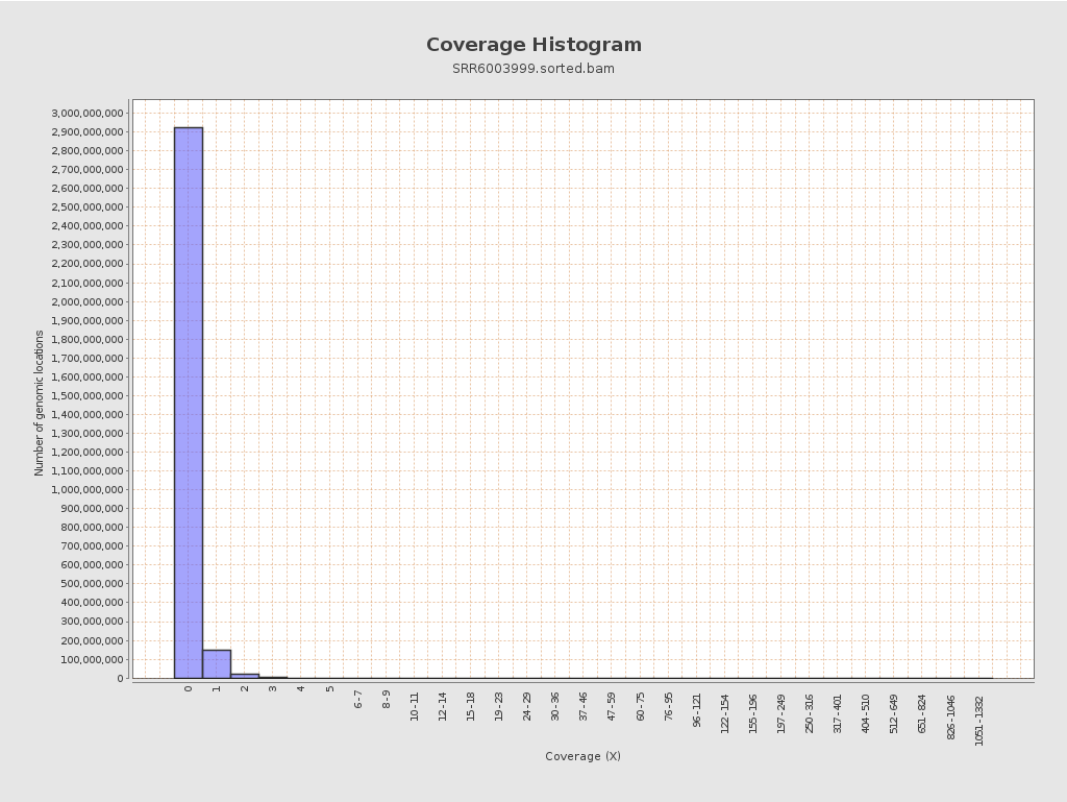
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15577857	0.0625	1.0781
chr2	243199373	13428612	0.0552	0.7778
chr3	198022430	8269205	0.0418	0.238
chr4	191154276	15006910	0.0785	0.3574
chr5	180915260	13283430	0.0734	0.3179
chr6	171115067	14492482	0.0847	0.3943
chr7	159138663	11604299	0.0729	0.771

chr8	146364022	14937841	0.1021	0.5534
chr9	141213431	9006403	0.0638	0.5694
chr10	135534747	11131757	0.0821	0.4931
chr11	135006516	10536776	0.078	0.5212
chr12	133851895	9007997	0.0673	0.3119
chr13	115169878	8387641	0.0728	0.314
chr14	107349540	4843725	0.0451	0.3342
chr15	102531392	3042122	0.0297	0.2214
chr16	90354753	5138098	0.0569	0.3715
chr17	81195210	4538703	0.0559	0.3077
chr18	78077248	6580121	0.0843	1.2538
chr19	59128983	5544364	0.0938	0.7826
chr20	63025520	6146980	0.0975	0.3948
chr21	48129895	3399325	0.0706	0.3597
chr22	51304566	2699777	0.0526	0.2659
chrMT	16571	99180	5.9852	4.7782
chrX	155270560	10340277	0.0666	0.3706
chrY	59373566	515163	0.0087	0.1877

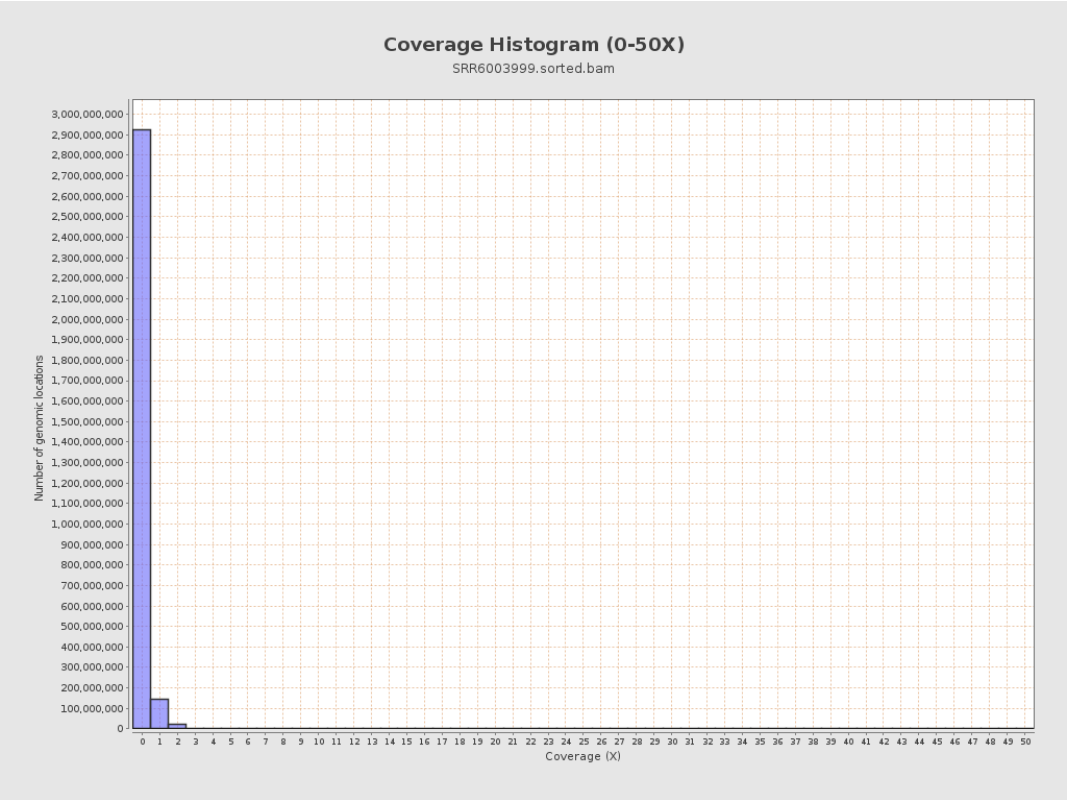
3. Results : Coverage across reference



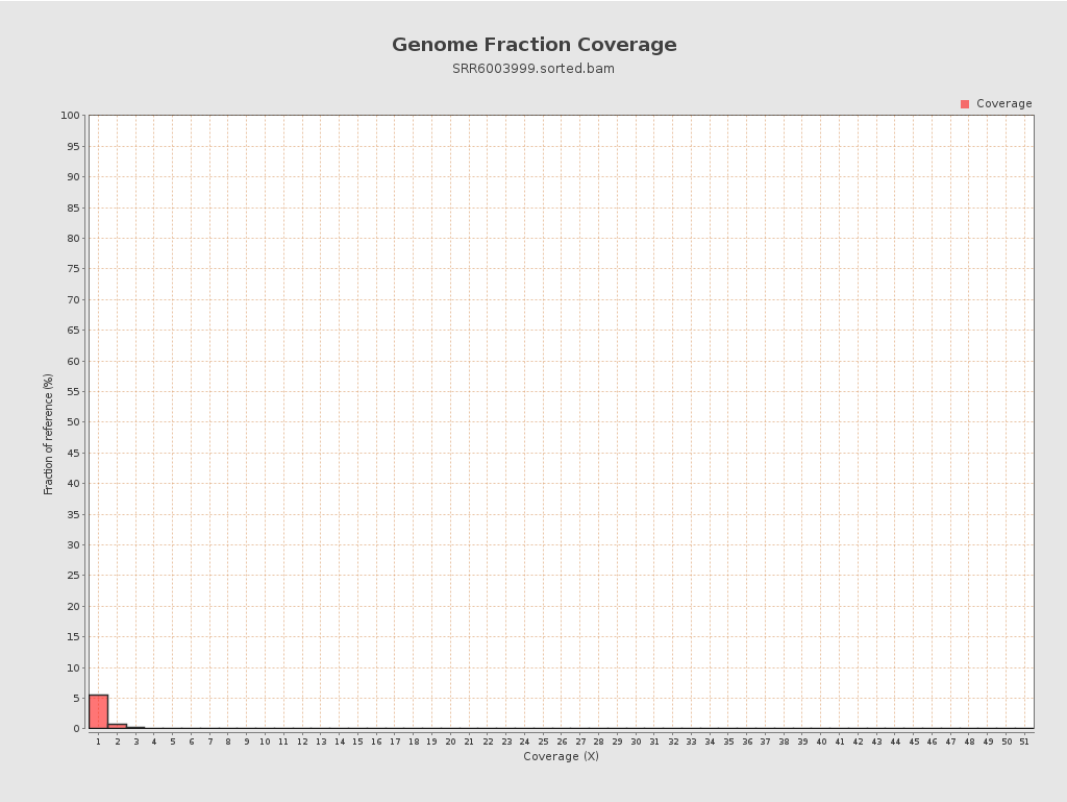
4. Results : Coverage Histogram



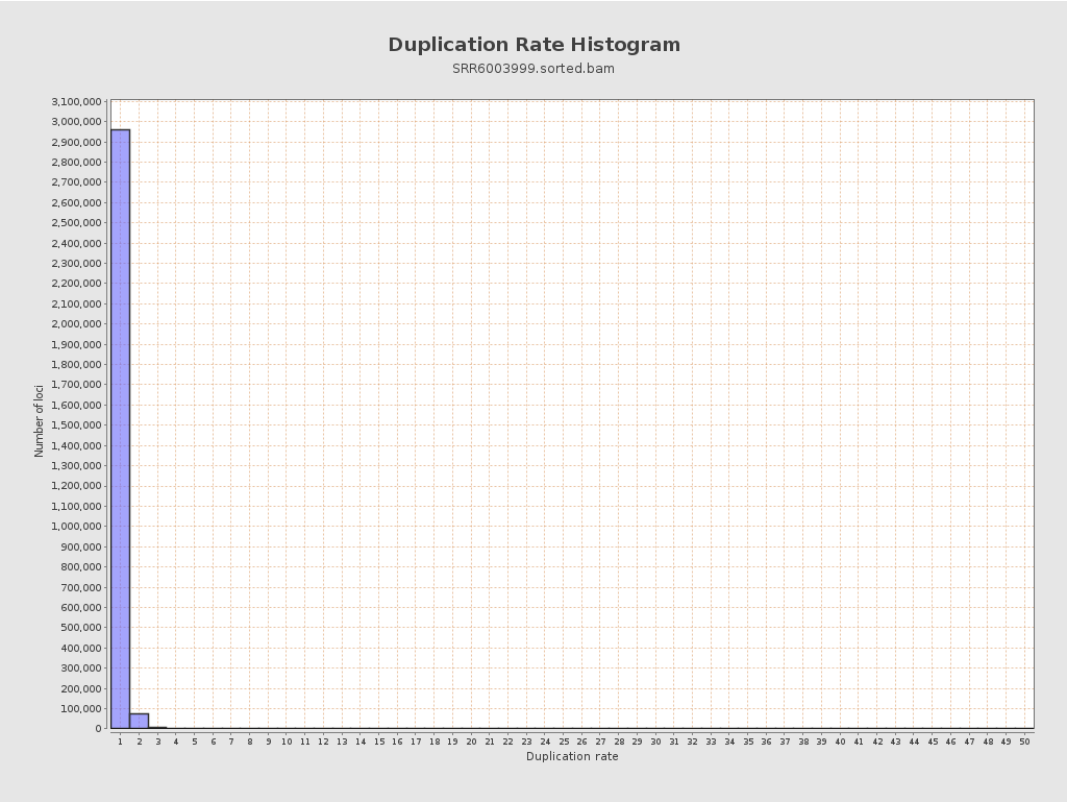
5. Results : Coverage Histogram (0-50X)



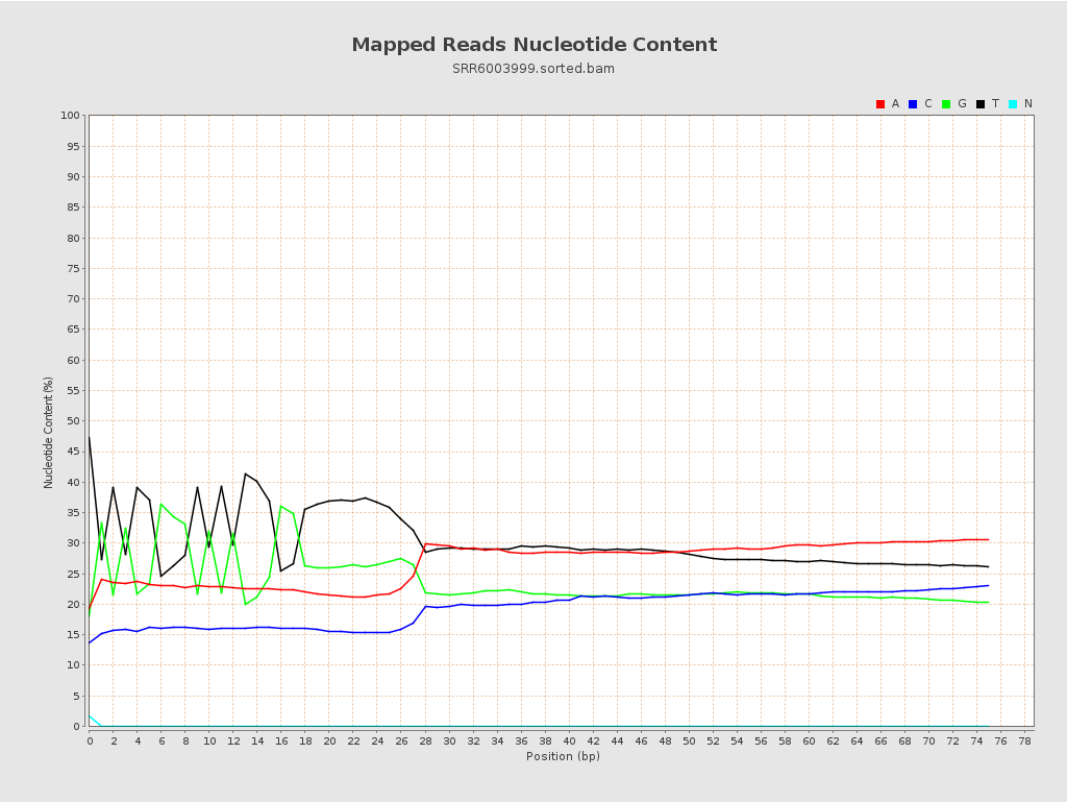
6. Results : Genome Fraction Coverage



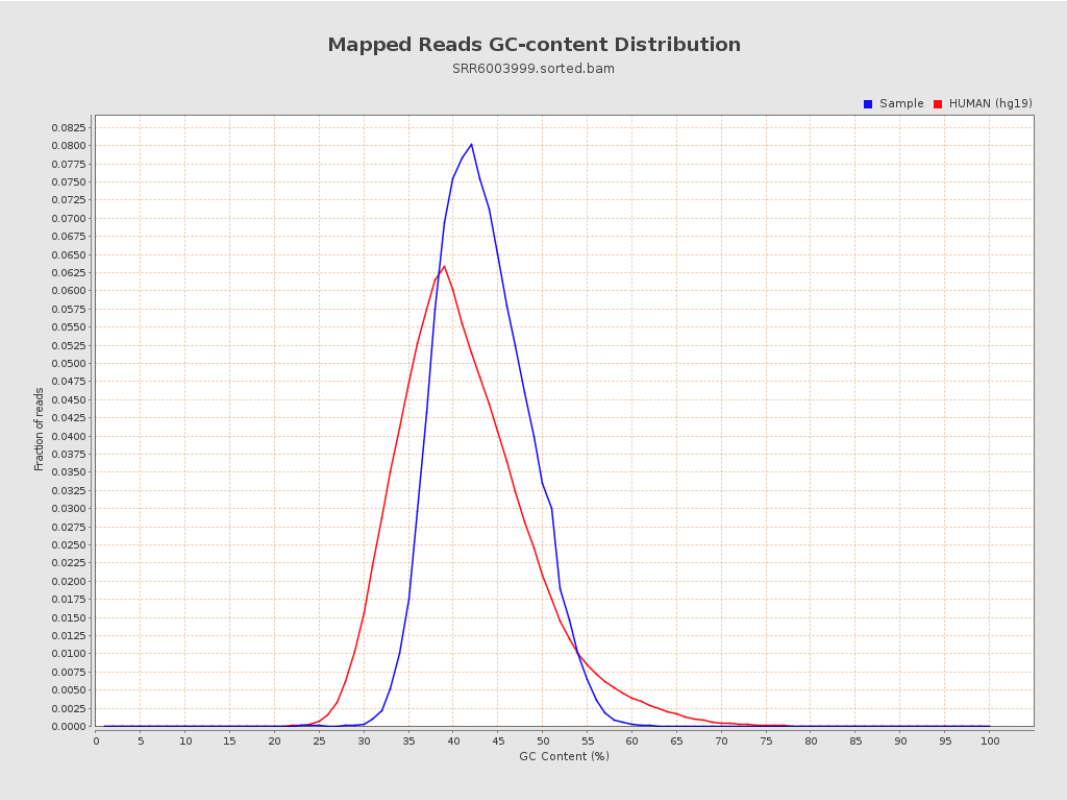
7. Results : Duplication Rate Histogram



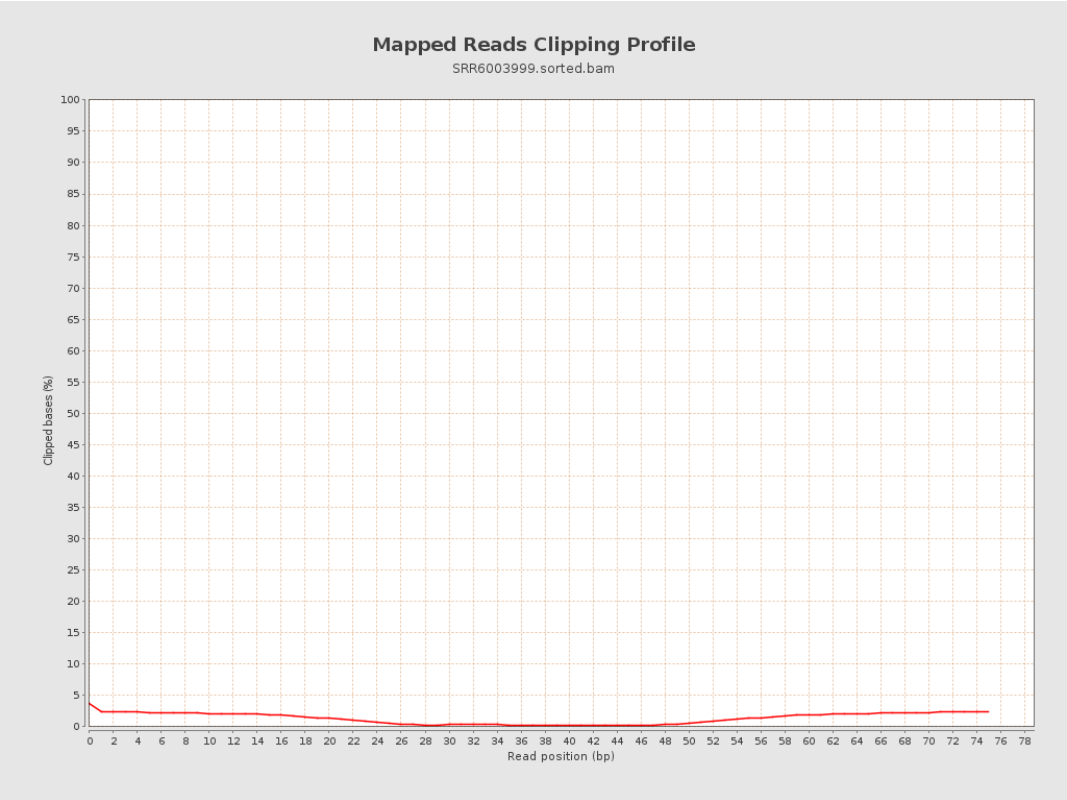
8. Results : Mapped Reads Nucleotide Content



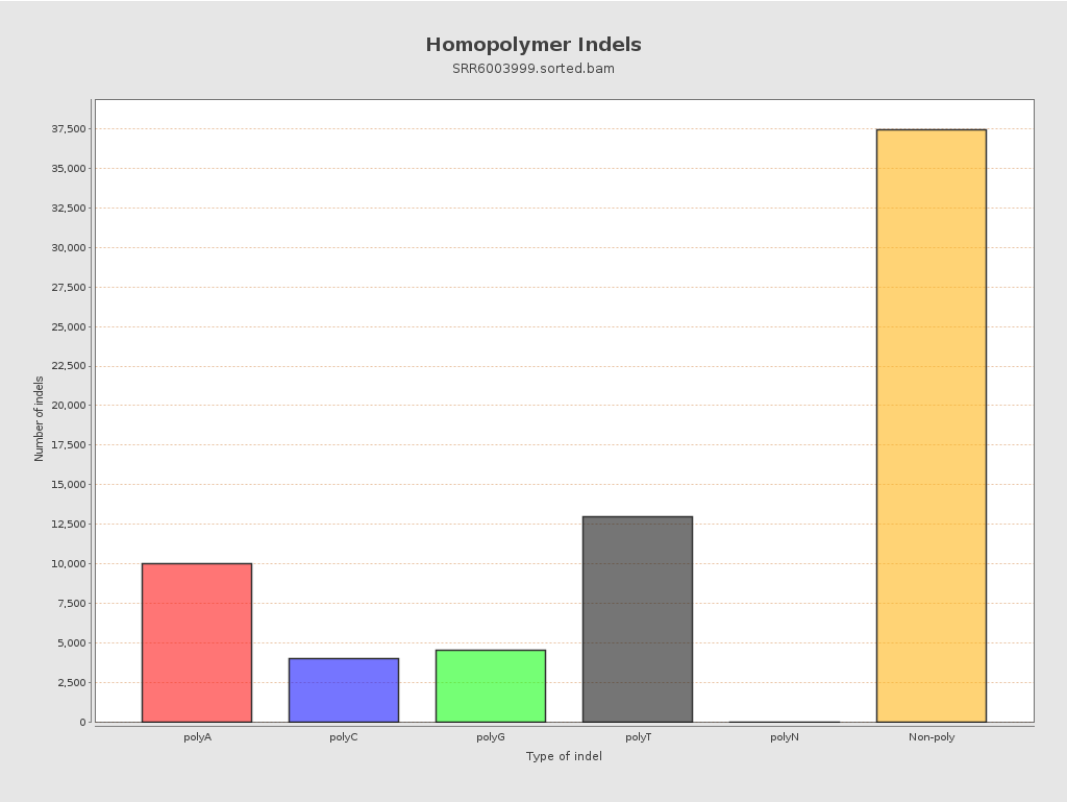
9. Results : Mapped Reads GC-content Distribution



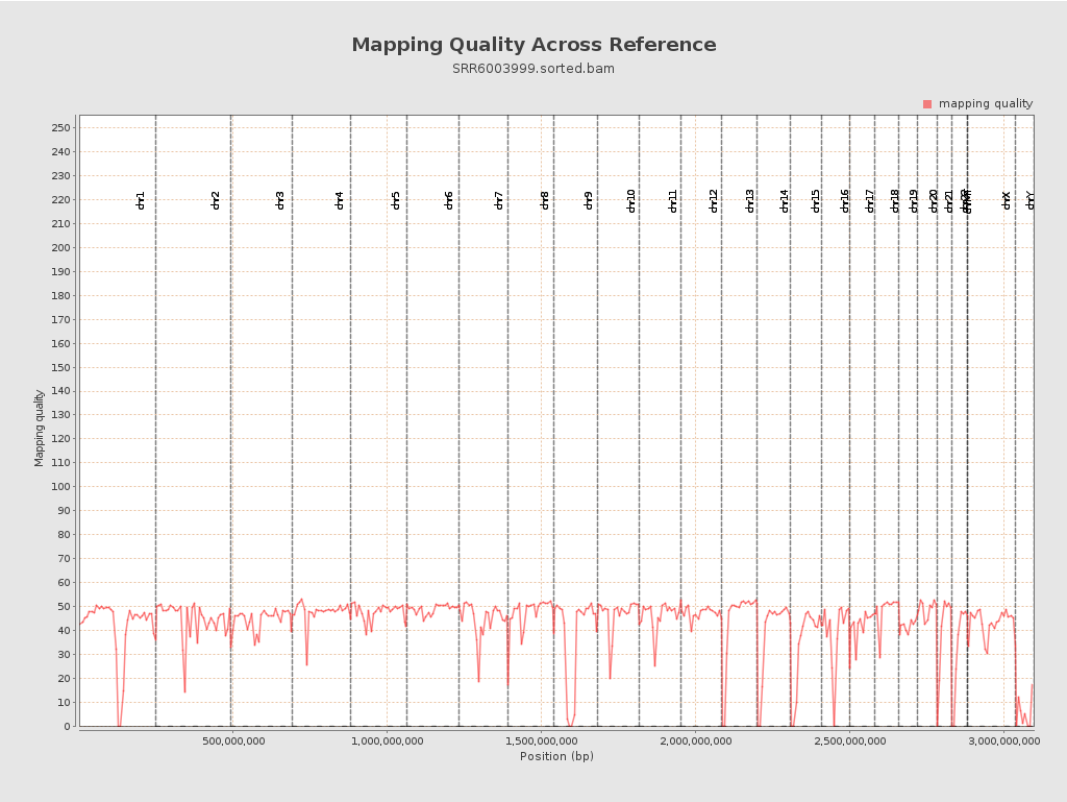
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram