Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:19:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080903.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_SRR3080903 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080903.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:19:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080903.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,014,087
Mapped reads	3,628,467 / 90.39%
Unmapped reads	385,620 / 9.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,219 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	188,478 / 4.7%
Duplication rate	4.25%
Clipped reads	1,347,309 / 33.56%

2.2. ACGT Content

Number/percentage of A's	71,434,466 / 28.79%
Number/percentage of C's	43,528,362 / 17.54%
Number/percentage of T's	80,237,866 / 32.34%
Number/percentage of G's	51,749,516 / 20.85%
Number/percentage of N's	1,193,322 / 0.48%
GC Percentage	38.4%

2.3. Coverage

Mean	0.0802

Standard Deviation	0.5148

2.4. Mapping Quality

Mean Mapping Quality	48.03

2.5. Mismatches and indels

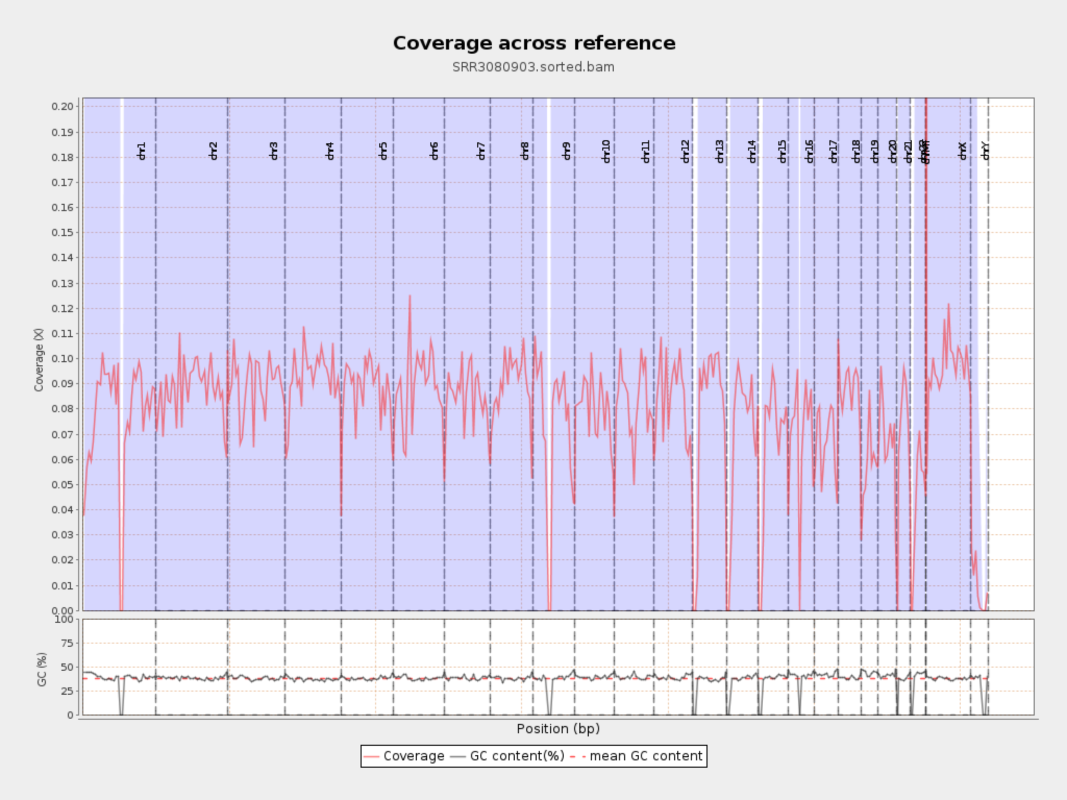
General error rate	1.16%
Mismatches	2,840,758
Insertions	18,759
Mapped reads with at least one insertion	0.51%
Deletions	54,974
Mapped reads with at least one deletion	1.5%
Homopolymer indels	49.93%

2.6. Chromosome stats

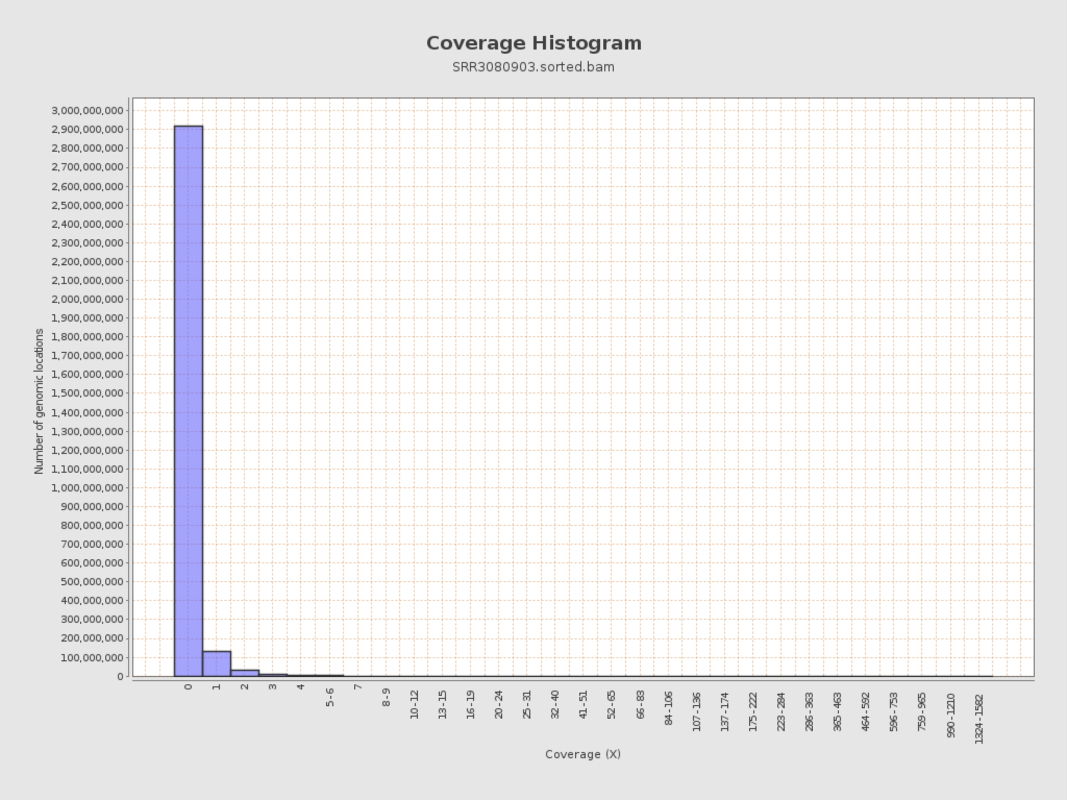
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19178606	0.0769	0.7094
chr2	243199373	21387437	0.0879	0.5031
chr3	198022430	17776459	0.0898	0.3996
chr4	191154276	17695404	0.0926	0.4158
chr5	180915260	15918178	0.088	0.3956
chr6	171115067	15385861	0.0899	0.5049
chr7	159138663	13483324	0.0847	0.6019

chr8	146364022	13129964	0.0897	1.0238
chr9	141213431	10404619	0.0737	0.4748
chr10	135534747	10966821	0.0809	0.4497
chr11	135006516	11146242	0.0826	0.4426
chr12	133851895	11231357	0.0839	0.3883
chr13	115169878	8872012	0.077	0.3706
chr14	107349540	7475556	0.0696	0.3675
chr15	102531392	6552486	0.0639	0.3358
chr16	90354753	6104066	0.0676	0.3651
chr17	81195210	5484898	0.0676	0.3733
chr18	78077248	6963434	0.0892	0.7732
chr19	59128983	3448100	0.0583	0.5171
chr20	63025520	4451459	0.0706	0.366
chr21	48129895	3346238	0.0695	0.373
chr22	51304566	2166055	0.0422	0.27
chrMT	16571	116969	7.0587	4.1845
chrX	155270560	15029170	0.0968	0.4404
chrY	59373566	519189	0.0087	0.1556

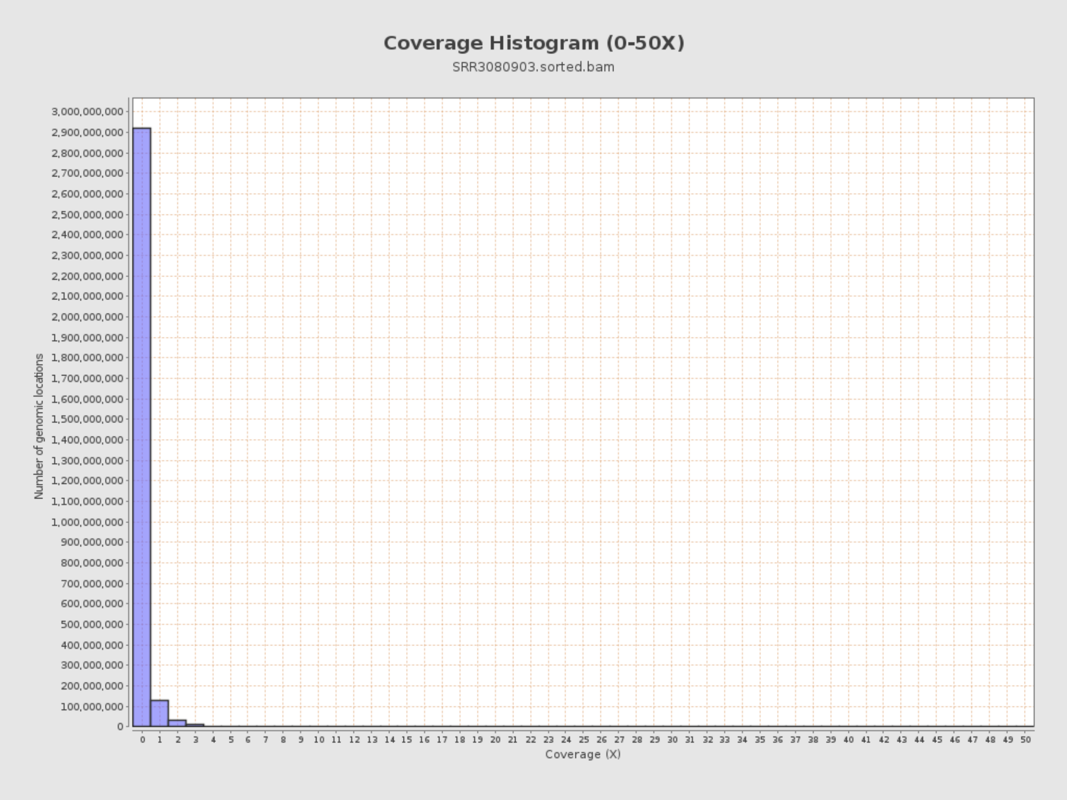
3. Results : Coverage across reference



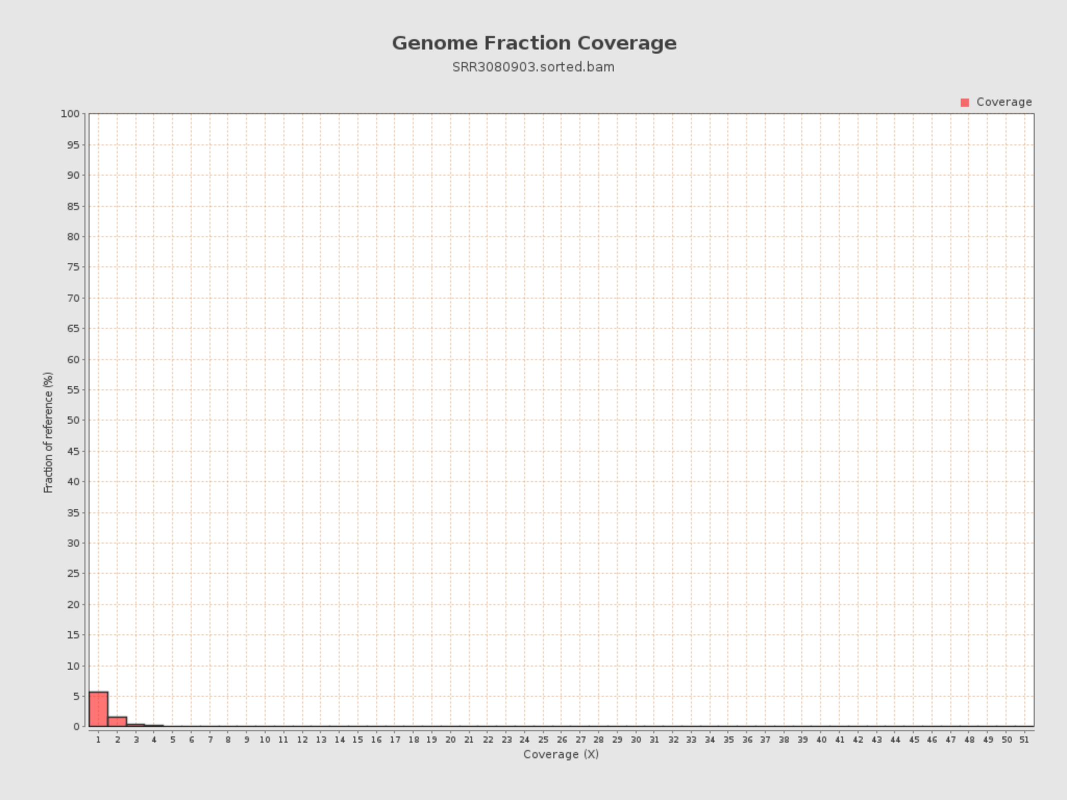
4. Results : Coverage Histogram



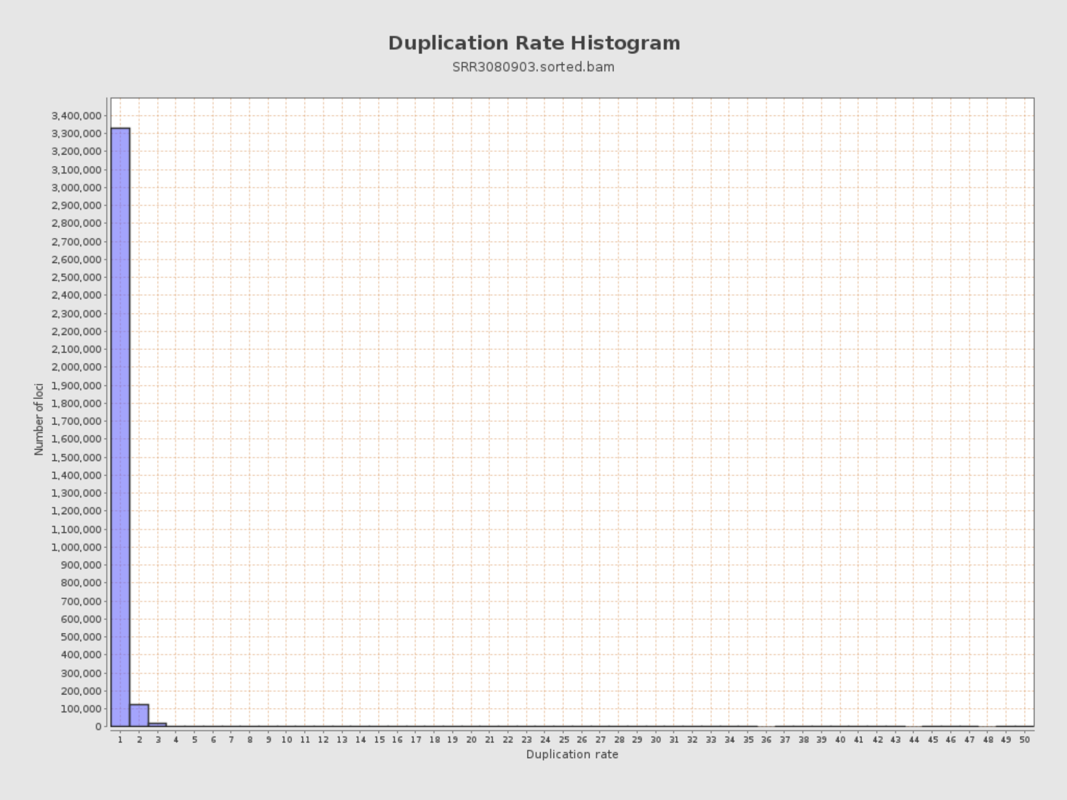
5. Results : Coverage Histogram (0-50X)



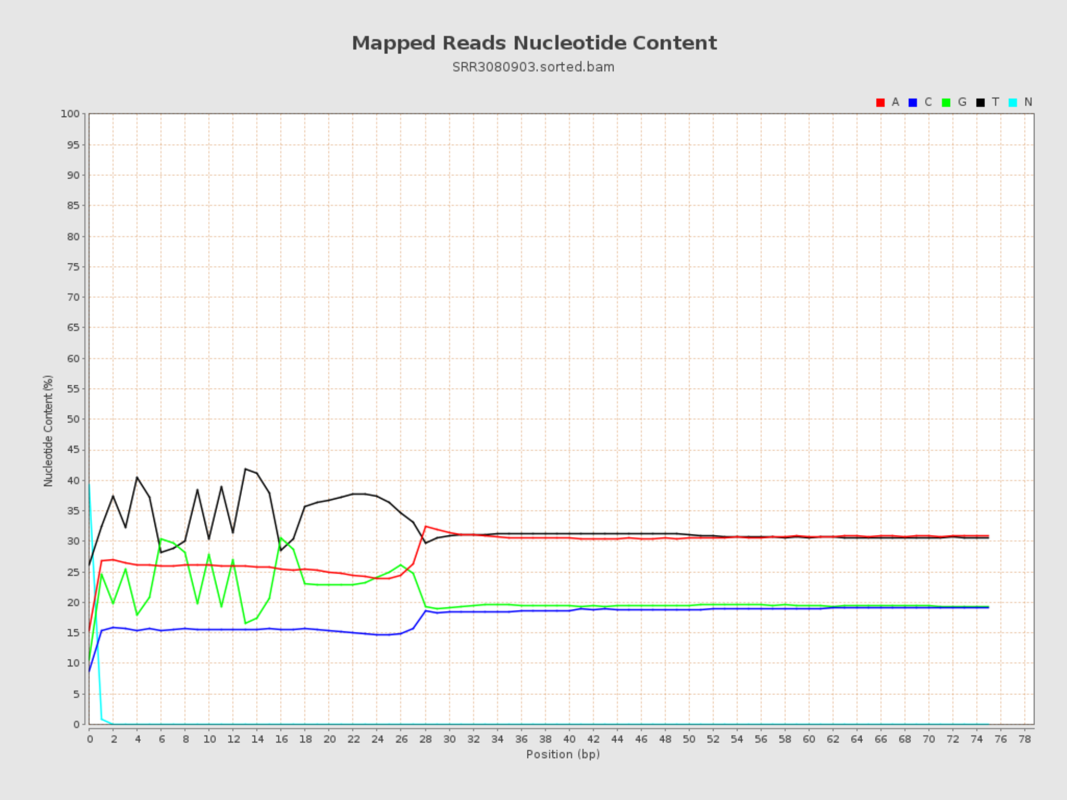
6. Results : Genome Fraction Coverage



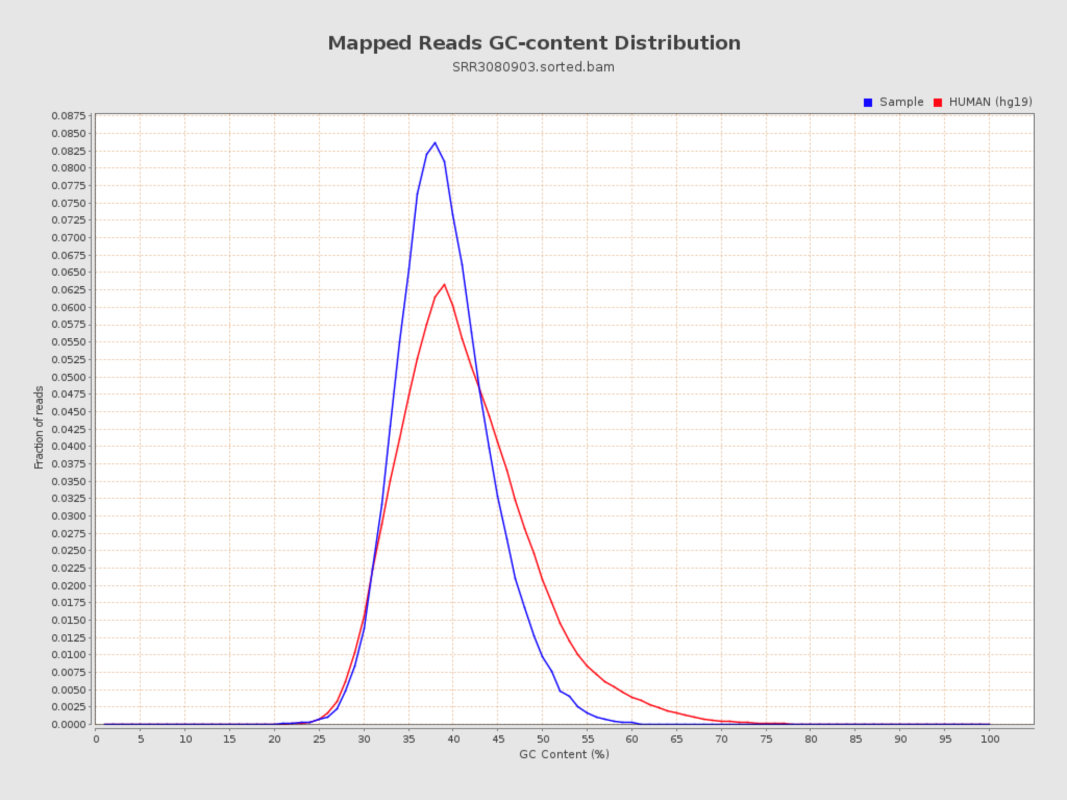
7. Results : Duplication Rate Histogram



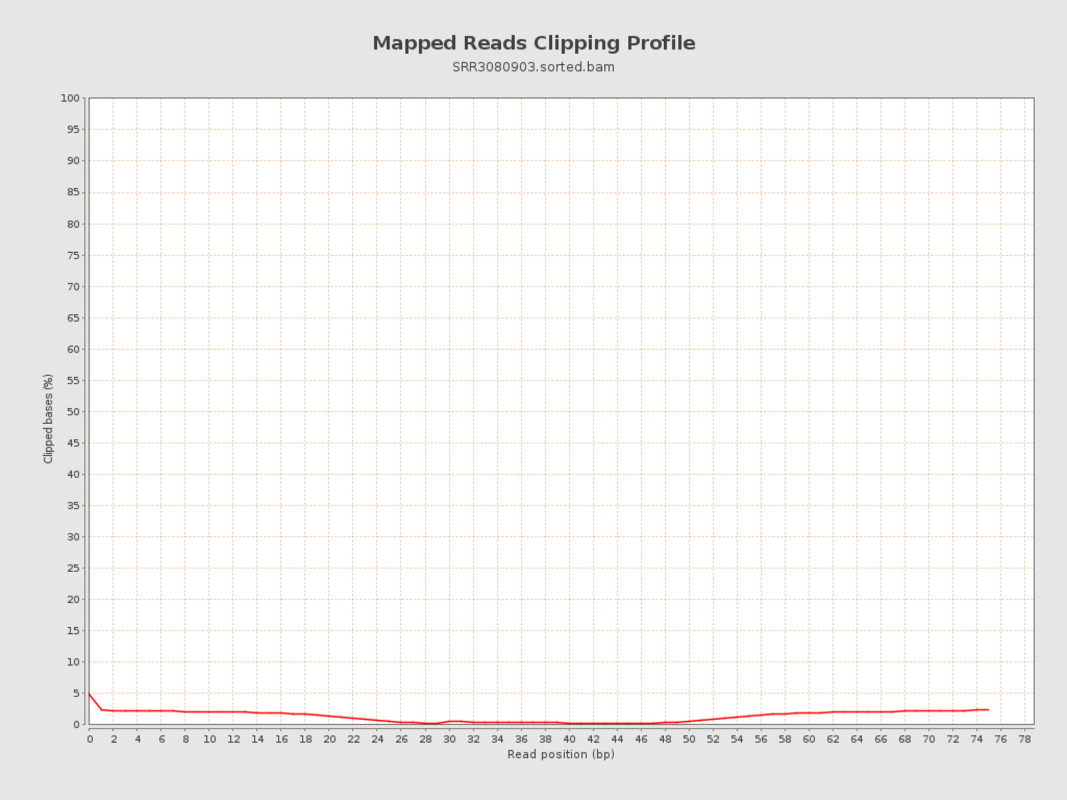
8. Results : Mapped Reads Nucleotide Content



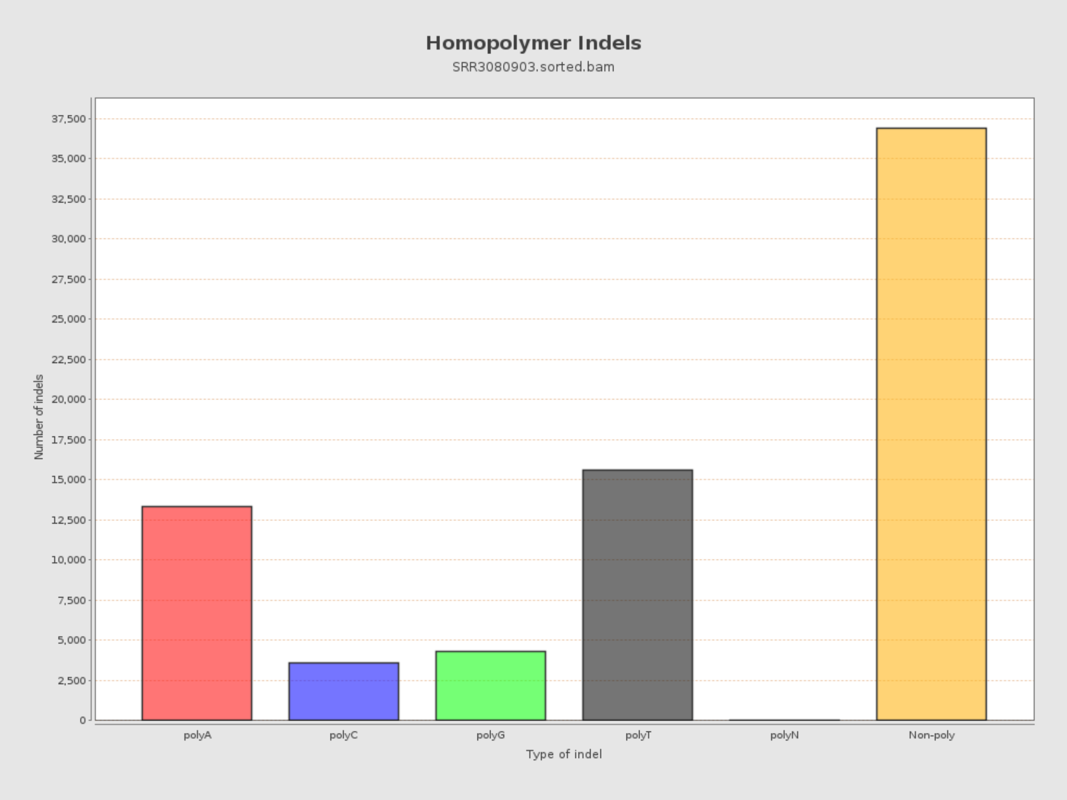
9. Results : Mapped Reads GC-content Distribution



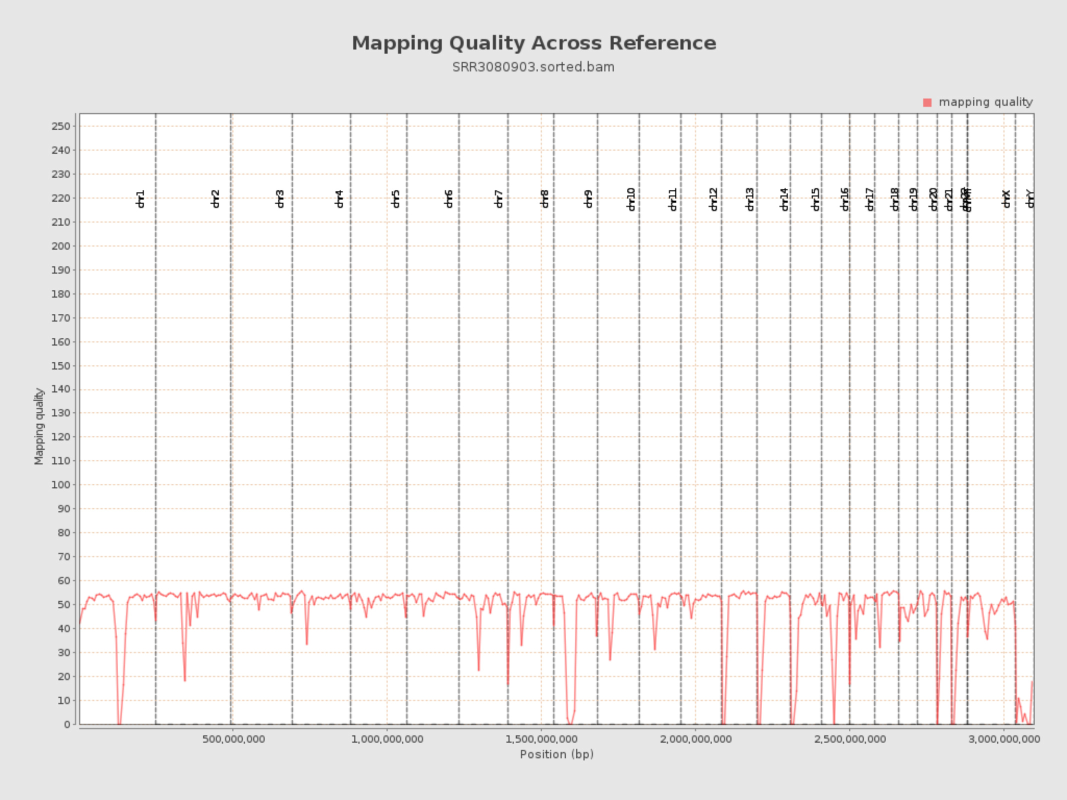
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram