Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:23:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080998.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_SRR3080998 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080998.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:23:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080998.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,213,869
Mapped reads	2,836,886 / 88.27%
Unmapped reads	376,983 / 11.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,397 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	121,073 / 3.77%
Duplication rate	3.55%
Clipped reads	1,520,855 / 47.32%

2.2. ACGT Content

Number/percentage of A's	50,990,213 / 27.93%
Number/percentage of C's	36,545,839 / 20.02%
Number/percentage of T's	54,109,960 / 29.64%
Number/percentage of G's	40,897,750 / 22.4%
Number/percentage of N's	2,294 / 0%
GC Percentage	42.42%

2.3. Coverage

Mean	0.059

Standard Deviation	0.3758

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

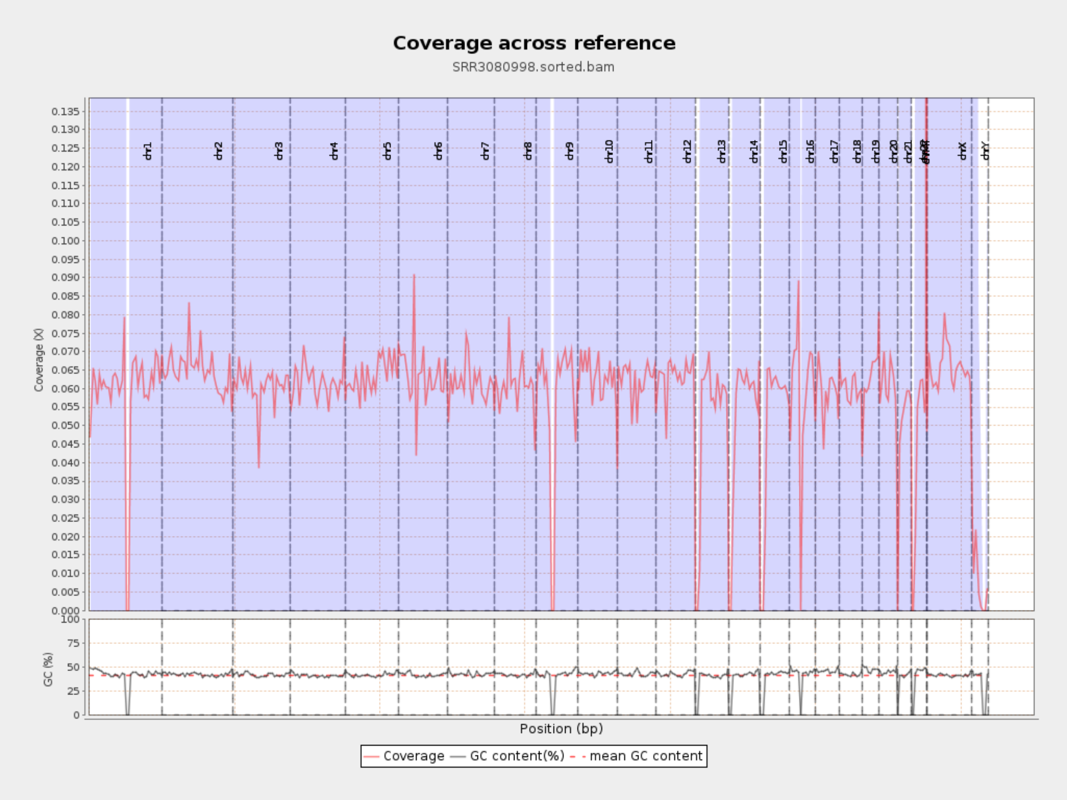
General error rate	0.73%
Mismatches	1,303,756
Insertions	12,310
Mapped reads with at least one insertion	0.43%
Deletions	34,668
Mapped reads with at least one deletion	1.21%
Homopolymer indels	46.83%

2.6. Chromosome stats

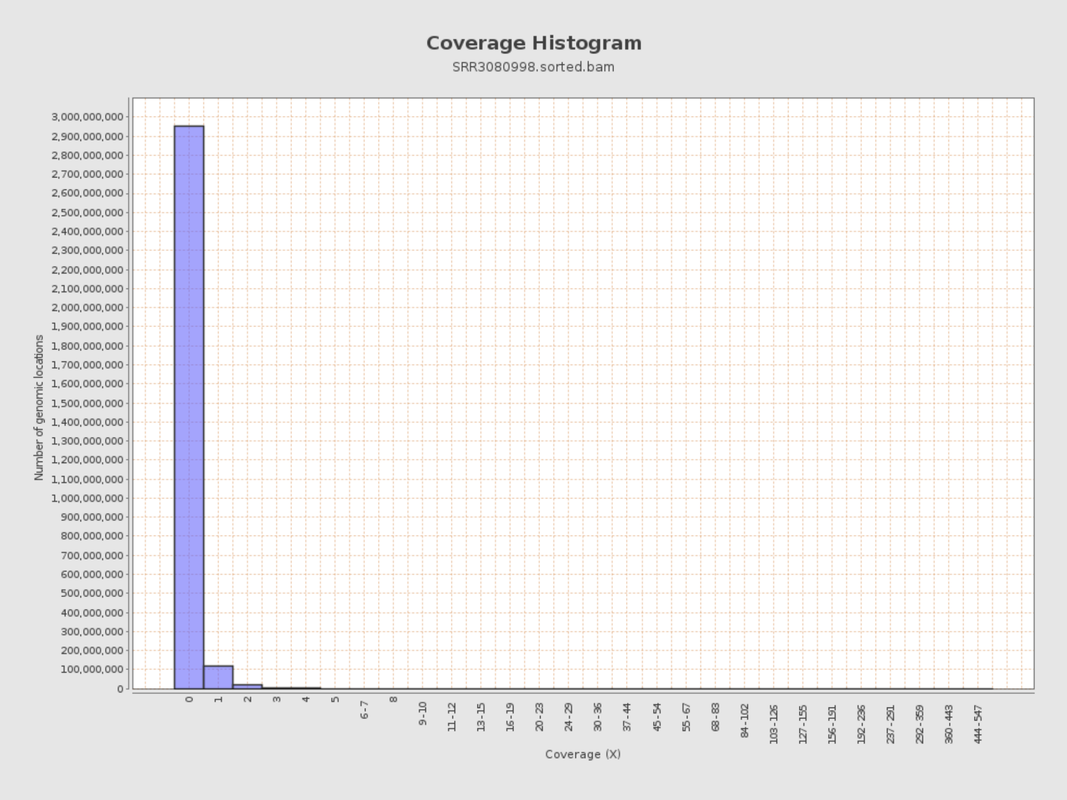
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14553988	0.0584	0.5483
chr2	243199373	15836969	0.0651	0.4232
chr3	198022430	11999221	0.0606	0.3003
chr4	191154276	11809049	0.0618	0.3172
chr5	180915260	11493747	0.0635	0.3078
chr6	171115067	10936909	0.0639	0.399
chr7	159138663	9805411	0.0616	0.4751

chr8	146364022	8914217	0.0609	0.3889
chr9	141213431	7949129	0.0563	0.3539
chr10	135534747	8618774	0.0636	0.3614
chr11	135006516	8361711	0.0619	0.3624
chr12	133851895	8444680	0.0631	0.3078
chr13	115169878	5802212	0.0504	0.2735
chr14	107349540	5478573	0.051	0.2856
chr15	102531392	5107141	0.0498	0.2847
chr16	90354753	5383091	0.0596	0.3229
chr17	81195210	4772085	0.0588	0.3146
chr18	78077248	4720138	0.0605	0.5824
chr19	59128983	3737127	0.0632	0.4352
chr20	63025520	3836609	0.0609	0.3103
chr21	48129895	2365979	0.0492	0.2904
chr22	51304566	2069418	0.0403	0.2434
chrMT	16571	48785	2.944	2.3383
chrX	155270560	10119813	0.0652	0.3353
chrY	59373566	442152	0.0074	0.1556

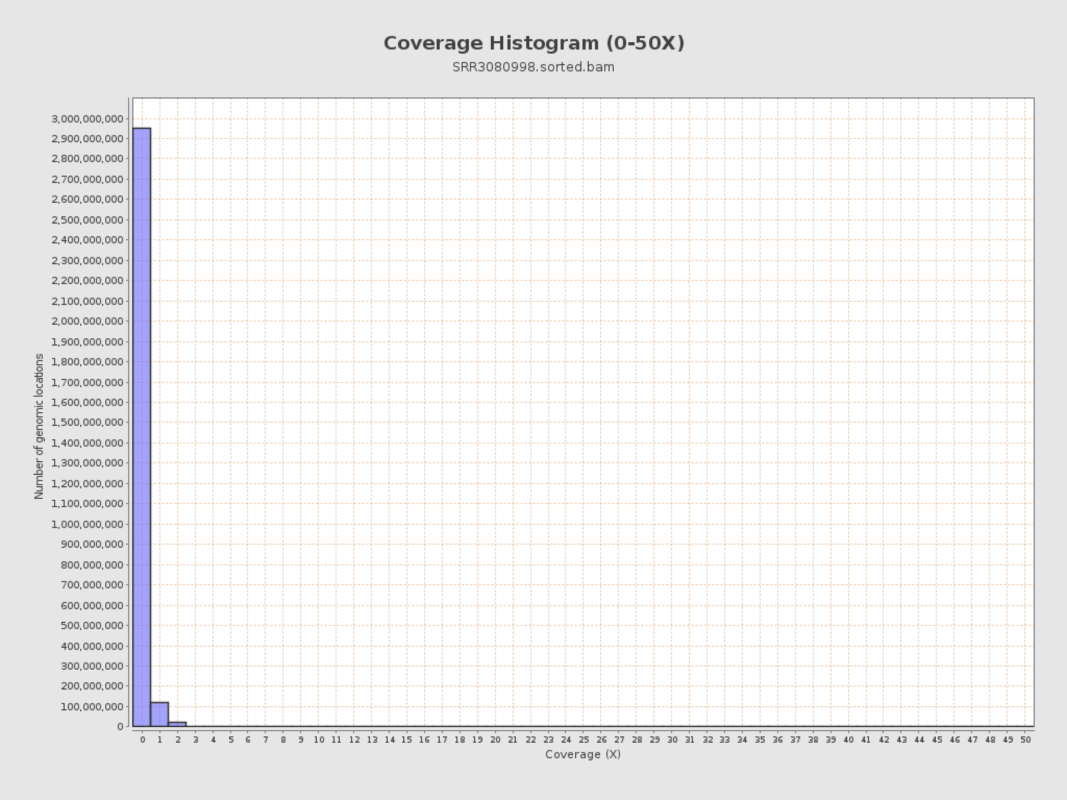
3. Results : Coverage across reference



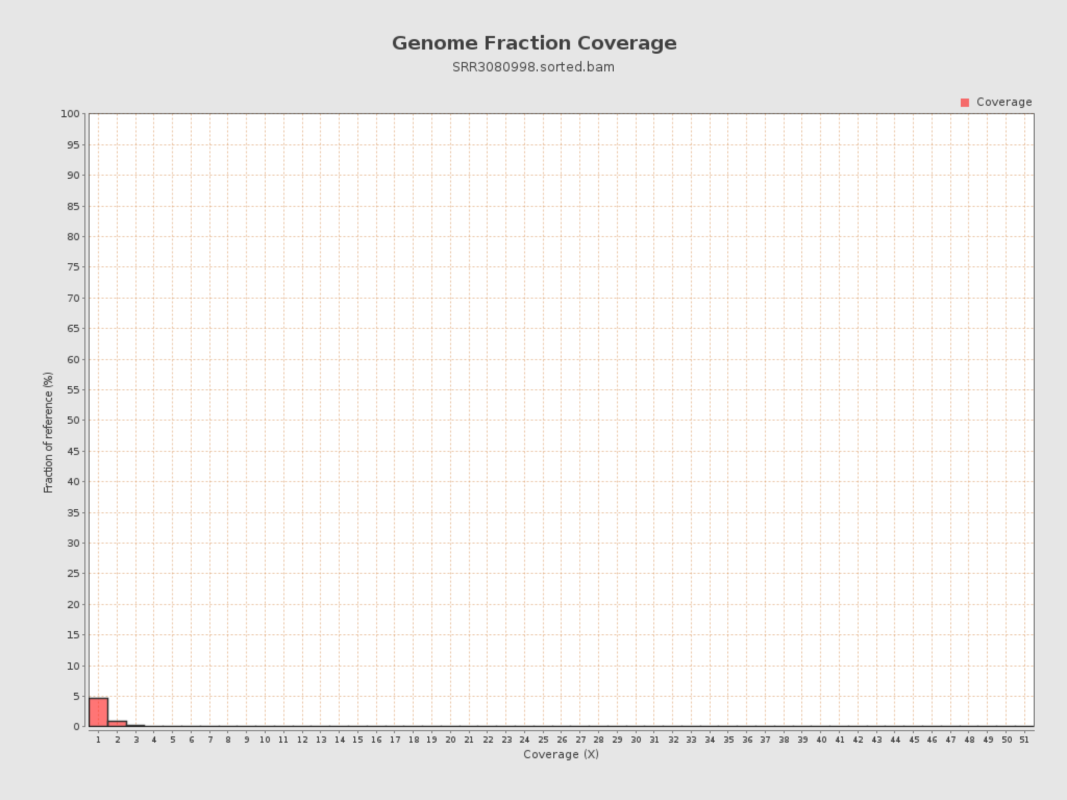
4. Results : Coverage Histogram



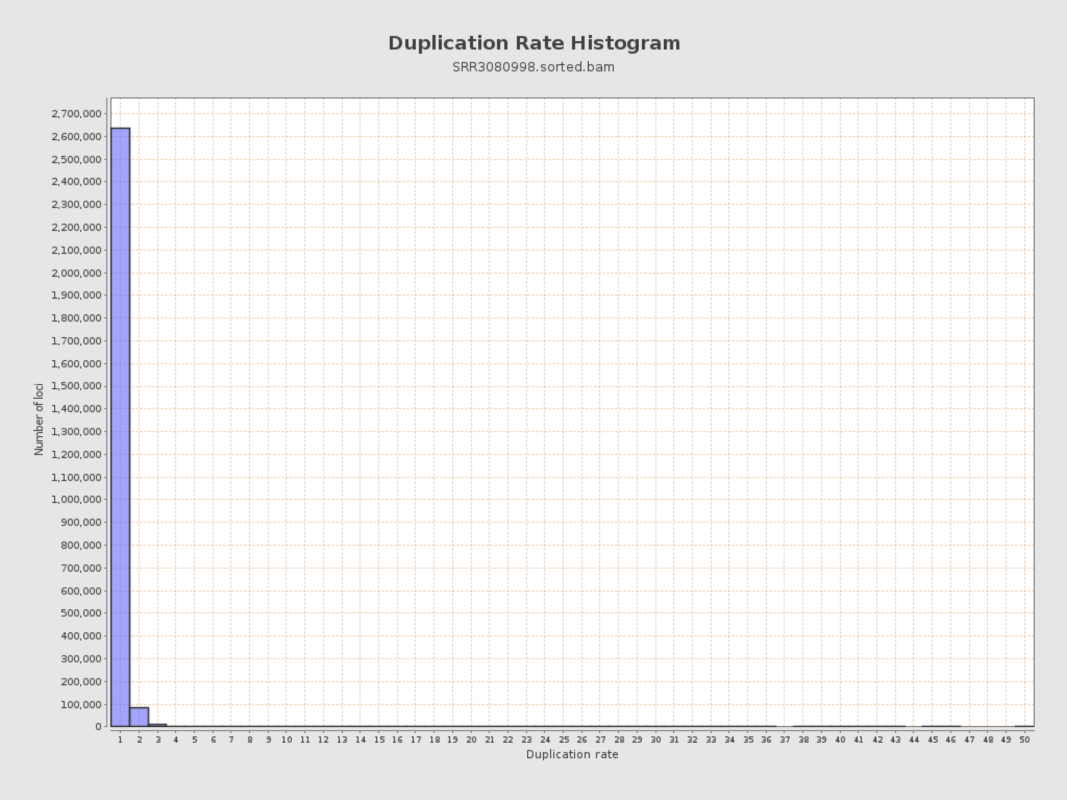
5. Results : Coverage Histogram (0-50X)



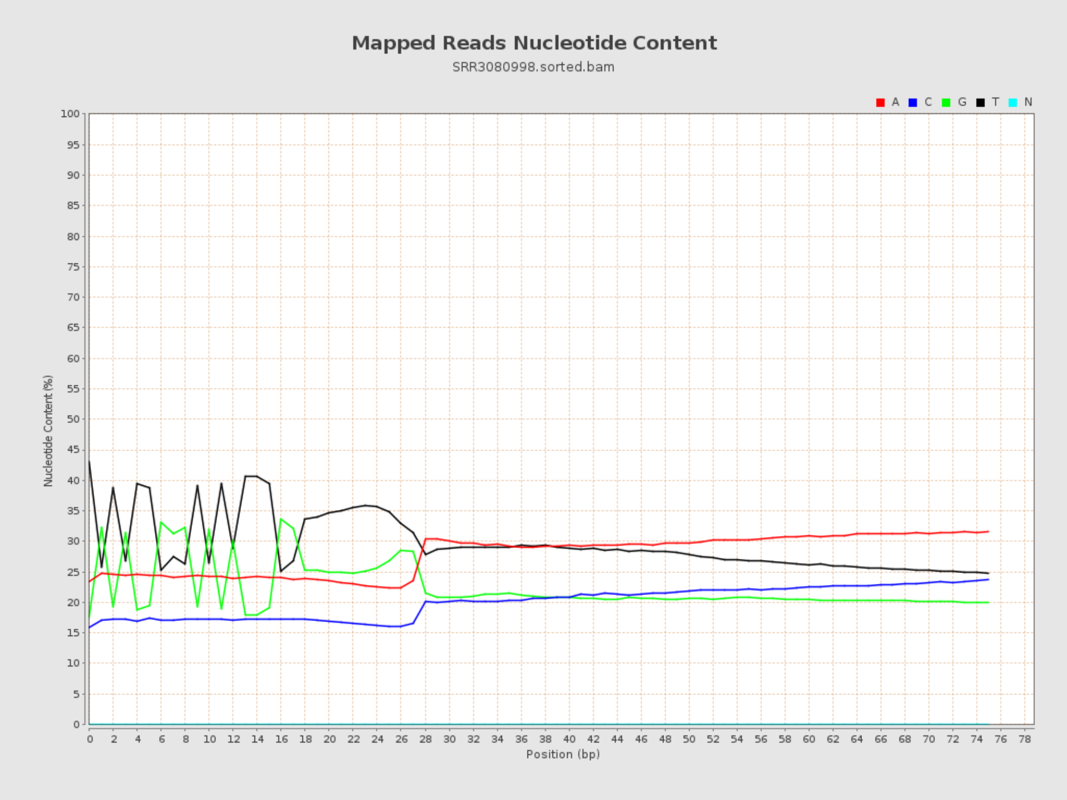
6. Results : Genome Fraction Coverage



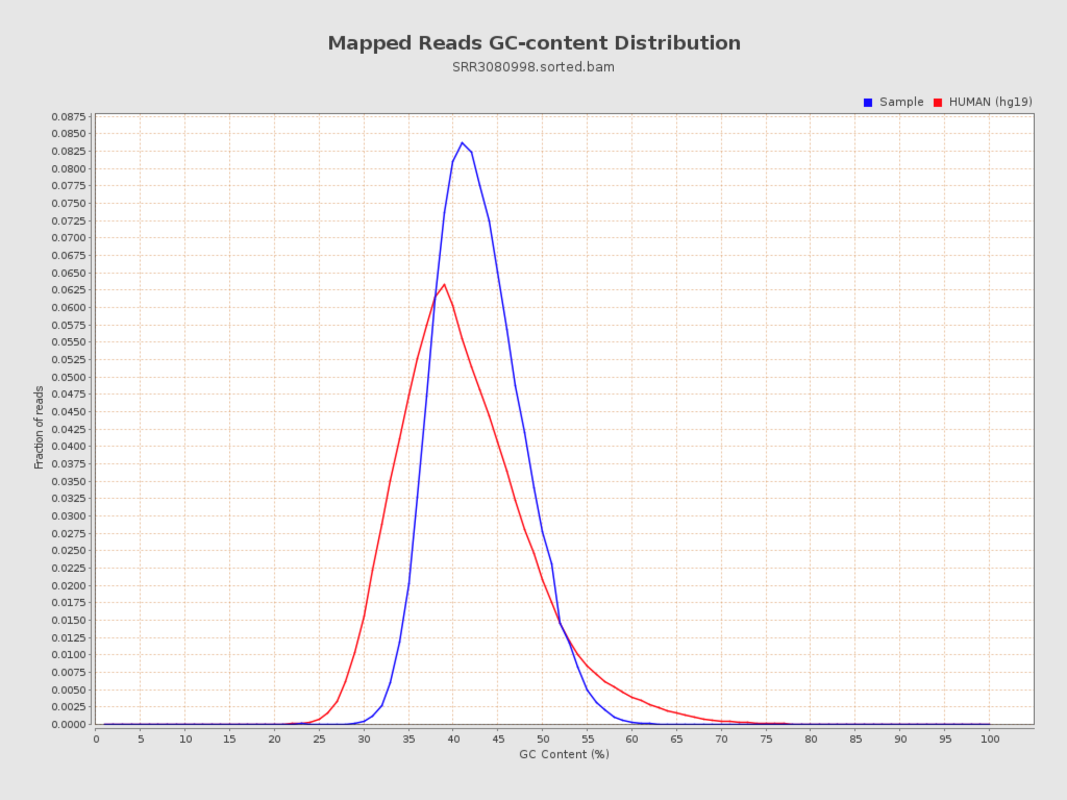
7. Results : Duplication Rate Histogram



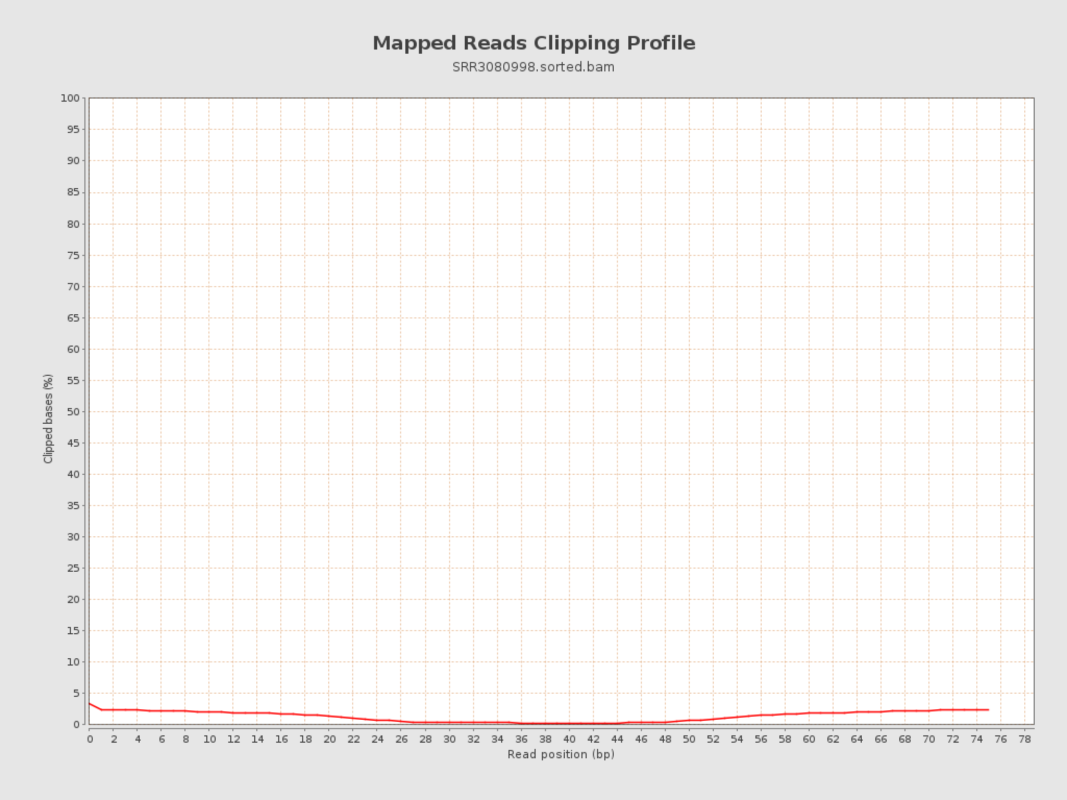
8. Results : Mapped Reads Nucleotide Content



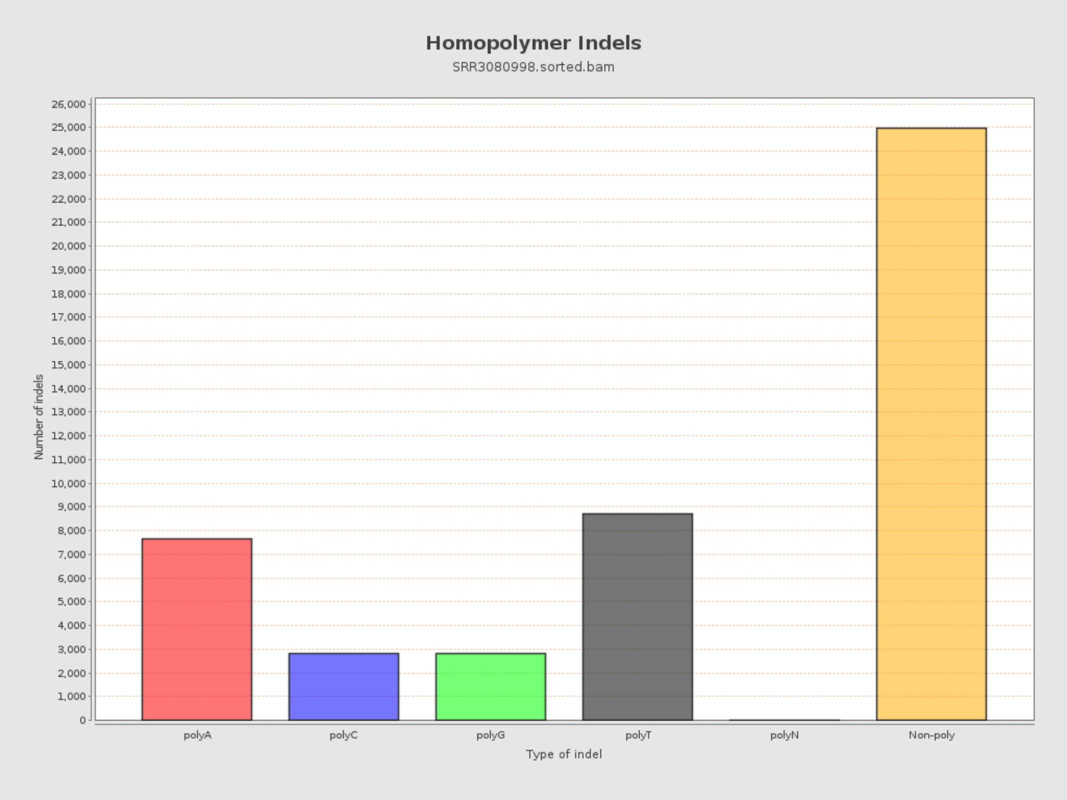
9. Results : Mapped Reads GC-content Distribution



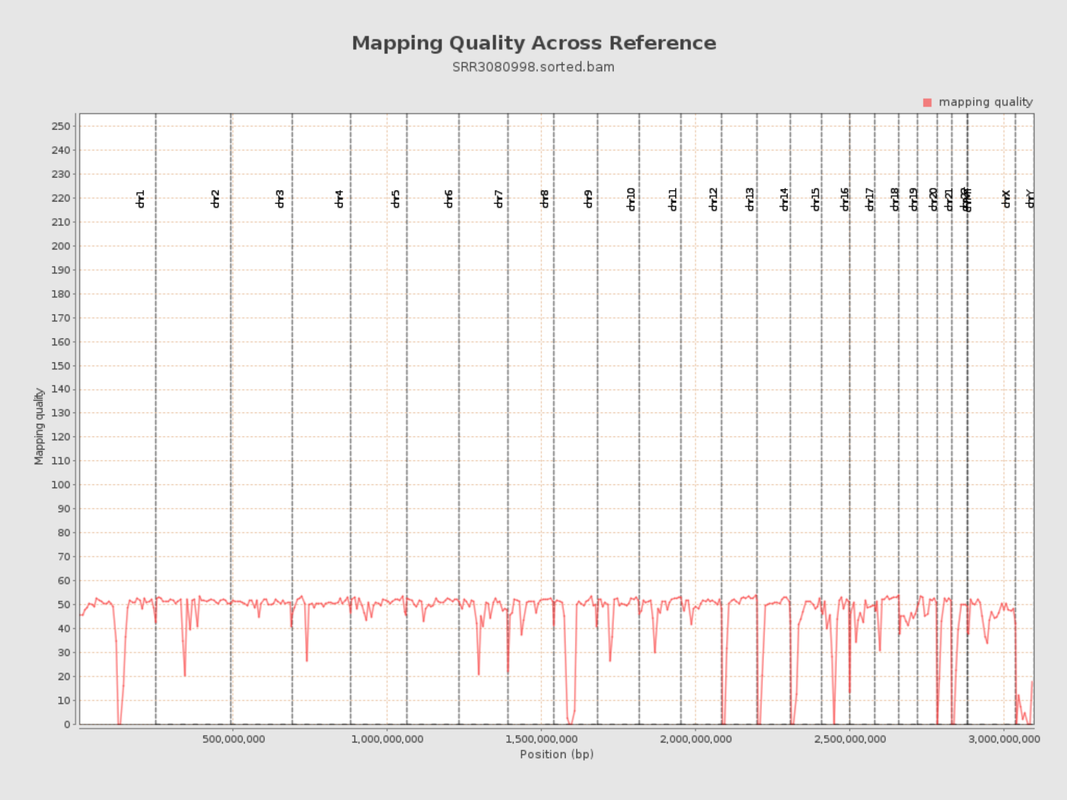
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram