Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:31:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080905.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_SRR3080905 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080905.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:31:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080905.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,923,747
Mapped reads	2,626,916 / 89.85%
Unmapped reads	296,831 / 10.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,300 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	104,487 / 3.57%
Duplication rate	3.02%
Clipped reads	1,007,628 / 34.46%

2.2. ACGT Content

Number/percentage of A's	51,130,648 / 28.59%
Number/percentage of C's	31,398,319 / 17.56%
Number/percentage of T's	57,735,889 / 32.28%
Number/percentage of G's	37,721,420 / 21.09%
Number/percentage of N's	858,621 / 0.48%
GC Percentage	38.65%

2.3. Coverage

Mean	0.0578

Standard Deviation	0.4633

2.4. Mapping Quality

Mean Mapping Quality	47.77

2.5. Mismatches and indels

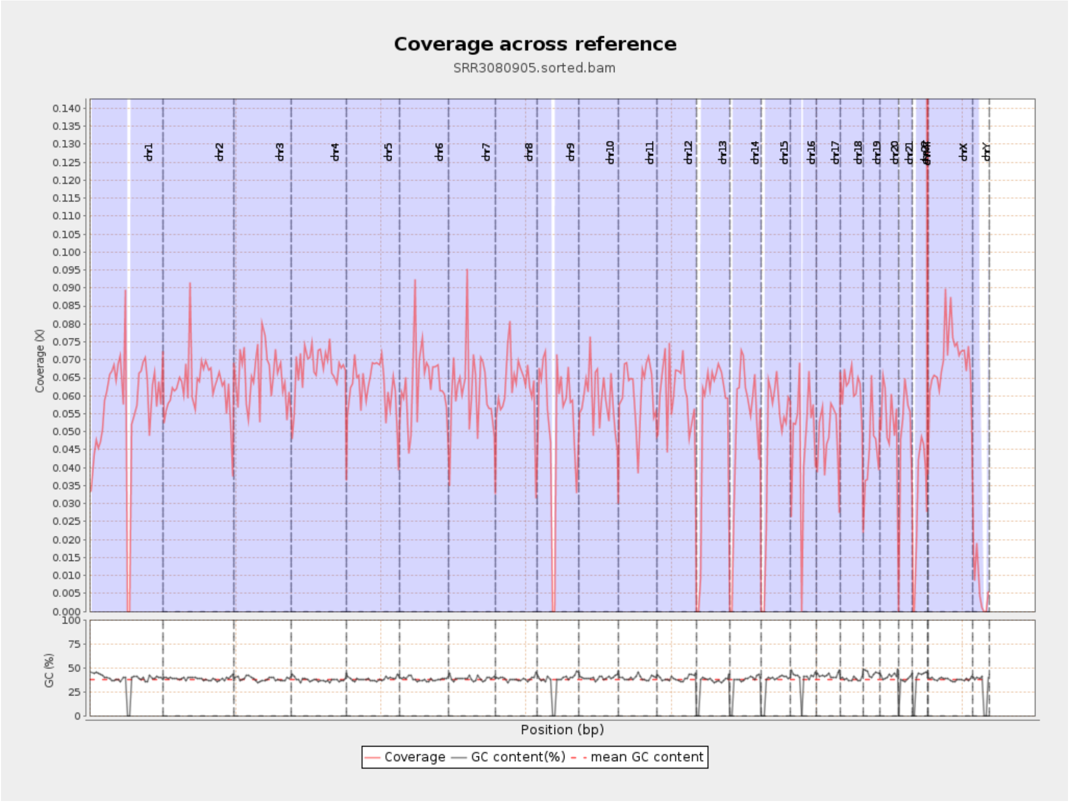
General error rate	1.17%
Mismatches	2,072,291
Insertions	13,903
Mapped reads with at least one insertion	0.53%
Deletions	39,938
Mapped reads with at least one deletion	1.51%
Homopolymer indels	49.71%

2.6. Chromosome stats

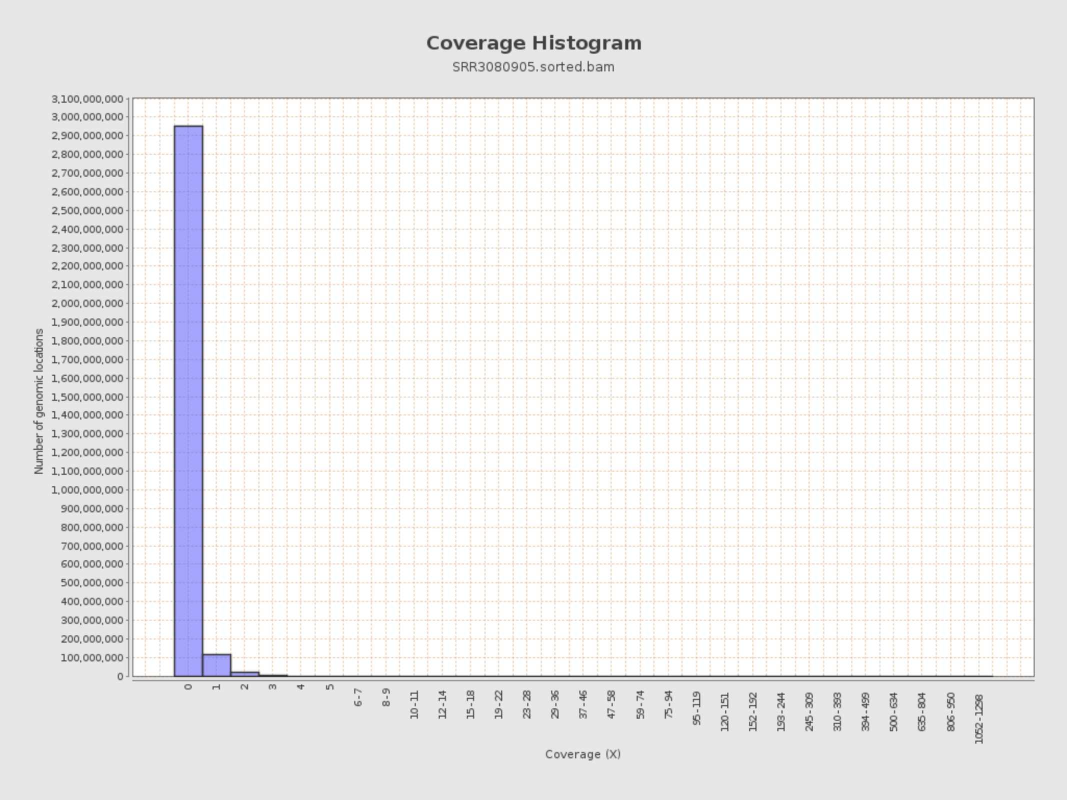
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14037353	0.0563	0.7576
chr2	243199373	15254482	0.0627	0.4592
chr3	198022430	13021384	0.0658	0.3094
chr4	191154276	12979113	0.0679	0.3261
chr5	180915260	11329482	0.0626	0.3035
chr6	171115067	10864872	0.0635	0.3996
chr7	159138663	9884222	0.0621	0.6282

chr8	146364022	9140264	0.0624	0.8371
chr9	141213431	7490506	0.053	0.4357
chr10	135534747	8045226	0.0594	0.3924
chr11	135006516	8170296	0.0605	0.4232
chr12	133851895	8069440	0.0603	0.2992
chr13	115169878	6056413	0.0526	0.2754
chr14	107349540	5427142	0.0506	0.2967
chr15	102531392	4858435	0.0474	0.2621
chr16	90354753	4336645	0.048	0.2844
chr17	81195210	3895011	0.048	0.3215
chr18	78077248	4883470	0.0625	0.7944
chr19	59128983	2659806	0.045	0.5009
chr20	63025520	3378794	0.0536	0.2958
chr21	48129895	2320920	0.0482	0.2916
chr22	51304566	1560765	0.0304	0.2069
chrMT	16571	53947	3.2555	2.4837
chrX	155270560	10812396	0.0696	0.3499
chrY	59373566	380259	0.0064	0.1371

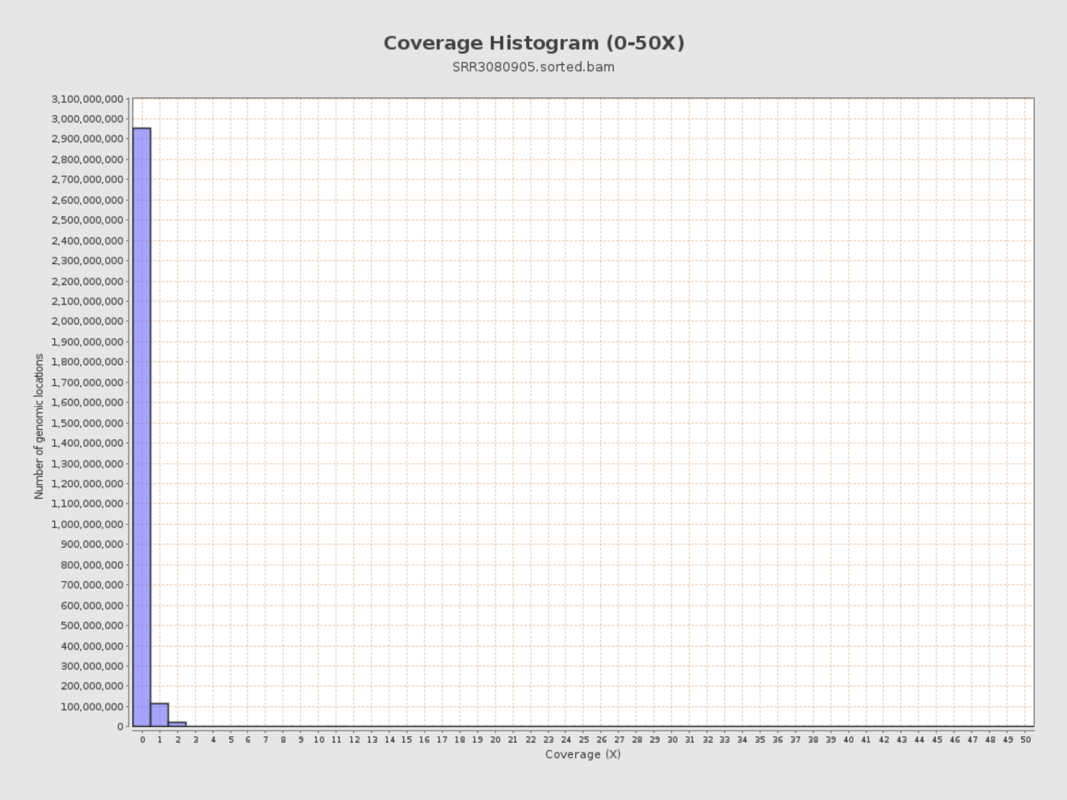
3. Results : Coverage across reference



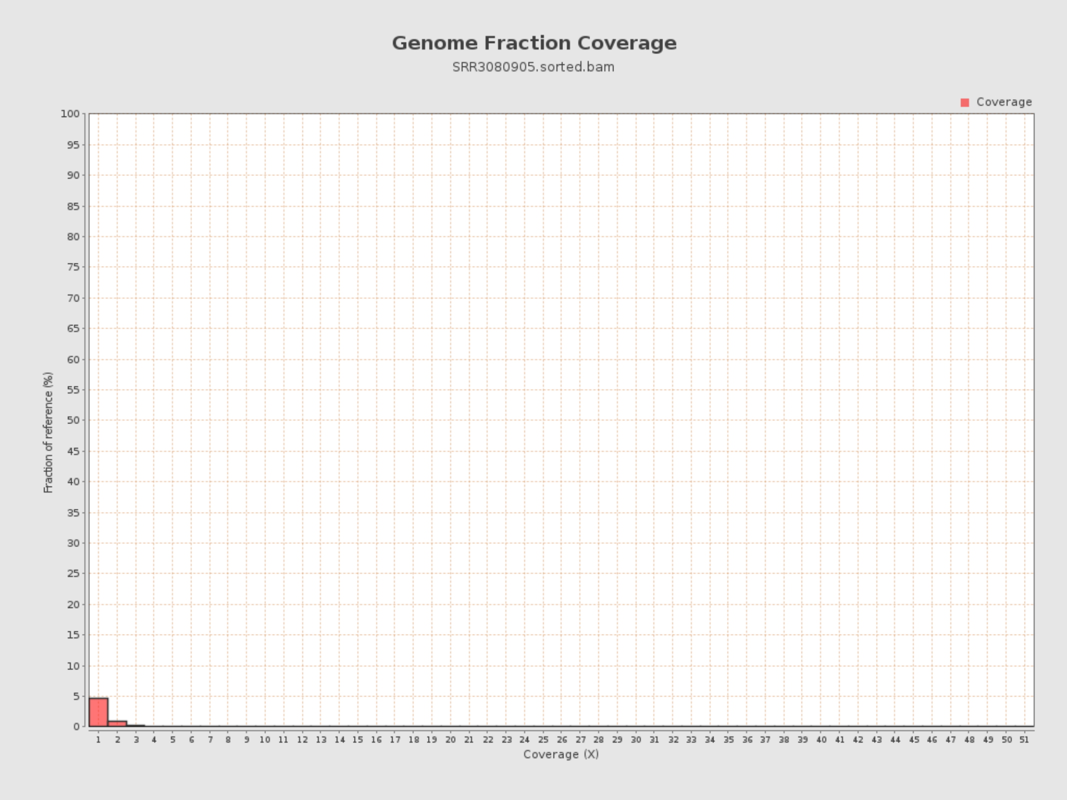
4. Results : Coverage Histogram



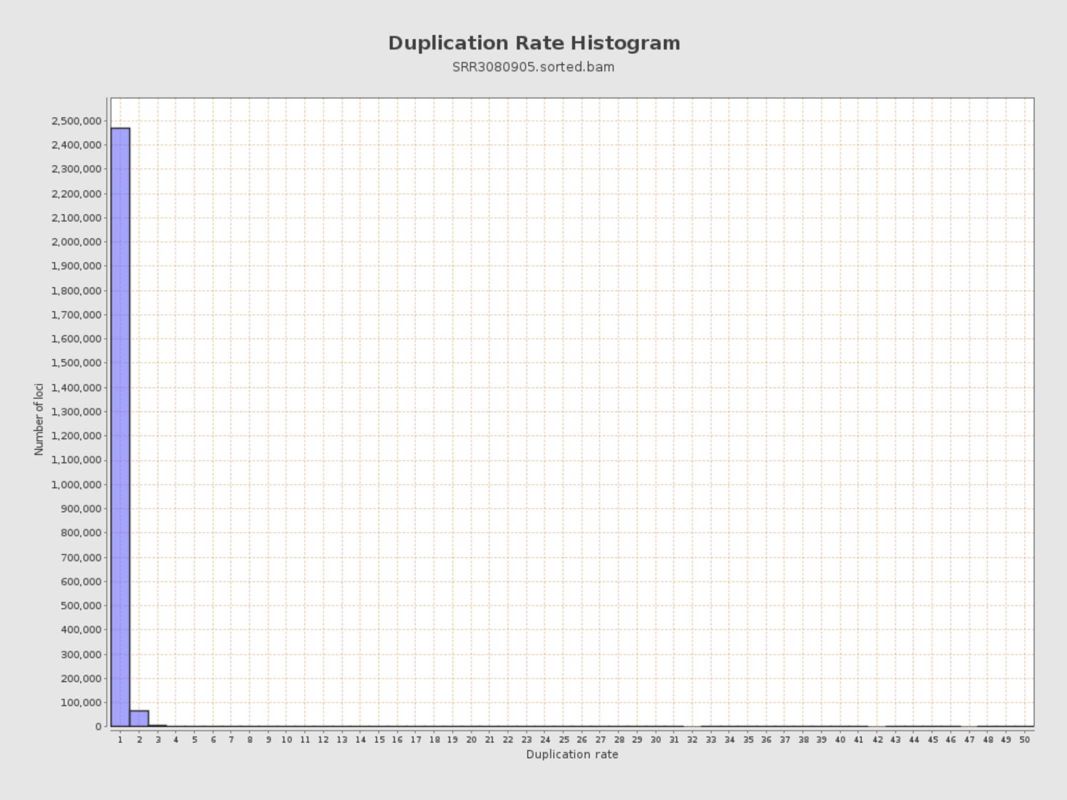
5. Results : Coverage Histogram (0-50X)



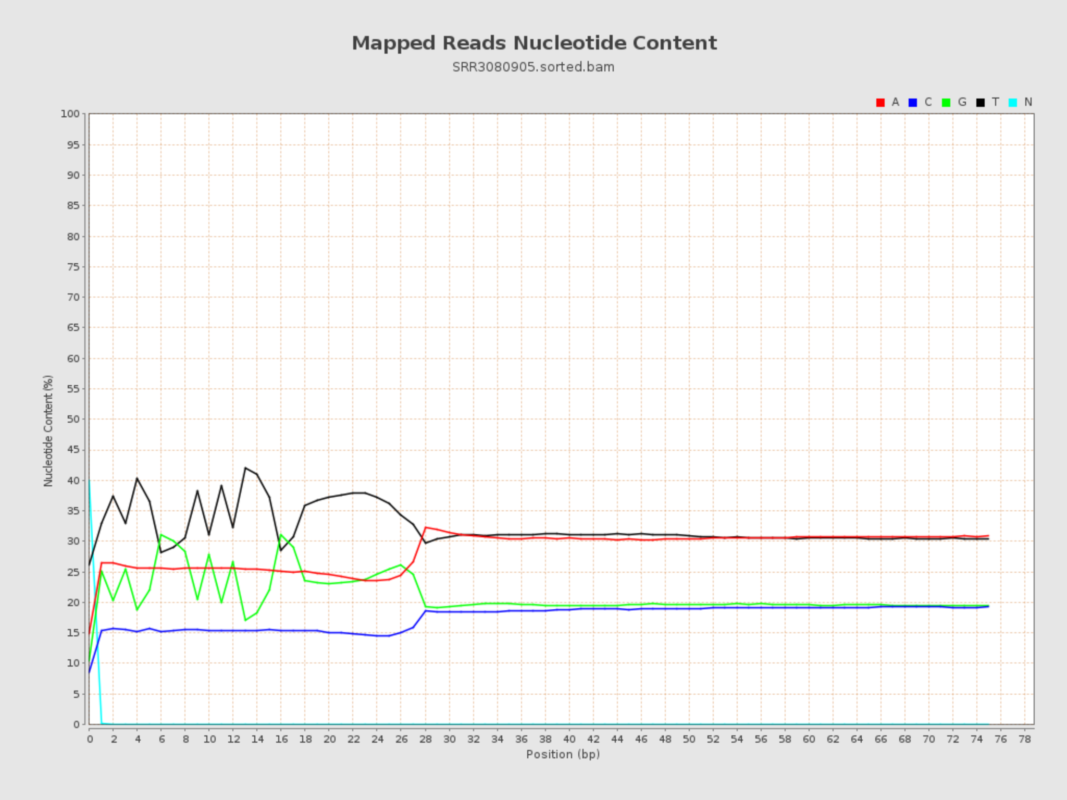
6. Results : Genome Fraction Coverage



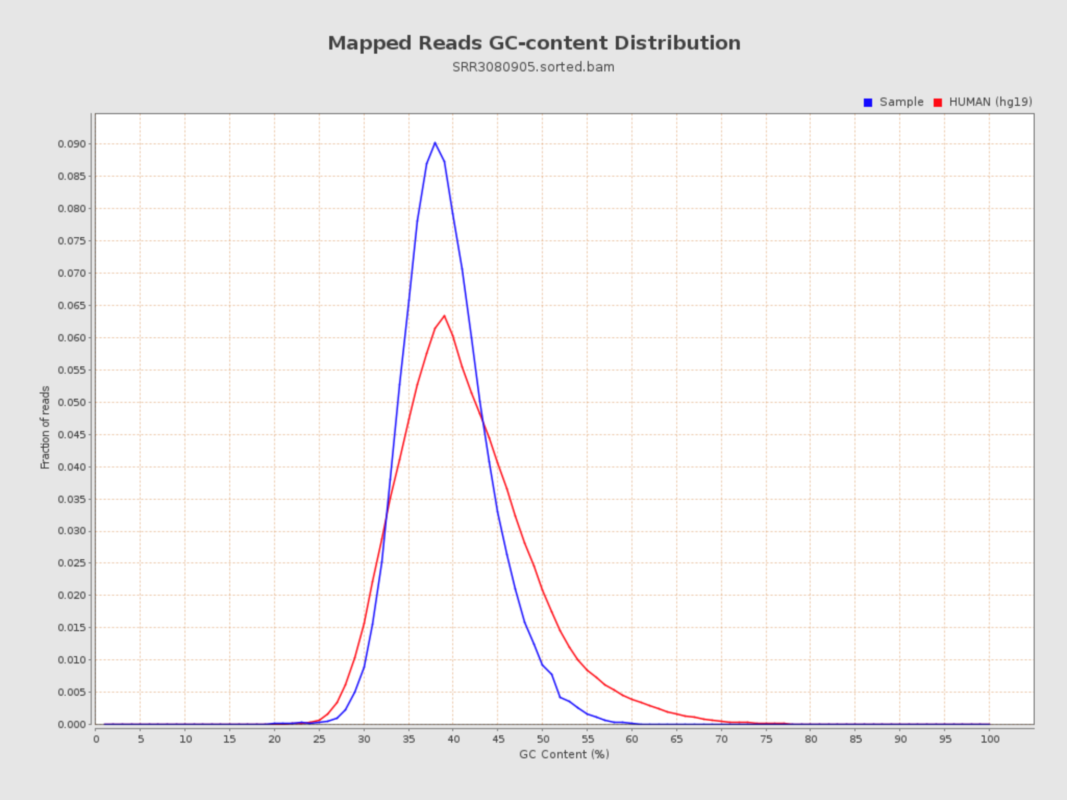
7. Results : Duplication Rate Histogram



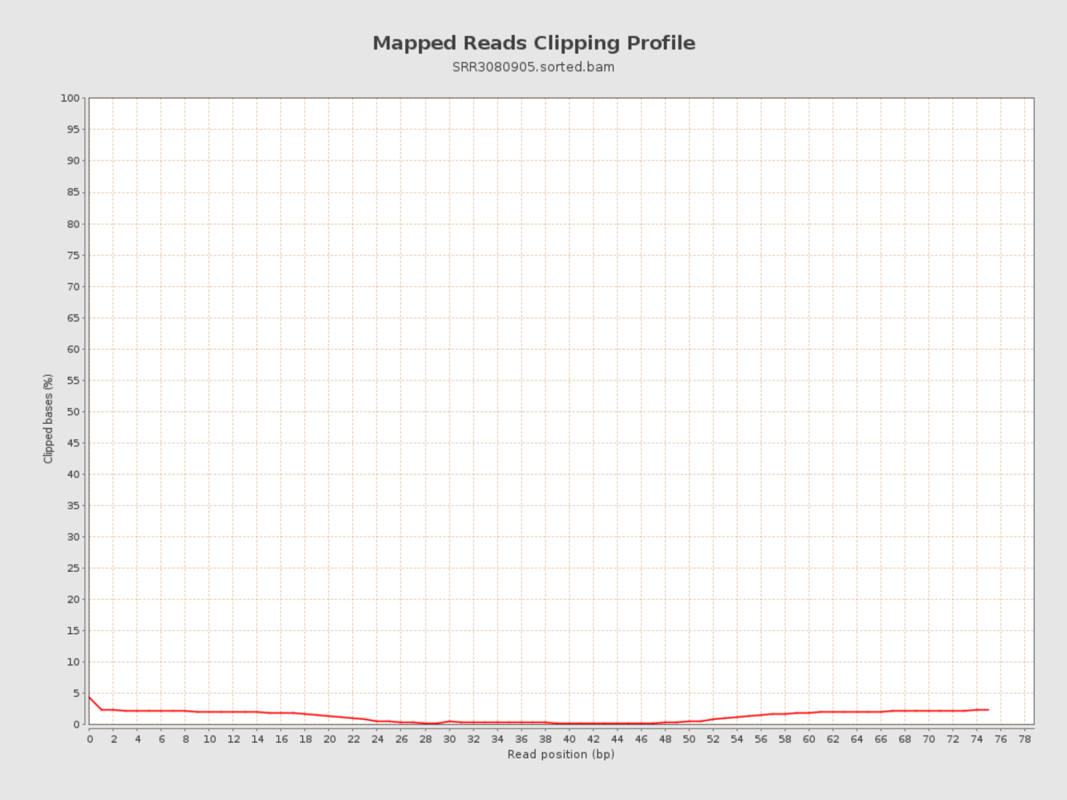
8. Results : Mapped Reads Nucleotide Content



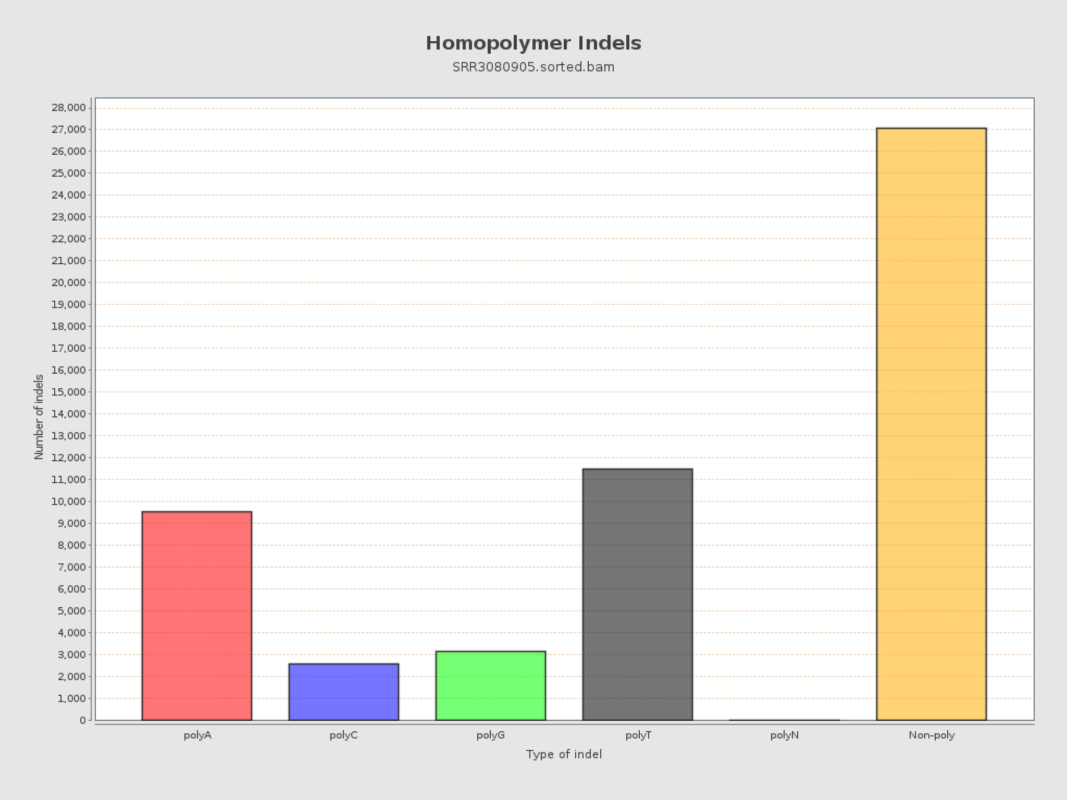
9. Results : Mapped Reads GC-content Distribution



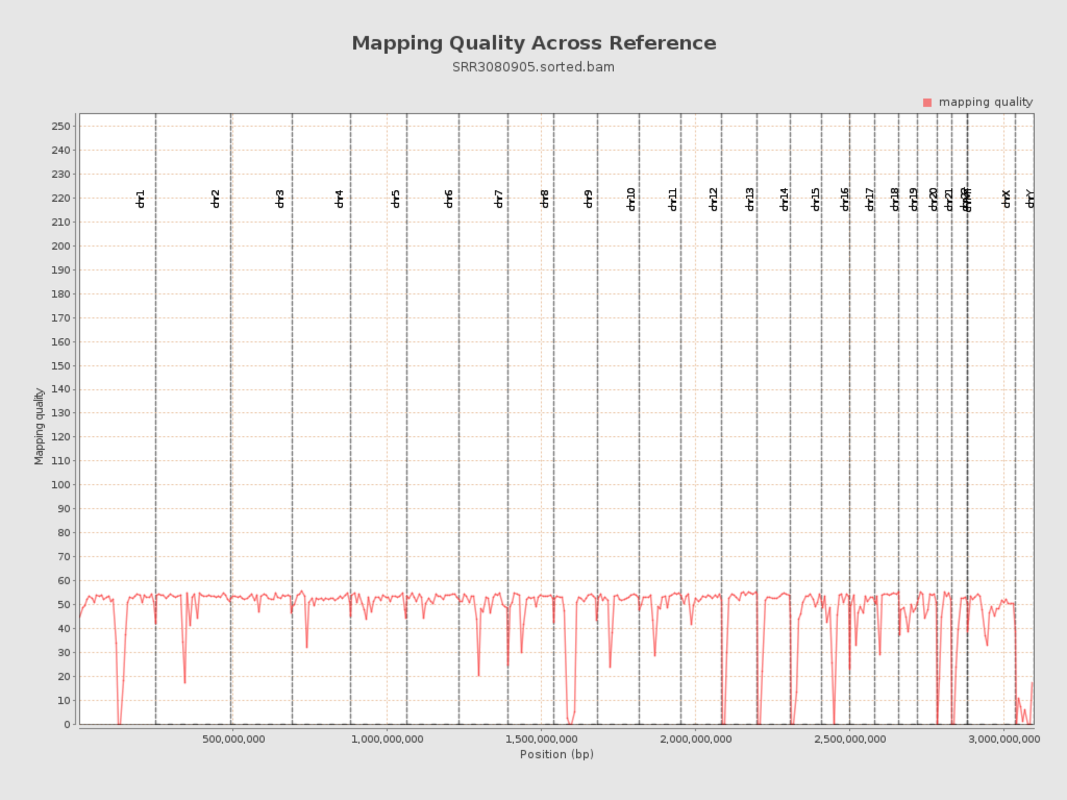
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram