Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:14:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082903.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_SRR3082903 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082903.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:14:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082903.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,274,630
Mapped reads	2,817,872 / 86.05%
Unmapped reads	456,758 / 13.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,466 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	126,786 / 3.87%
Duplication rate	3.85%
Clipped reads	1,249,253 / 38.15%

2.2. ACGT Content

Number/percentage of A's	52,086,146 / 27.73%
Number/percentage of C's	32,707,506 / 17.41%
Number/percentage of T's	62,316,561 / 33.17%
Number/percentage of G's	40,688,555 / 21.66%
Number/percentage of N's	48,604 / 0.03%
GC Percentage	39.07%

2.3. Coverage

Mean	0.0607

Standard Deviation	0.3774

2.4. Mapping Quality

Mean Mapping Quality	47.59

2.5. Mismatches and indels

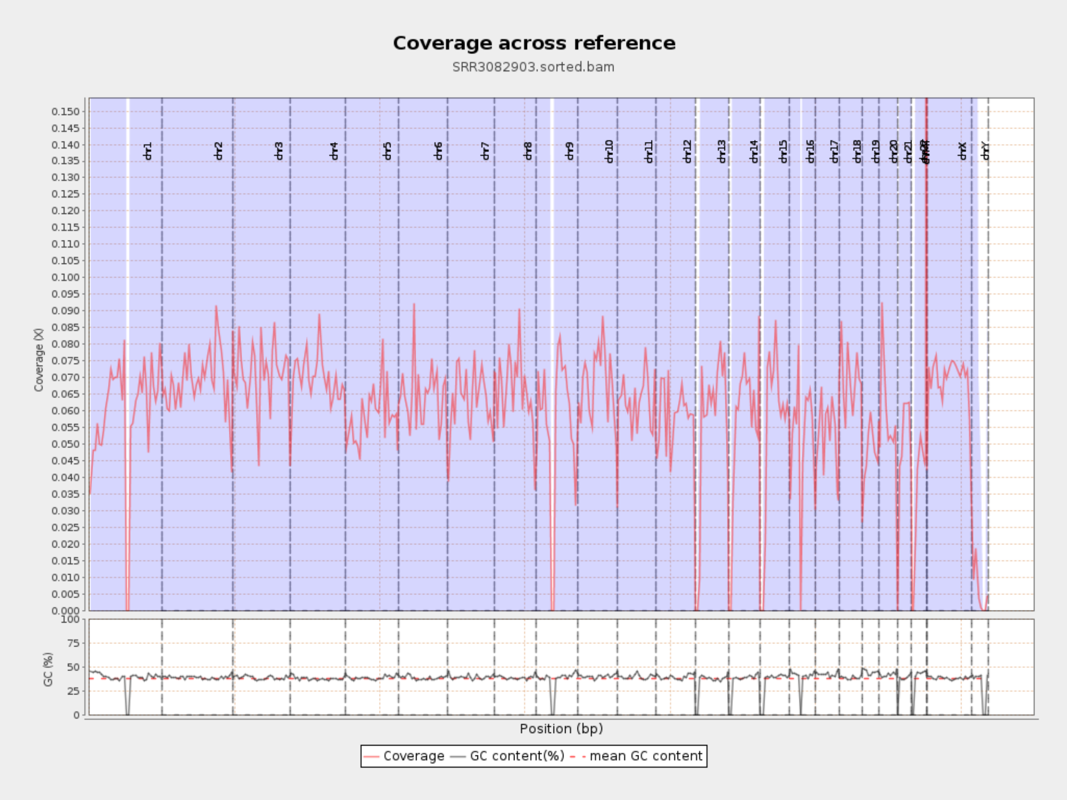
General error rate	0.95%
Mismatches	1,754,157
Insertions	16,235
Mapped reads with at least one insertion	0.57%
Deletions	43,164
Mapped reads with at least one deletion	1.52%
Homopolymer indels	49.45%

2.6. Chromosome stats

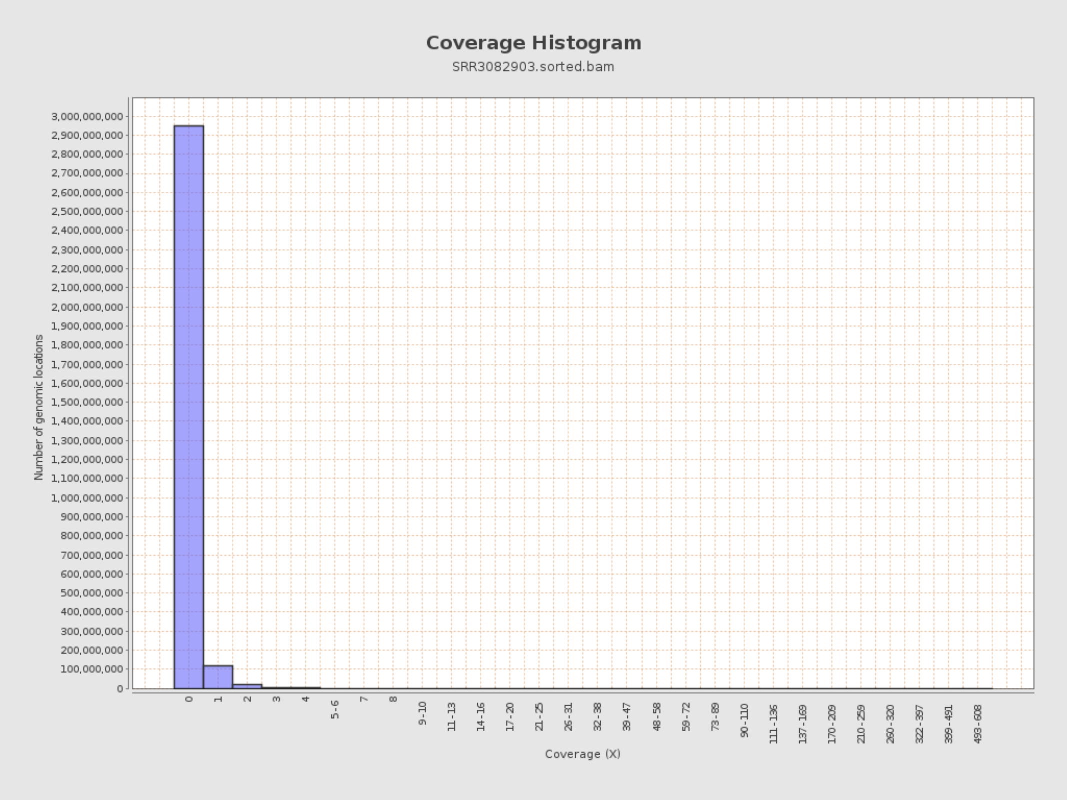
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14750428	0.0592	0.5291
chr2	243199373	16819455	0.0692	0.4338
chr3	198022430	14173700	0.0716	0.3232
chr4	191154276	13349696	0.0698	0.3294
chr5	180915260	10606532	0.0586	0.2928
chr6	171115067	11027744	0.0644	0.4323
chr7	159138663	10102523	0.0635	0.4203

chr8	146364022	9698784	0.0663	0.5005
chr9	141213431	7894475	0.0559	0.3824
chr10	135534747	9353935	0.069	0.3382
chr11	135006516	8480881	0.0628	0.3407
chr12	133851895	7779916	0.0581	0.2969
chr13	115169878	6350826	0.0551	0.2857
chr14	107349540	5784730	0.0539	0.3027
chr15	102531392	5588940	0.0545	0.2824
chr16	90354753	4718907	0.0522	0.2985
chr17	81195210	4233229	0.0521	0.2929
chr18	78077248	5433191	0.0696	0.5816
chr19	59128983	2838941	0.048	0.3773
chr20	63025520	3749973	0.0595	0.3061
chr21	48129895	2346008	0.0487	0.2832
chr22	51304566	1695800	0.0331	0.2176
chrMT	16571	21852	1.3187	1.4419
chrX	155270560	10734150	0.0691	0.3321
chrY	59373566	382516	0.0064	0.1354

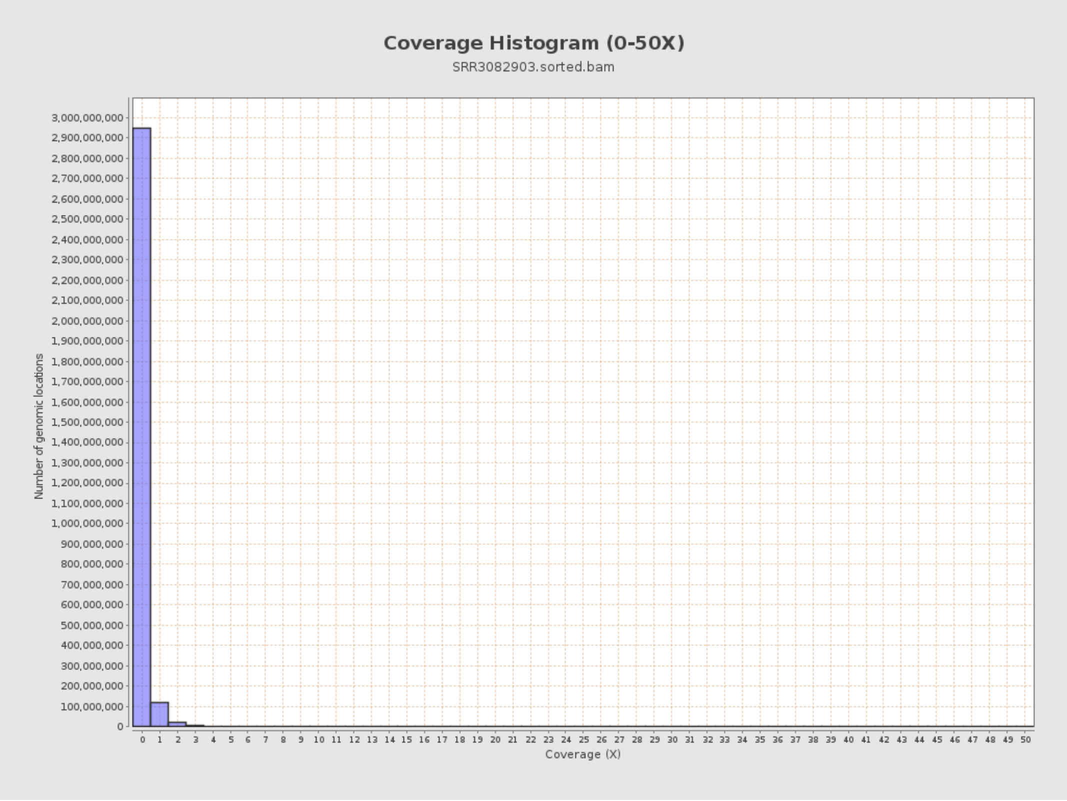
3. Results : Coverage across reference



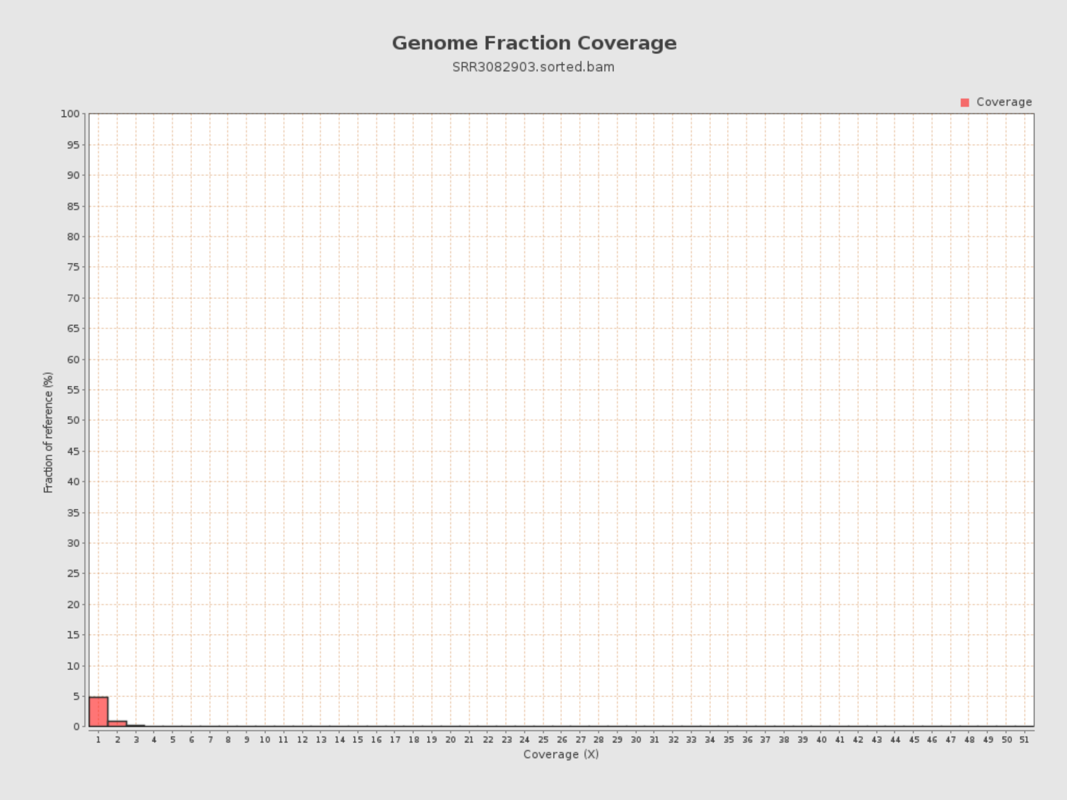
4. Results : Coverage Histogram



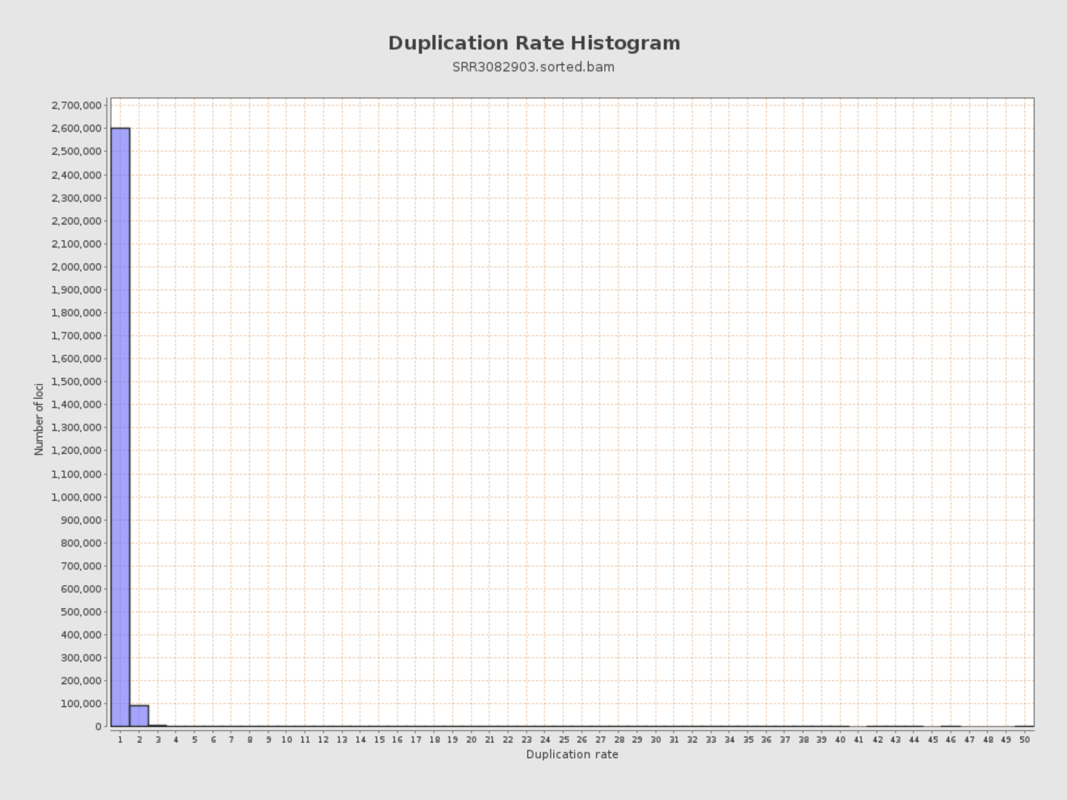
5. Results : Coverage Histogram (0-50X)



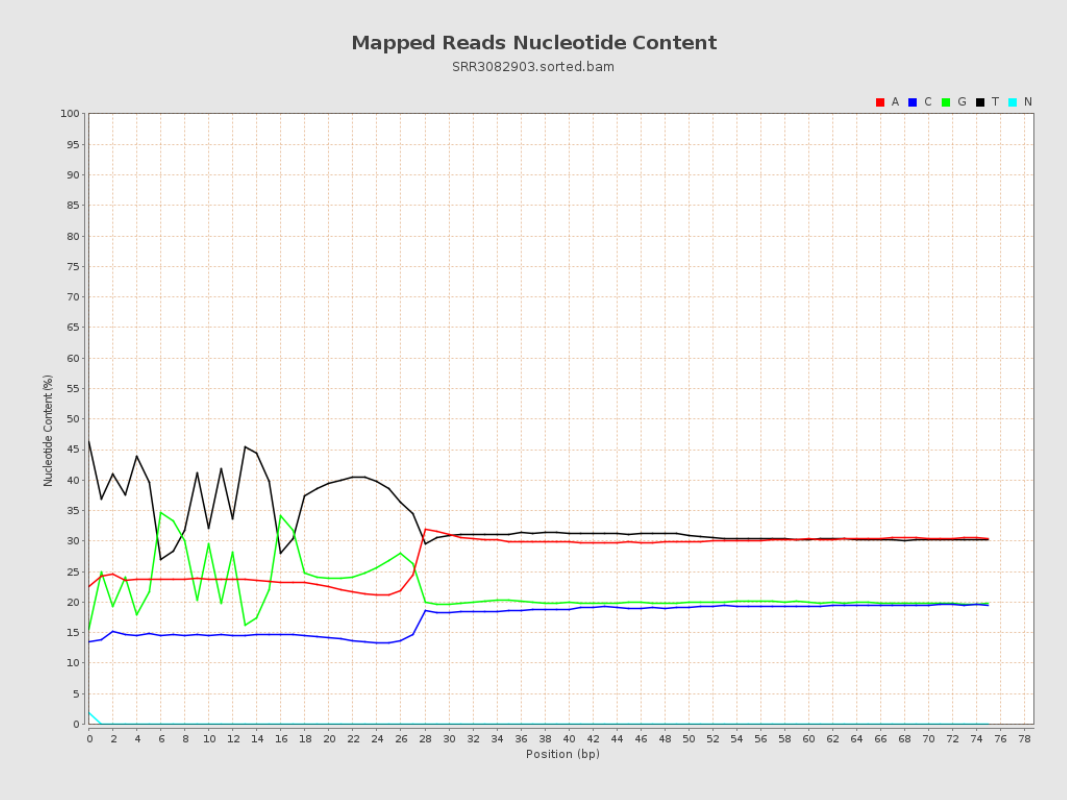
6. Results : Genome Fraction Coverage



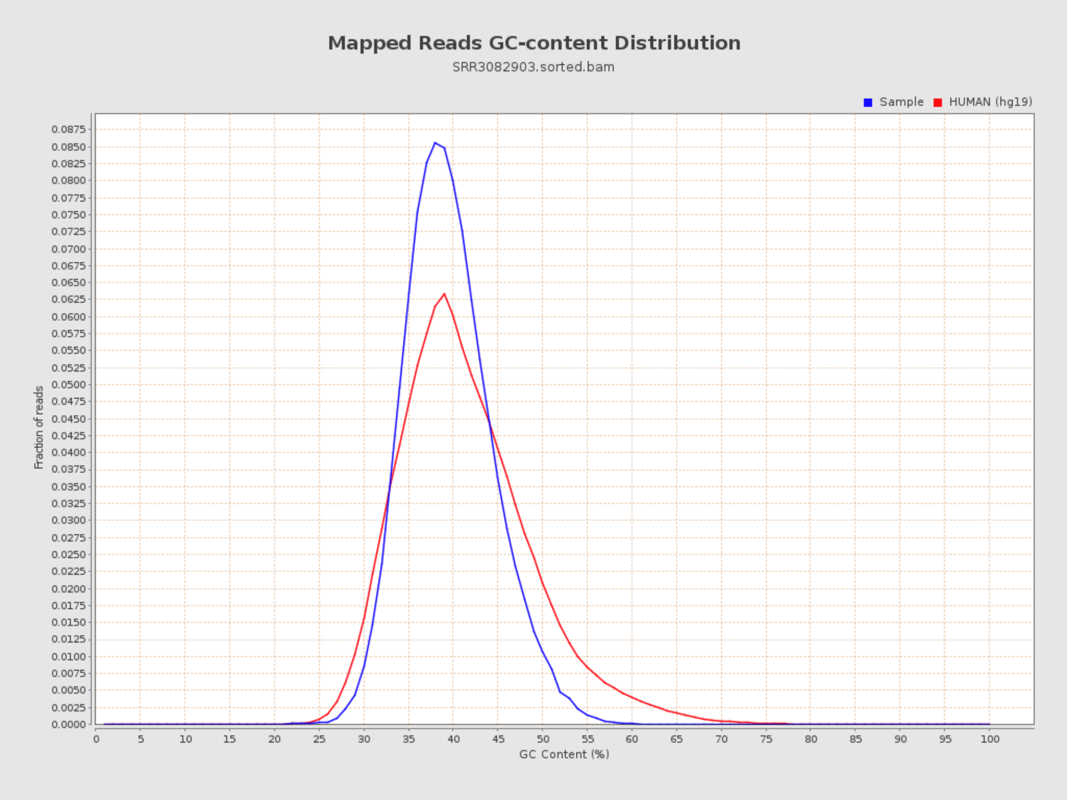
7. Results : Duplication Rate Histogram



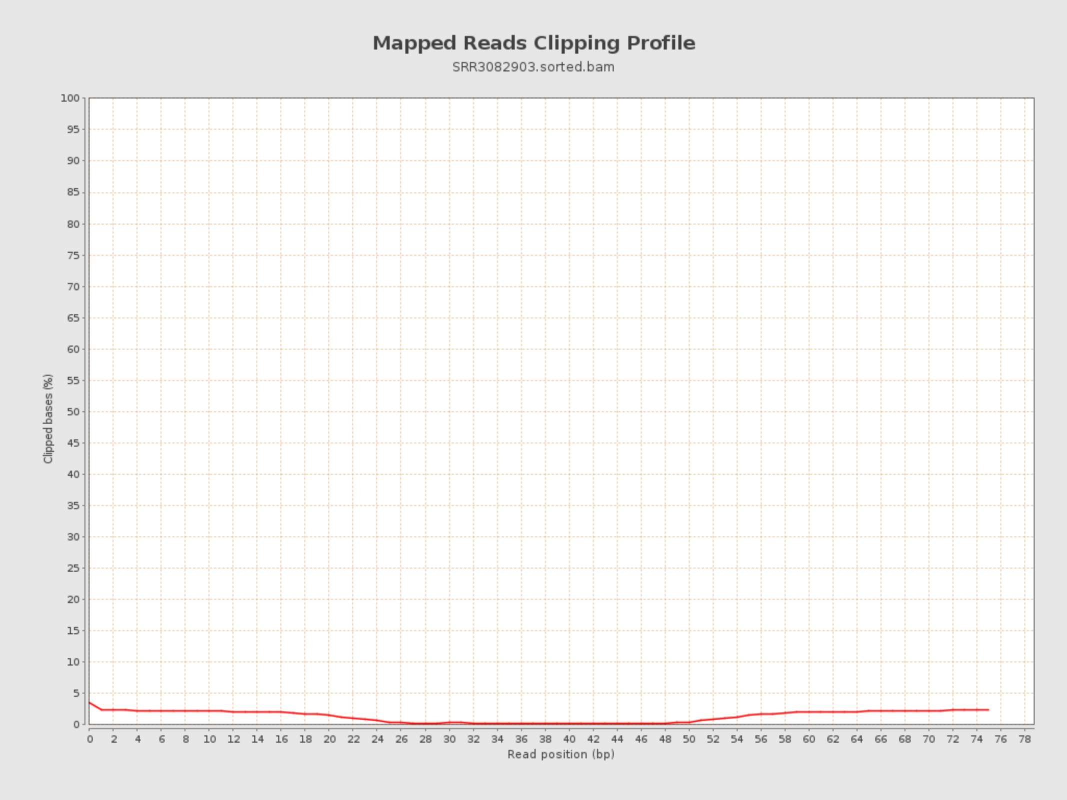
8. Results : Mapped Reads Nucleotide Content



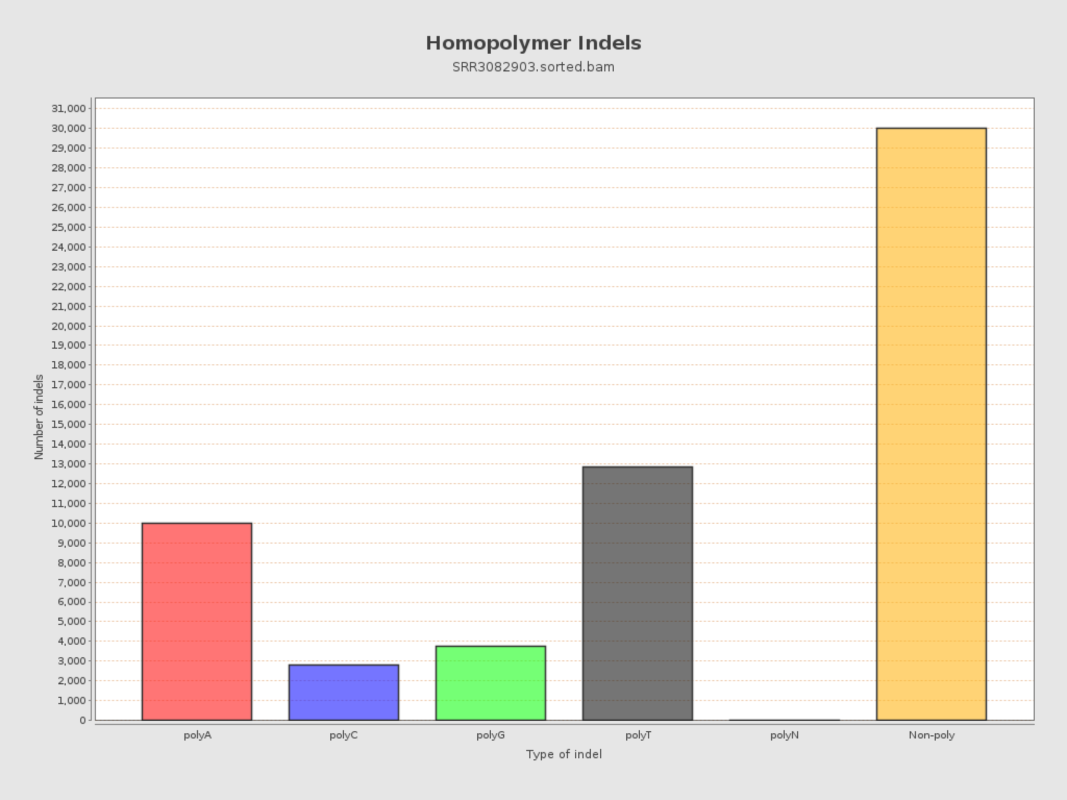
9. Results : Mapped Reads GC-content Distribution



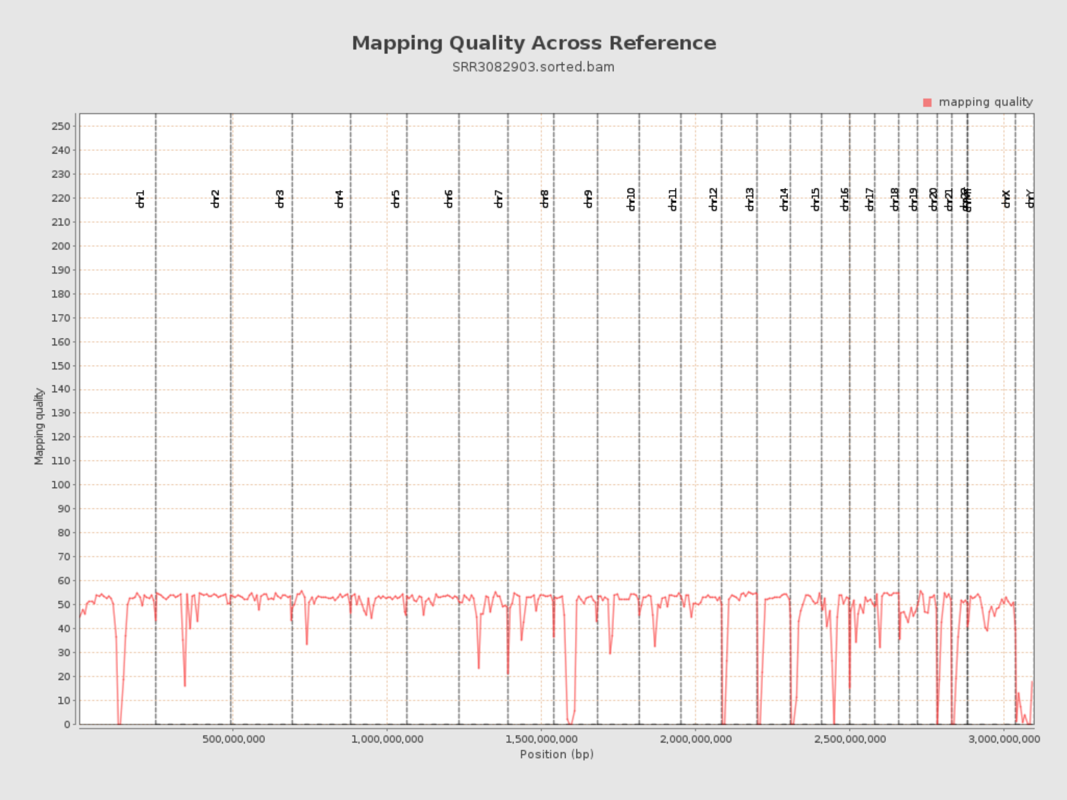
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram