Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:34:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003993.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_SRR6003993 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003993.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:34:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003993.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,467,749
Mapped reads	3,813,322 / 85.35%
Unmapped reads	654,427 / 14.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,291 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	268,727 / 6.01%
Duplication rate	5.61%
Clipped reads	1,683,006 / 37.67%

2.2. ACGT Content

Number/percentage of A's	71,757,140 / 28.17%
Number/percentage of C's	45,000,868 / 17.67%
Number/percentage of T's	83,990,235 / 32.97%
Number/percentage of G's	53,944,243 / 21.18%
Number/percentage of N's	28,218 / 0.01%
GC Percentage	38.84%

2.3. Coverage

Mean	0.0823

Standard Deviation	0.6973

2.4. Mapping Quality

Mean Mapping Quality	46.19

2.5. Mismatches and indels

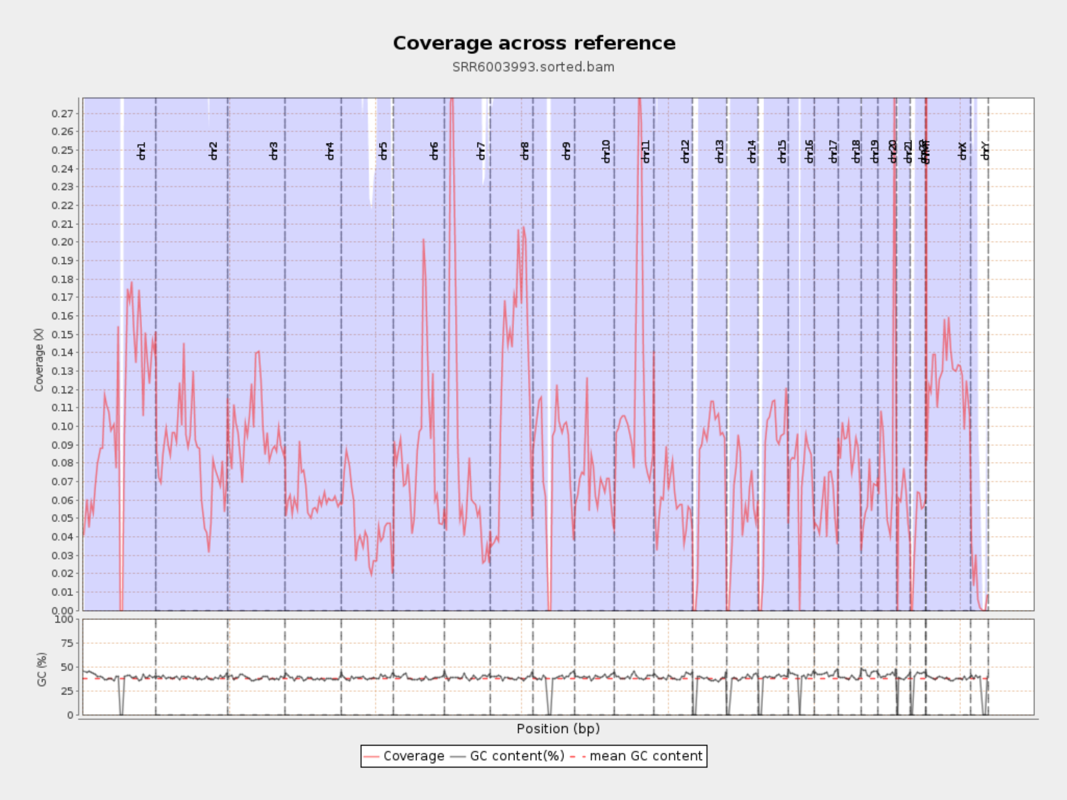
General error rate	0.96%
Mismatches	2,416,926
Insertions	22,385
Mapped reads with at least one insertion	0.58%
Deletions	75,123
Mapped reads with at least one deletion	1.95%
Homopolymer indels	47.26%

2.6. Chromosome stats

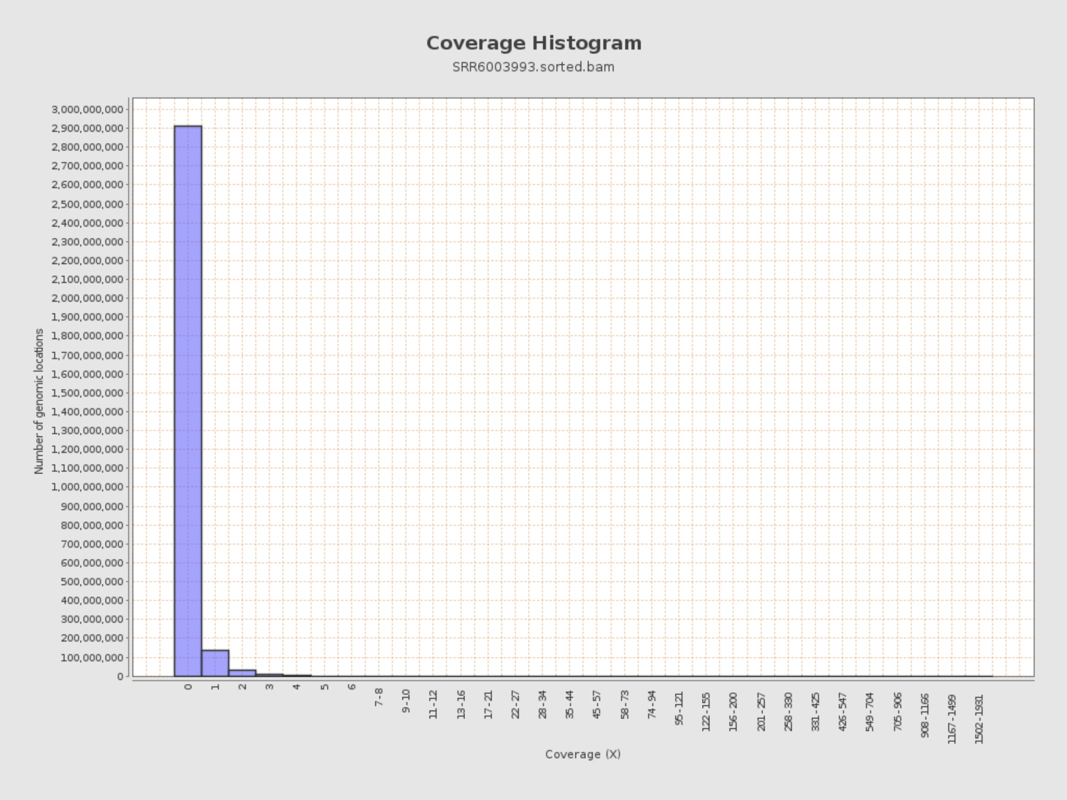
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26398482	0.1059	1.4055
chr2	243199373	20146760	0.0828	0.7694
chr3	198022430	19542397	0.0987	0.4138
chr4	191154276	11617588	0.0608	0.353
chr5	180915260	8068996	0.0446	0.2798
chr6	171115067	14999076	0.0877	0.4188
chr7	159138663	13035550	0.0819	0.4997

chr8	146364022	18825092	0.1286	1.2749
chr9	141213431	11591257	0.0821	0.632
chr10	135534747	9530521	0.0703	0.5993
chr11	135006516	15992978	0.1185	0.6454
chr12	133851895	7788184	0.0582	0.3306
chr13	115169878	9473146	0.0823	0.3728
chr14	107349540	5905318	0.055	0.3566
chr15	102531392	8372949	0.0817	0.3742
chr16	90354753	6563517	0.0726	0.4206
chr17	81195210	4551783	0.0561	0.3493
chr18	78077248	6947218	0.089	1.2385
chr19	59128983	3557980	0.0602	0.8919
chr20	63025520	6496808	0.1031	0.4469
chr21	48129895	2585490	0.0537	0.3607
chr22	51304566	2202164	0.0429	0.2606
chrMT	16571	275811	16.6442	10.4654
chrX	155270560	19723743	0.127	0.5276
chrY	59373566	652513	0.011	0.2082

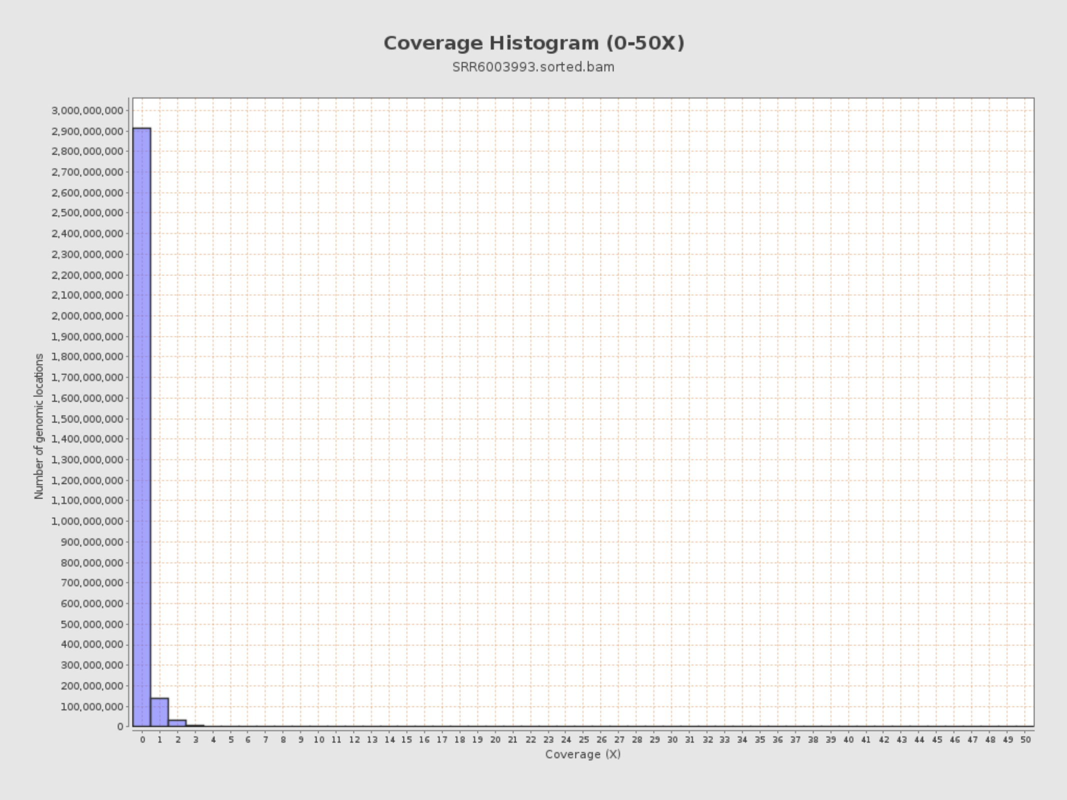
3. Results : Coverage across reference



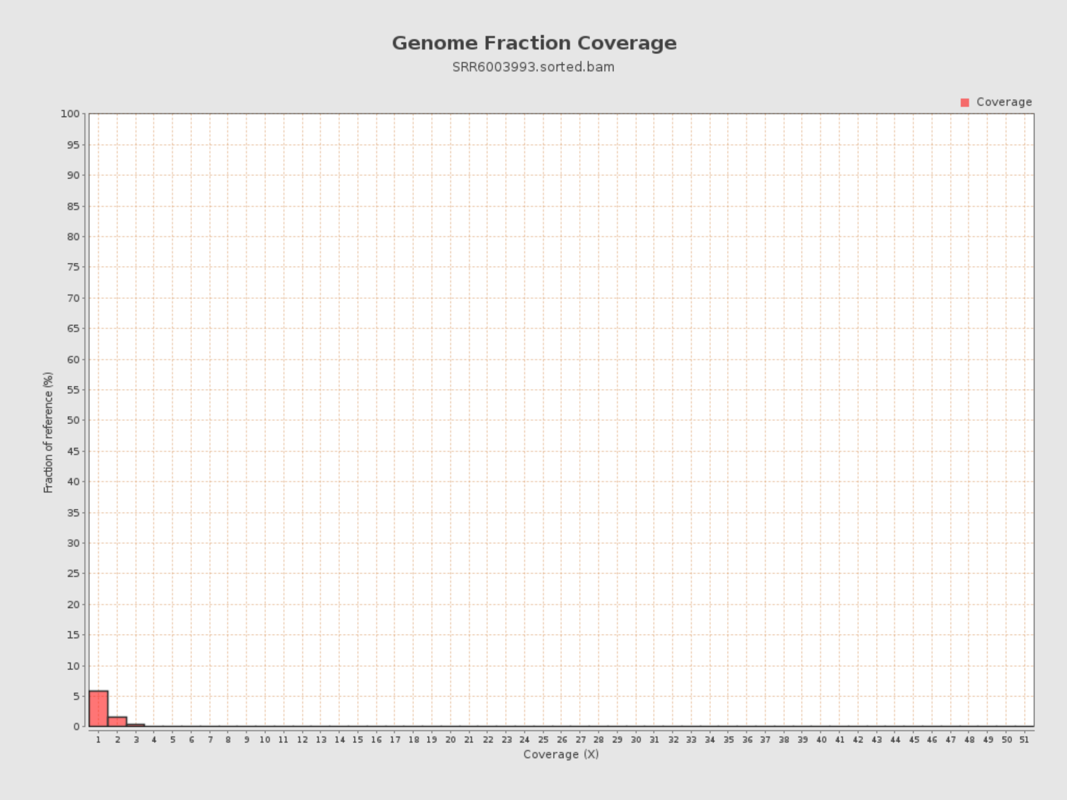
4. Results : Coverage Histogram



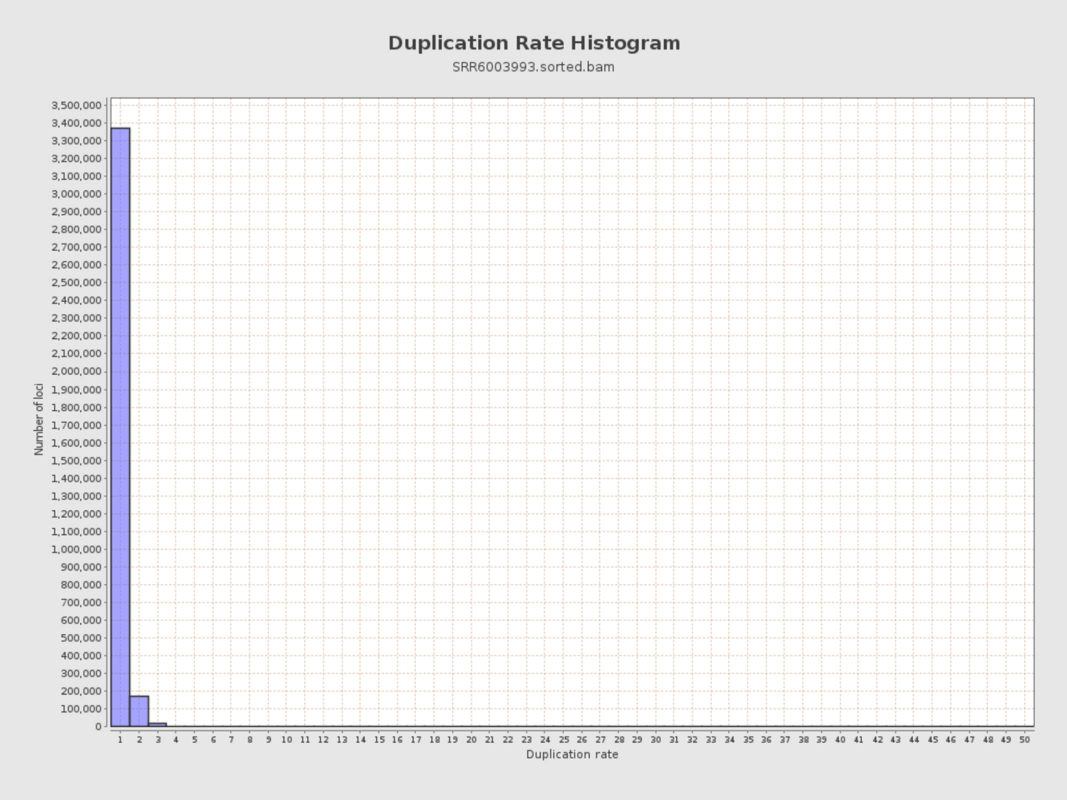
5. Results : Coverage Histogram (0-50X)



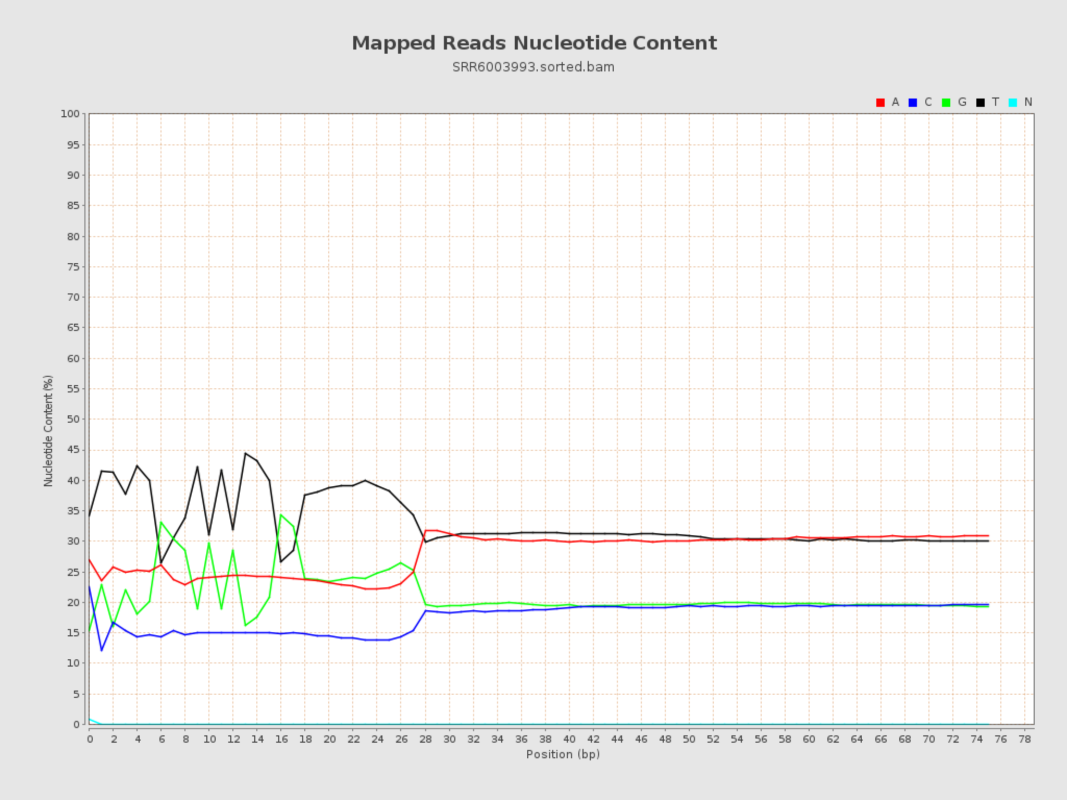
6. Results : Genome Fraction Coverage



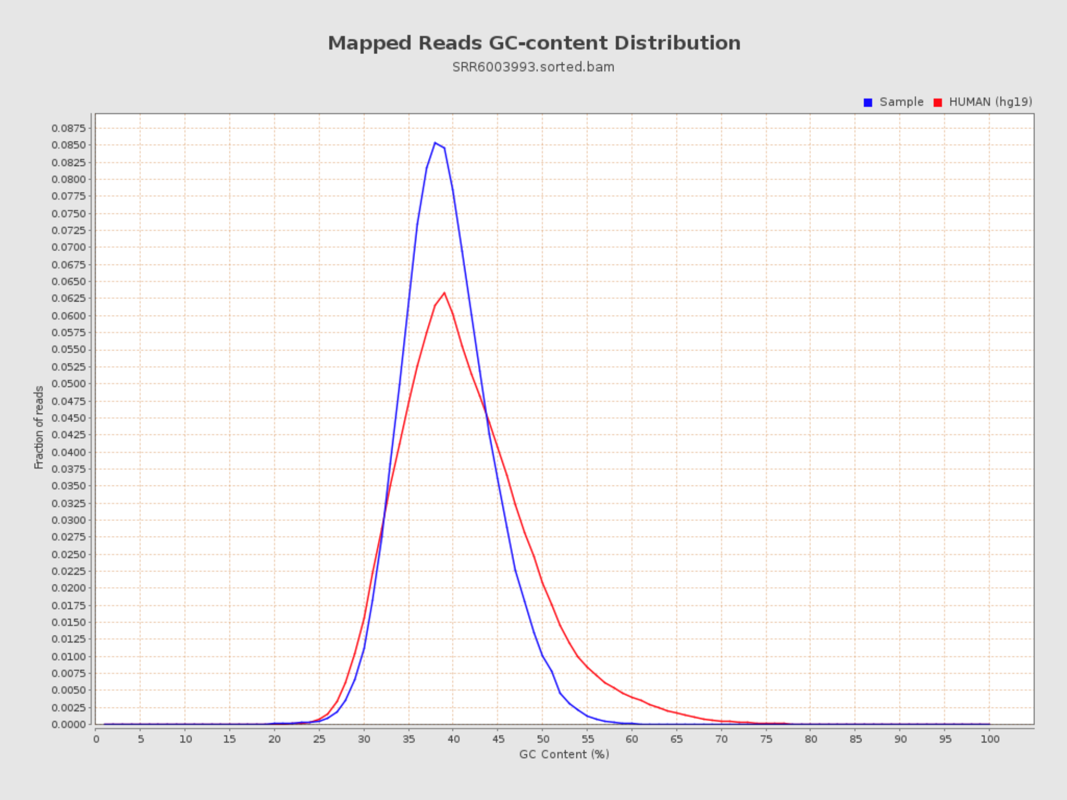
7. Results : Duplication Rate Histogram



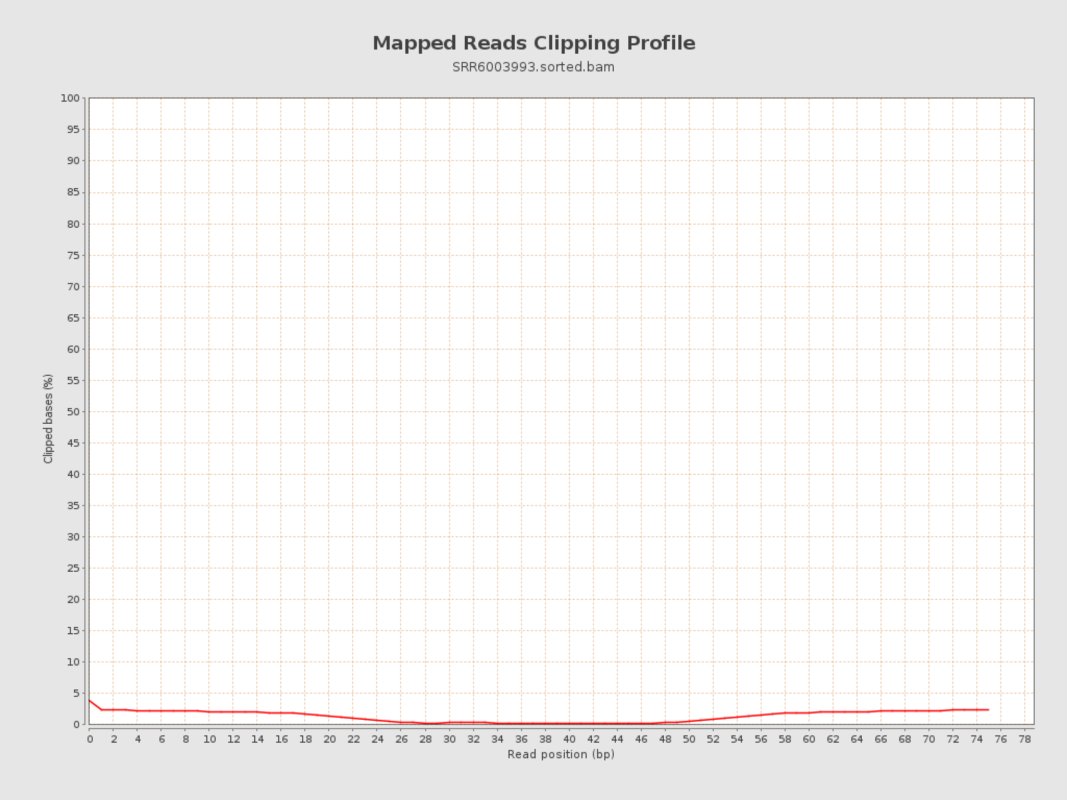
8. Results : Mapped Reads Nucleotide Content



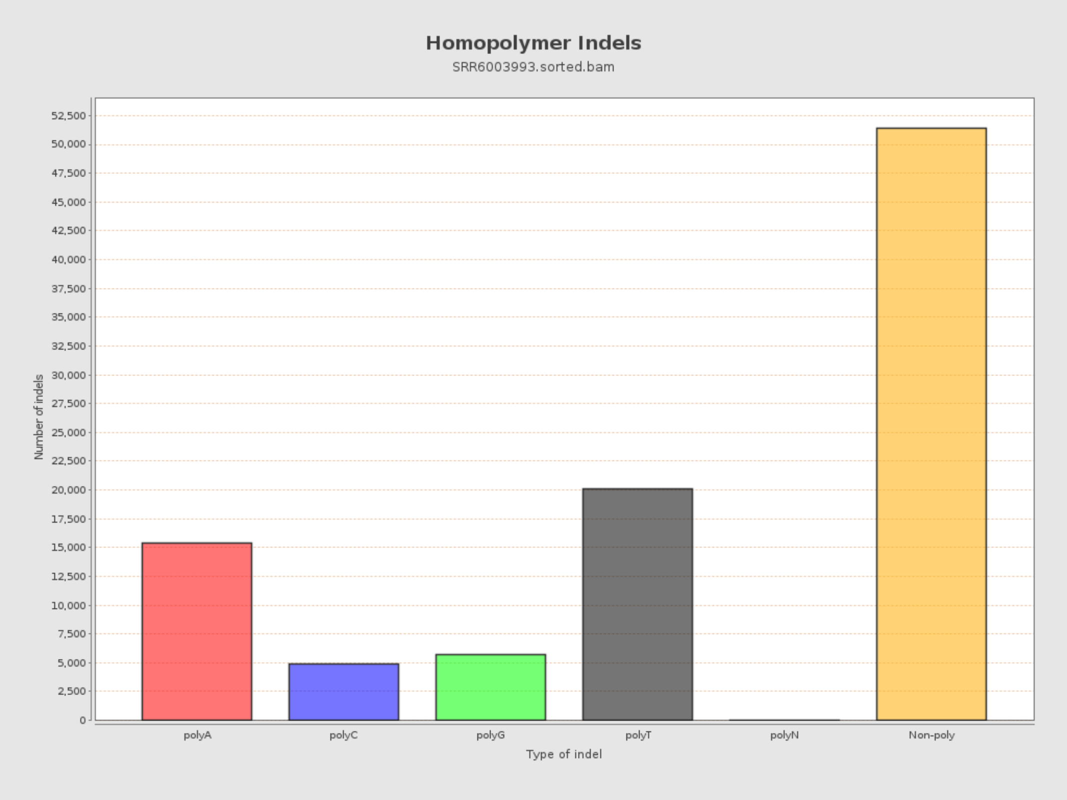
9. Results : Mapped Reads GC-content Distribution



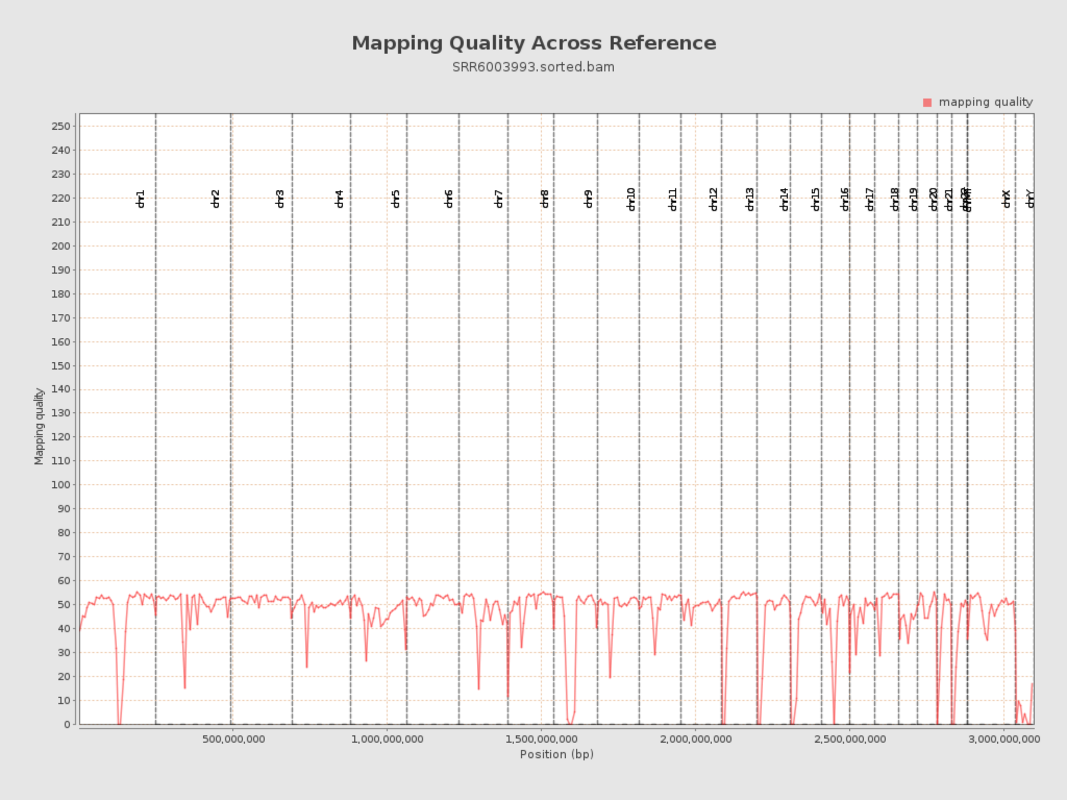
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram