Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:16:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080996.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_SRR3080996 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080996.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:16:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080996.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,526,304
Mapped reads	3,035,248 / 86.07%
Unmapped reads	491,056 / 13.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,636 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	133,960 / 3.8%
Duplication rate	3.62%
Clipped reads	1,614,694 / 45.79%

2.2. ACGT Content

Number/percentage of A's	54,712,020 / 28%
Number/percentage of C's	39,012,988 / 19.96%
Number/percentage of T's	58,024,755 / 29.69%
Number/percentage of G's	43,657,608 / 22.34%
Number/percentage of N's	2,580 / 0%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0631

Standard Deviation	0.398

2.4. Mapping Quality

Mean Mapping Quality	45.95

2.5. Mismatches and indels

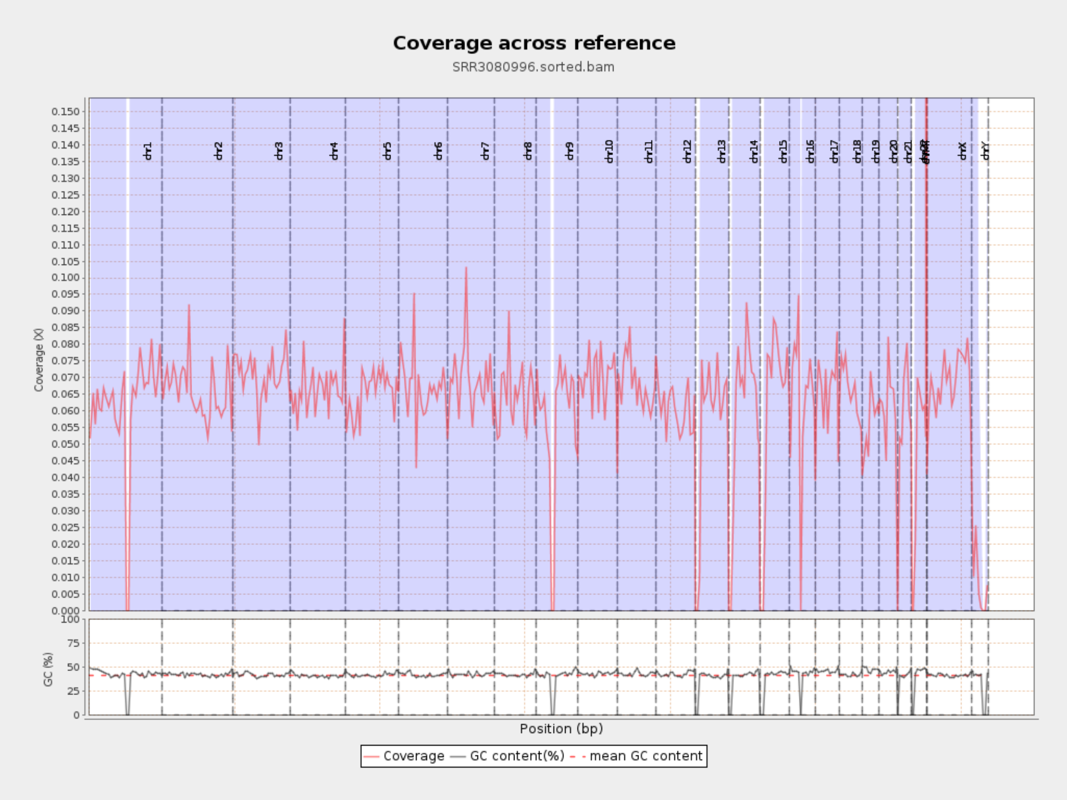
General error rate	0.74%
Mismatches	1,428,168
Insertions	13,015
Mapped reads with at least one insertion	0.43%
Deletions	39,609
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.44%

2.6. Chromosome stats

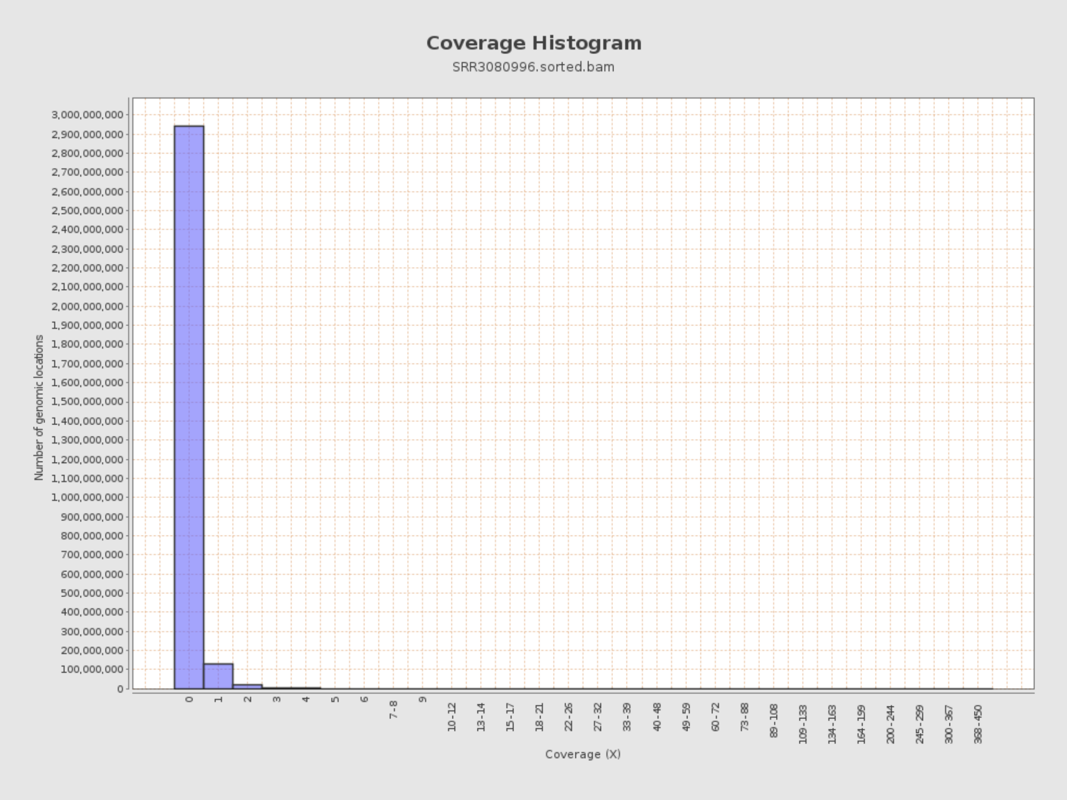
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15351406	0.0616	0.4969
chr2	243199373	16076158	0.0661	0.4454
chr3	198022430	14068280	0.071	0.3193
chr4	191154276	12716706	0.0665	0.3243
chr5	180915260	11805041	0.0653	0.3078
chr6	171115067	11486161	0.0671	0.4271
chr7	159138663	11030338	0.0693	0.6053

chr8	146364022	9396435	0.0642	0.4262
chr9	141213431	7983253	0.0565	0.3829
chr10	135534747	9572376	0.0706	0.3868
chr11	135006516	9159826	0.0678	0.4225
chr12	133851895	8109456	0.0606	0.3007
chr13	115169878	6371690	0.0553	0.2837
chr14	107349540	6291052	0.0586	0.3043
chr15	102531392	6293808	0.0614	0.3067
chr16	90354753	5791088	0.0641	0.3349
chr17	81195210	5398003	0.0665	0.3582
chr18	78077248	5184959	0.0664	0.6552
chr19	59128983	3349915	0.0567	0.4435
chr20	63025520	3852880	0.0611	0.3097
chr21	48129895	2691591	0.0559	0.3053
chr22	51304566	2250543	0.0439	0.2524
chrMT	16571	75691	4.5677	2.8393
chrX	155270560	10685950	0.0688	0.3514
chrY	59373566	487207	0.0082	0.1702

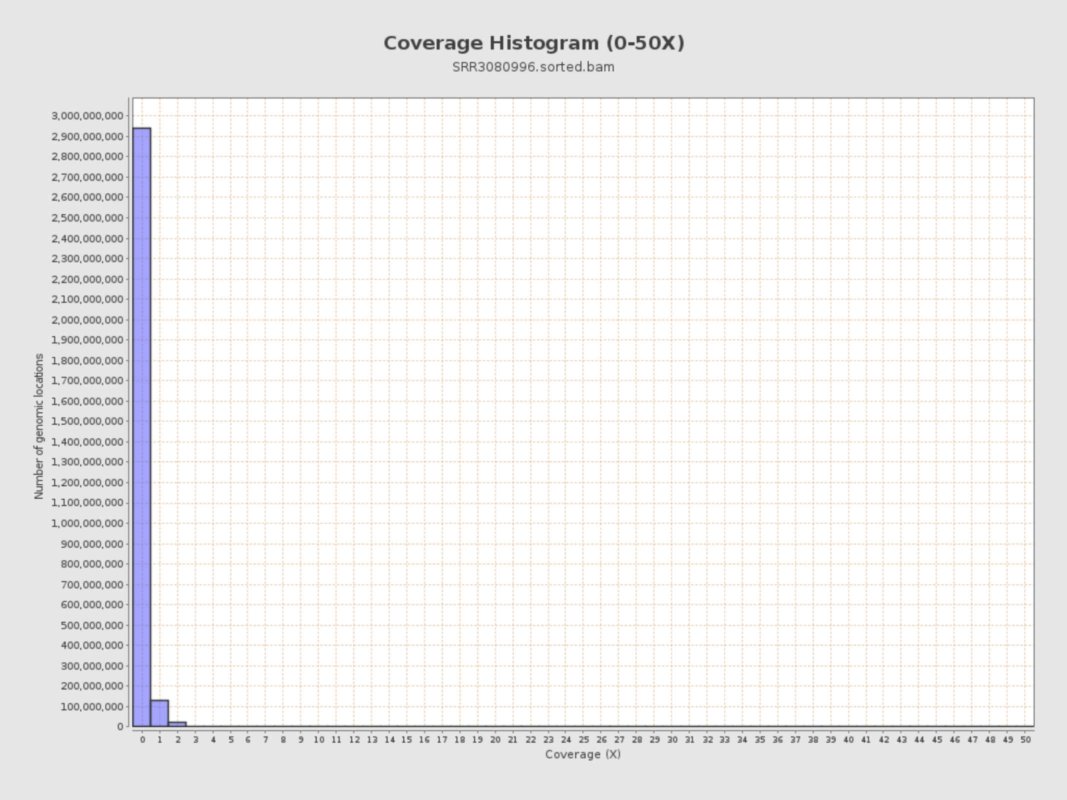
3. Results : Coverage across reference



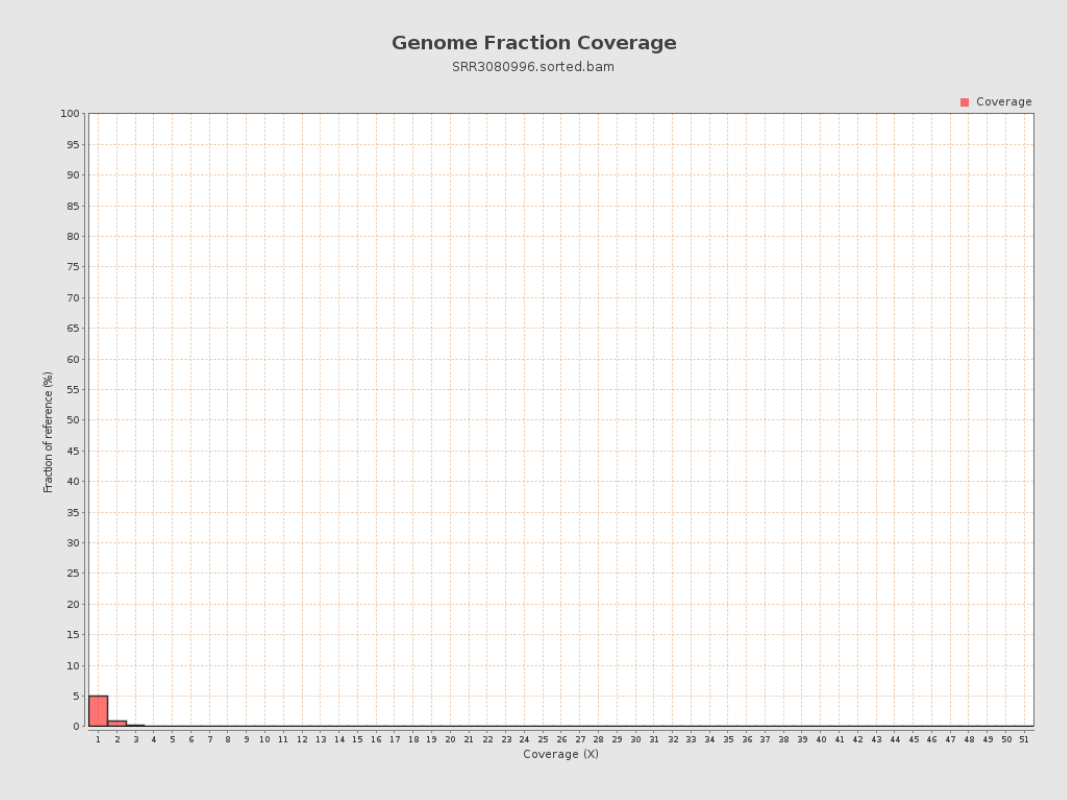
4. Results : Coverage Histogram



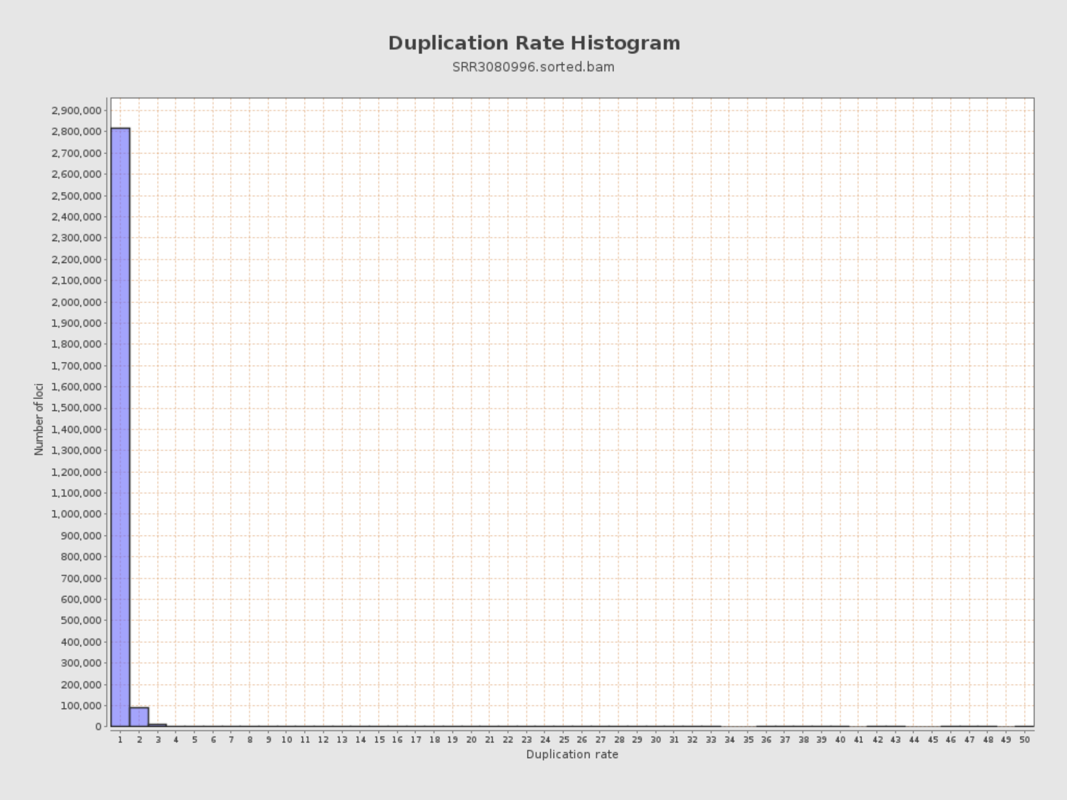
5. Results : Coverage Histogram (0-50X)



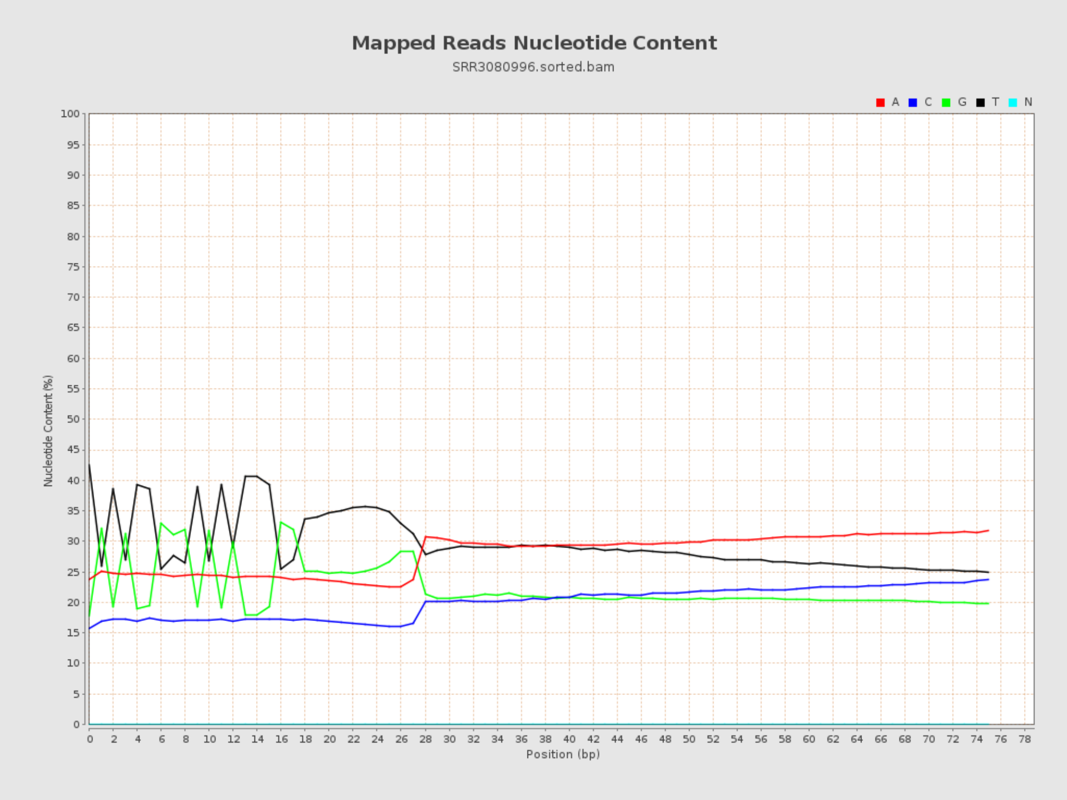
6. Results : Genome Fraction Coverage



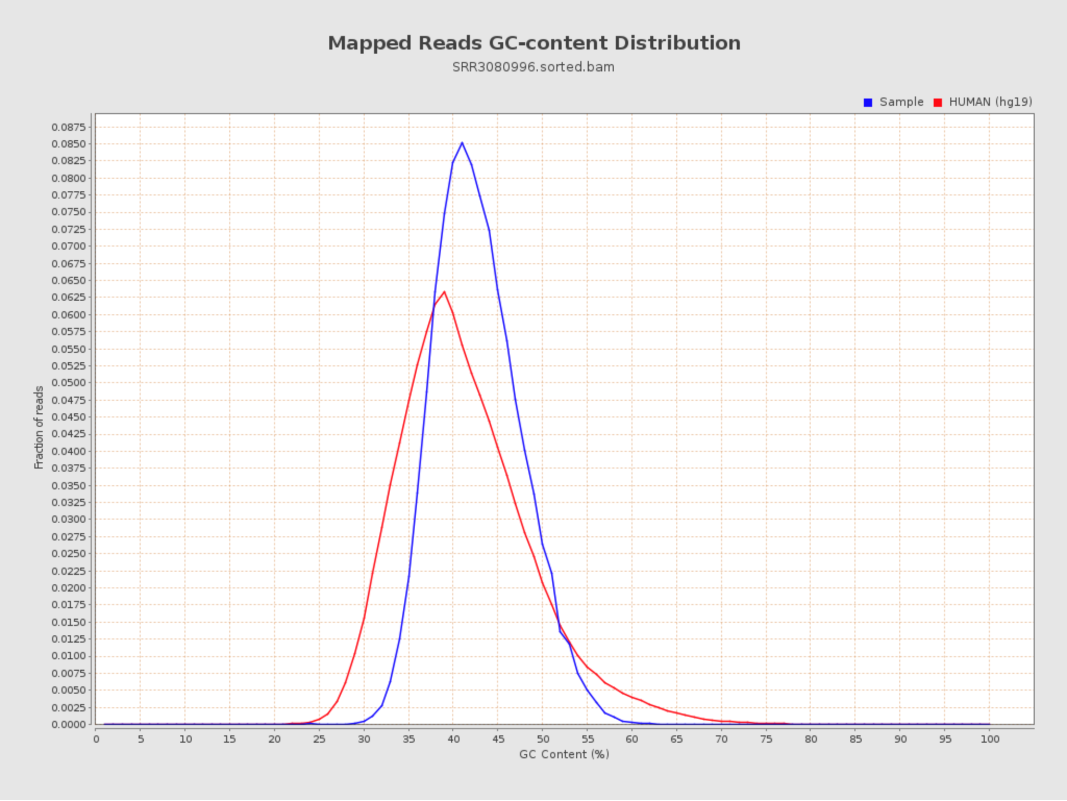
7. Results : Duplication Rate Histogram



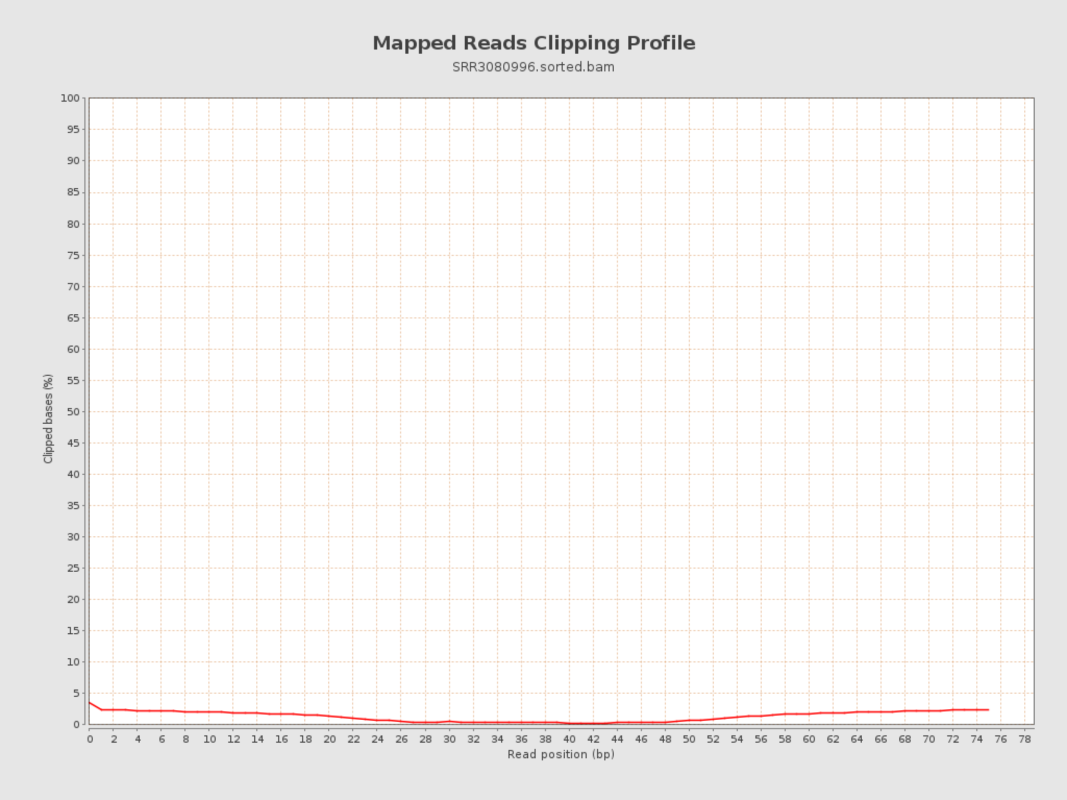
8. Results : Mapped Reads Nucleotide Content



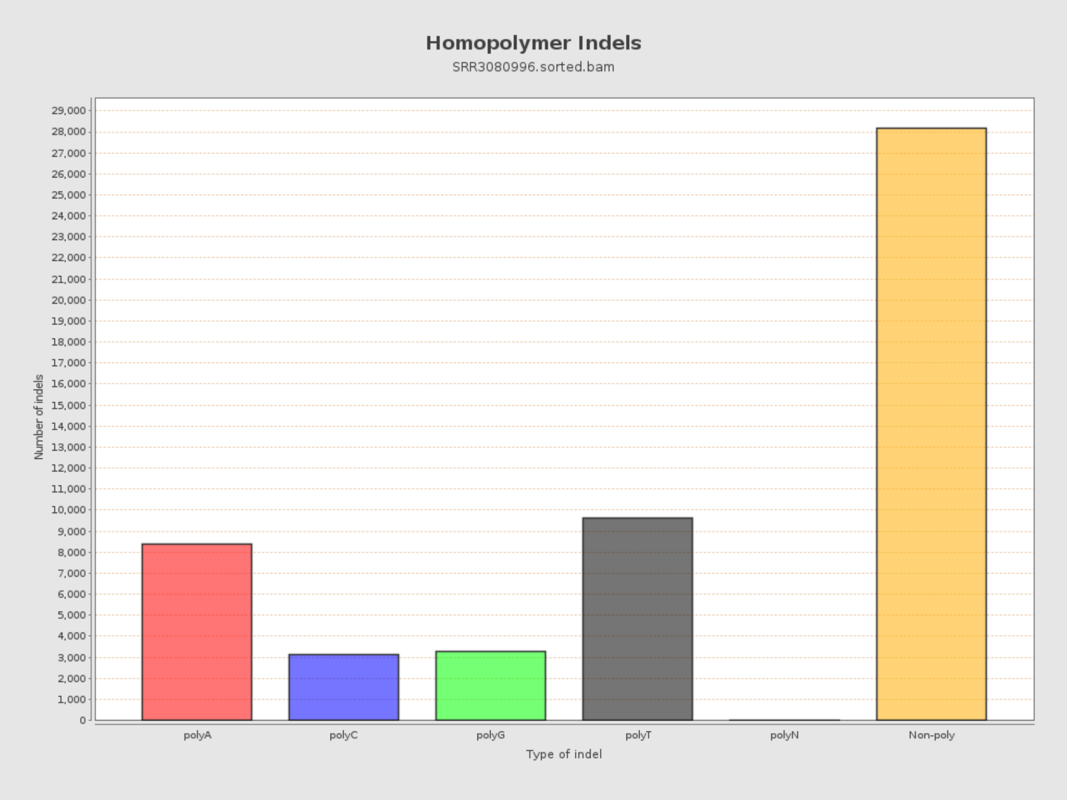
9. Results : Mapped Reads GC-content Distribution



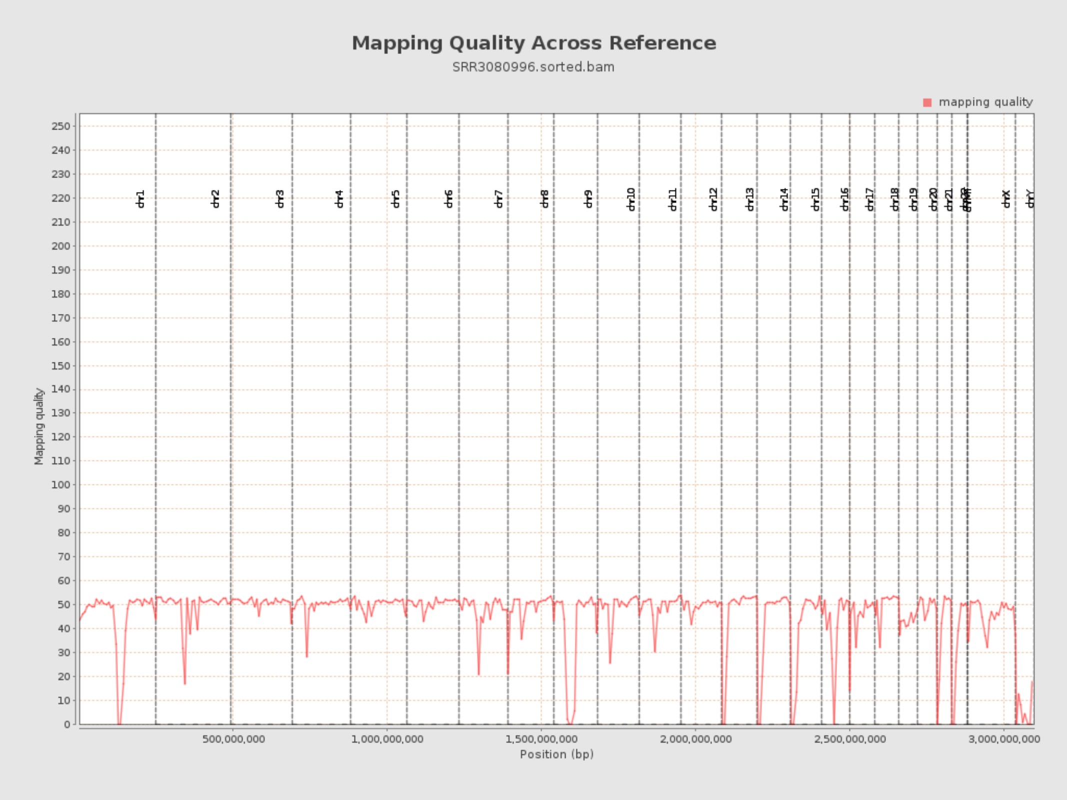
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram