Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:07:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080993.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_SRR3080993 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080993.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:06:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080993.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,481,960
Mapped reads	3,010,900 / 86.47%
Unmapped reads	471,060 / 13.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,469 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	118,213 / 3.4%
Duplication rate	2.76%
Clipped reads	1,533,991 / 44.06%

2.2. ACGT Content

Number/percentage of A's	54,358,396 / 27.78%
Number/percentage of C's	39,384,338 / 20.13%
Number/percentage of T's	57,621,402 / 29.45%
Number/percentage of G's	44,273,303 / 22.63%
Number/percentage of N's	2,547 / 0%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0632

Standard Deviation	0.5354

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

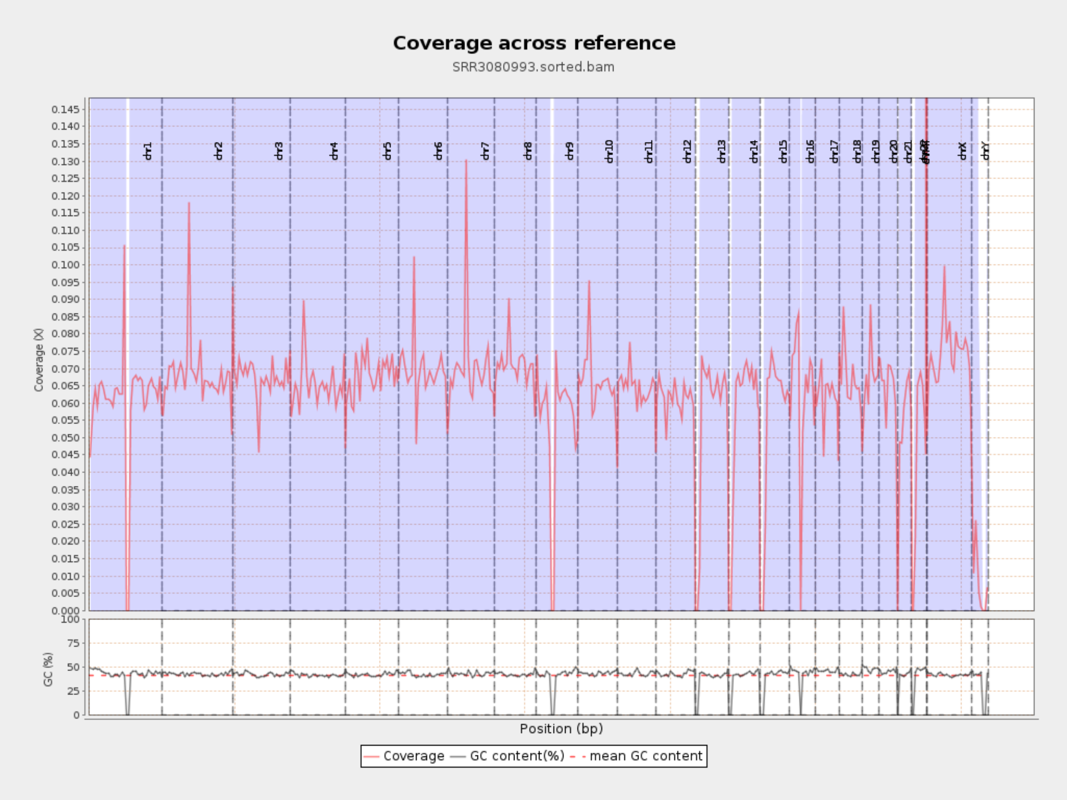
General error rate	0.78%
Mismatches	1,504,188
Insertions	13,912
Mapped reads with at least one insertion	0.46%
Deletions	38,274
Mapped reads with at least one deletion	1.26%
Homopolymer indels	45.82%

2.6. Chromosome stats

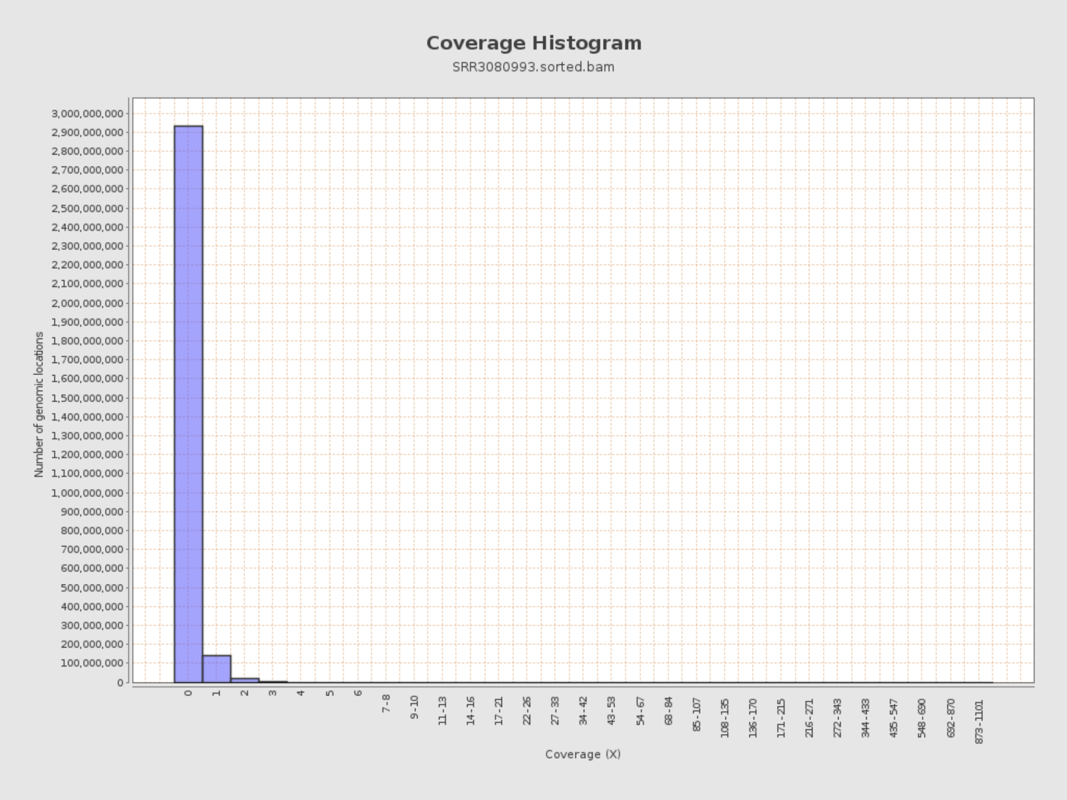
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14993928	0.0602	0.9202
chr2	243199373	16648475	0.0685	0.5833
chr3	198022430	13368324	0.0675	0.3267
chr4	191154276	12486837	0.0653	0.328
chr5	180915260	12321655	0.0681	0.3035
chr6	171115067	11895356	0.0695	0.4722
chr7	159138663	11317052	0.0711	0.9913

chr8	146364022	10372408	0.0709	0.4993
chr9	141213431	7601048	0.0538	0.4831
chr10	135534747	9013156	0.0665	0.4695
chr11	135006516	8693936	0.0644	0.4844
chr12	133851895	8170786	0.061	0.2915
chr13	115169878	6357953	0.0552	0.2678
chr14	107349540	5995086	0.0558	0.3157
chr15	102531392	5547275	0.0541	0.2869
chr16	90354753	5690104	0.063	0.3377
chr17	81195210	4962446	0.0611	0.345
chr18	78077248	5306976	0.068	1.0228
chr19	59128983	4004668	0.0677	0.694
chr20	63025520	4049285	0.0642	0.3076
chr21	48129895	2535602	0.0527	0.3041
chr22	51304566	2219128	0.0433	0.2364
chrMT	16571	64325	3.8818	2.8231
chrX	155270560	11568554	0.0745	0.4001
chrY	59373566	523048	0.0088	0.1888

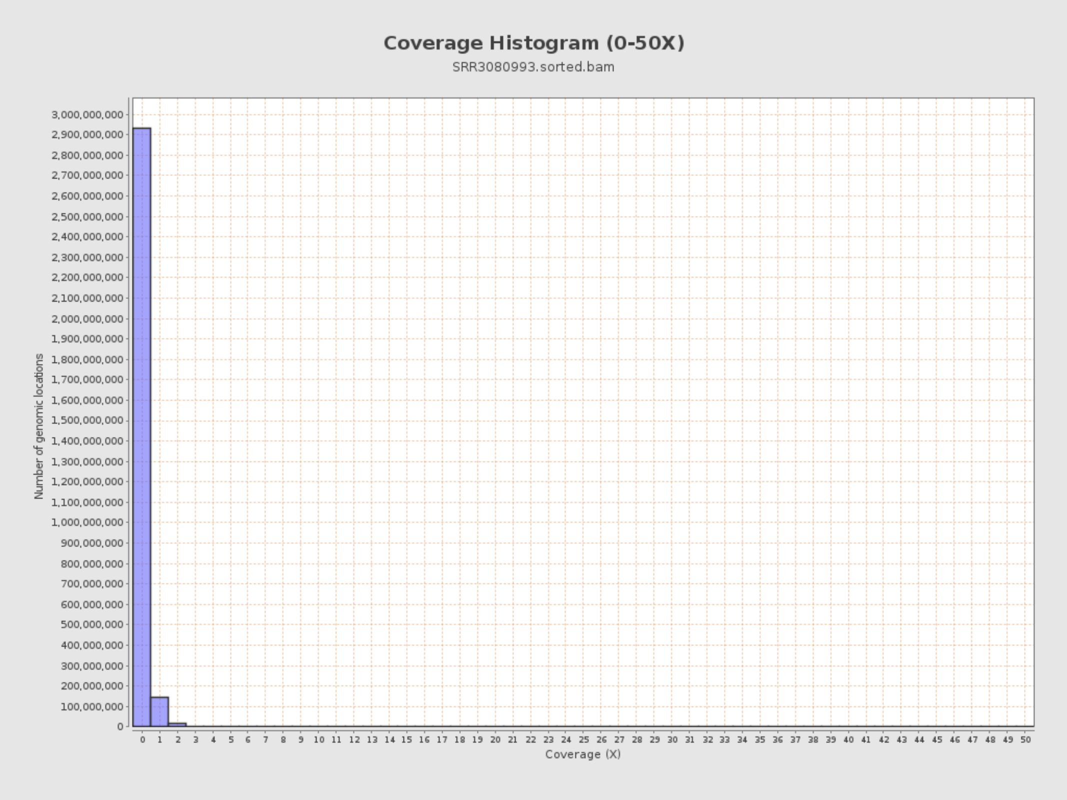
3. Results : Coverage across reference



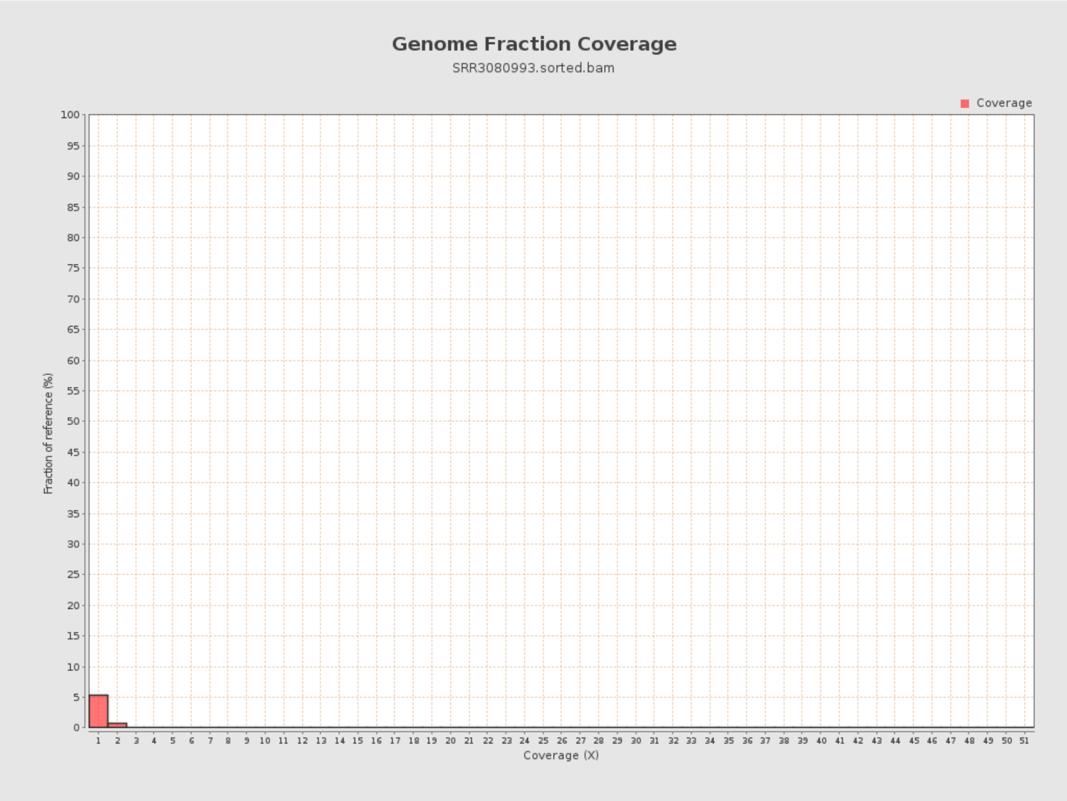
4. Results : Coverage Histogram



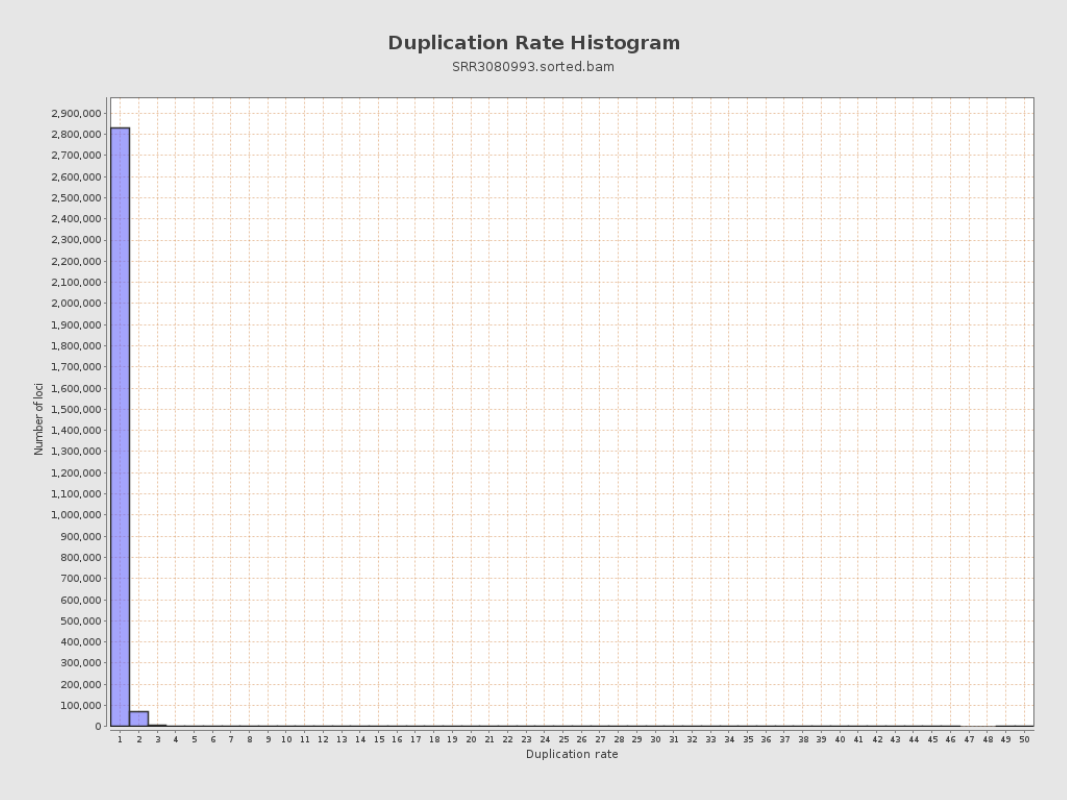
5. Results : Coverage Histogram (0-50X)



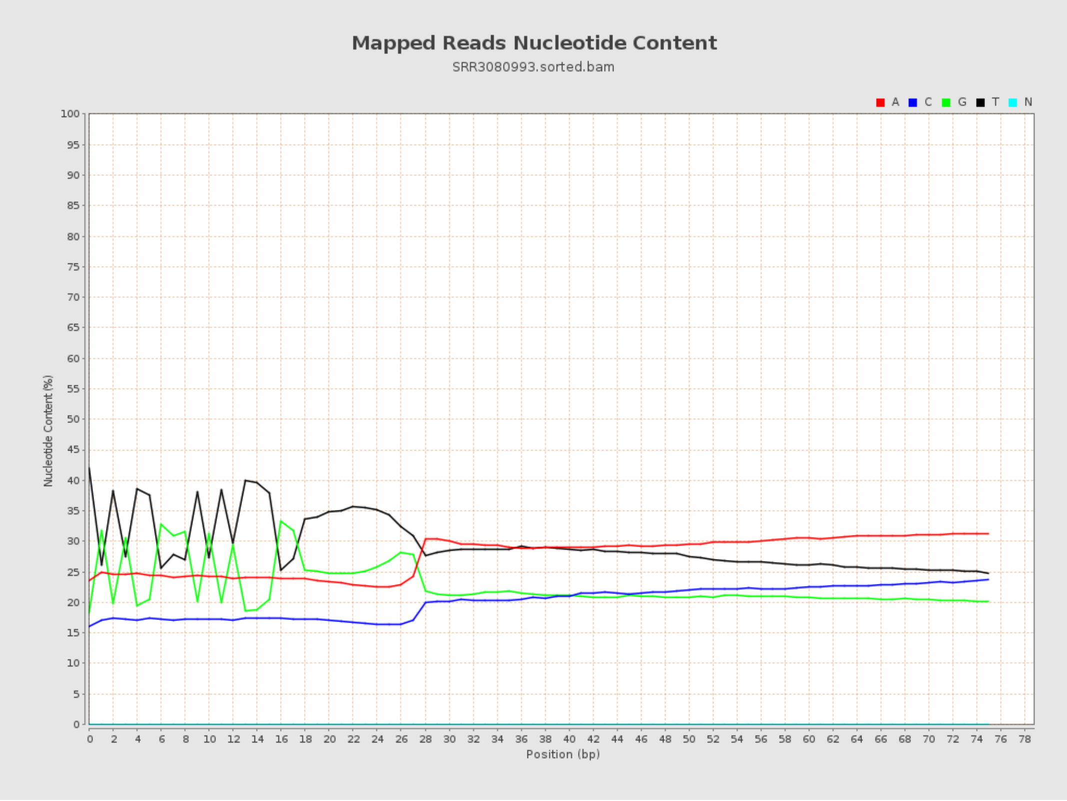
6. Results : Genome Fraction Coverage



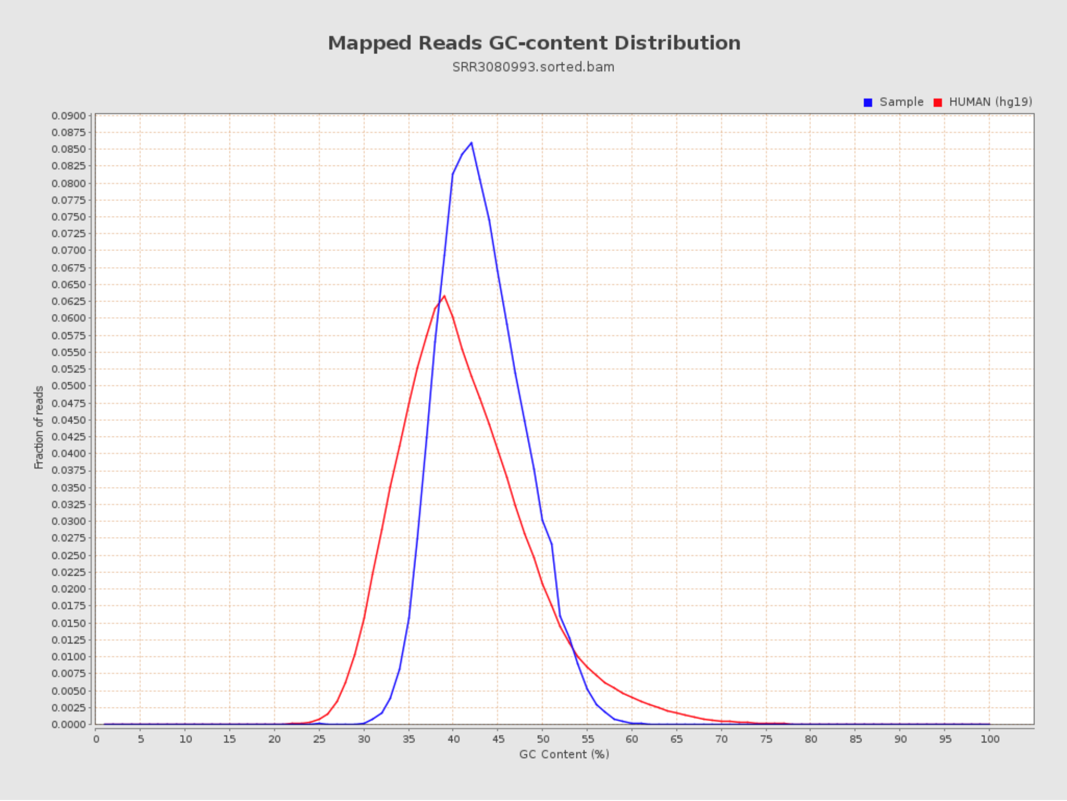
7. Results : Duplication Rate Histogram



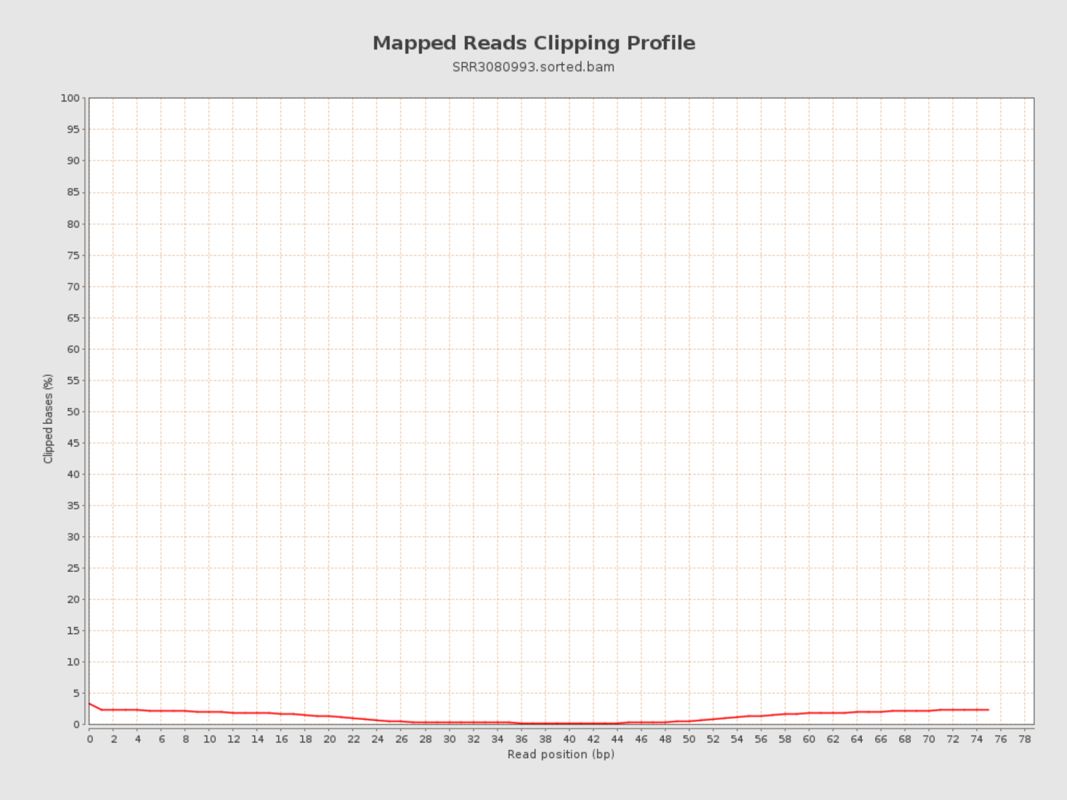
8. Results : Mapped Reads Nucleotide Content



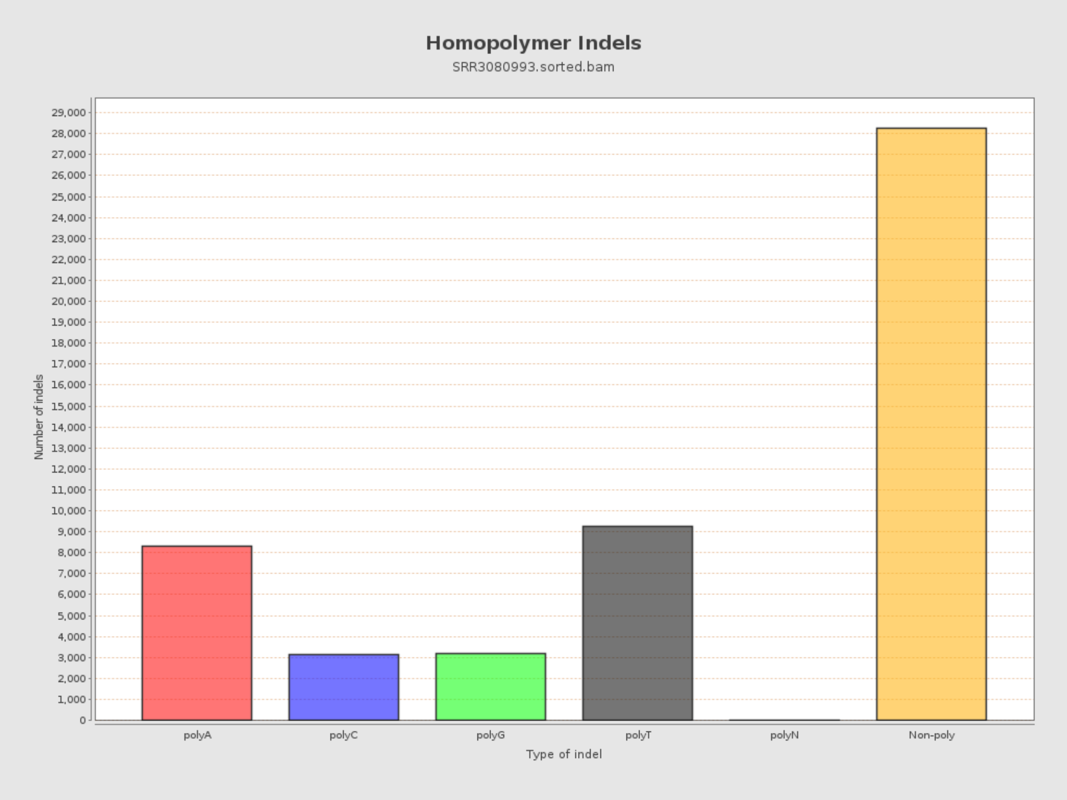
9. Results : Mapped Reads GC-content Distribution



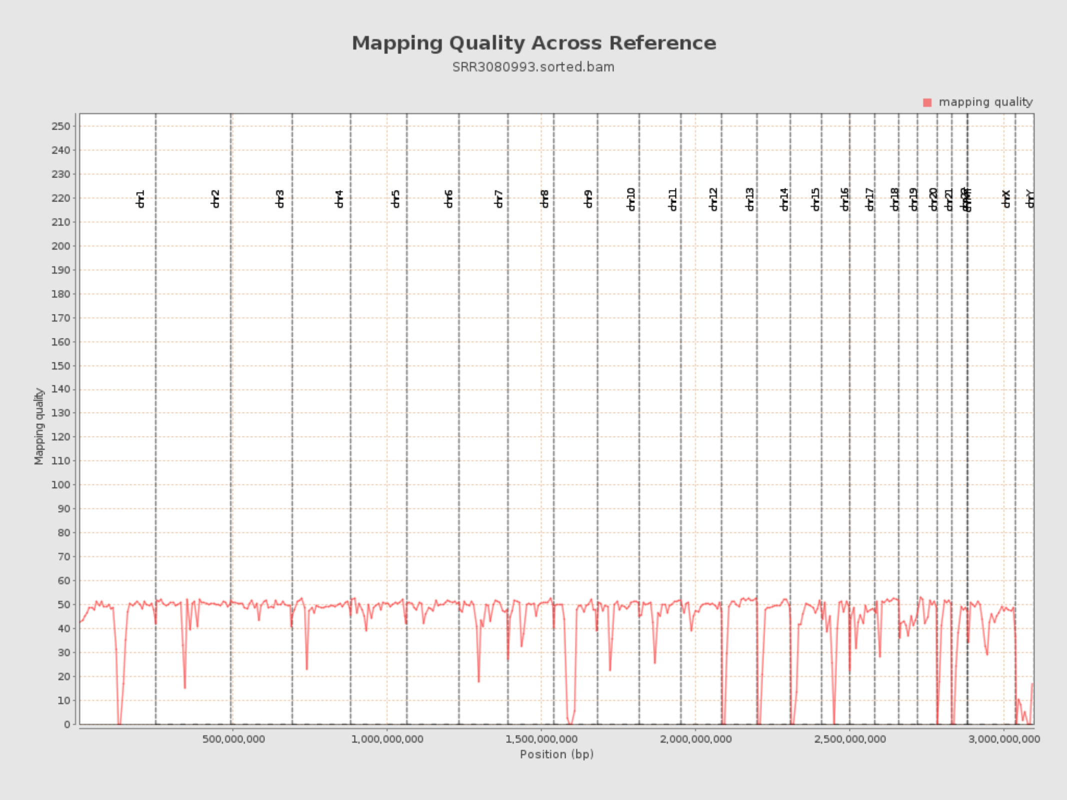
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram