Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:58:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080810.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_SRR3080810 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080810.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:58:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080810.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,636,127
Mapped reads	2,400,403 / 91.06%
Unmapped reads	235,724 / 8.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,985 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	156,014 / 5.92%
Duplication rate	5.49%
Clipped reads	943,290 / 35.78%

2.2. ACGT Content

Number/percentage of A's	46,646,923 / 28.57%
Number/percentage of C's	30,138,793 / 18.46%
Number/percentage of T's	51,883,852 / 31.78%
Number/percentage of G's	34,567,956 / 21.17%
Number/percentage of N's	23,068 / 0.01%
GC Percentage	39.63%

2.3. Coverage

Mean	0.0528

Standard Deviation	0.3908

2.4. Mapping Quality

Mean Mapping Quality	47.12

2.5. Mismatches and indels

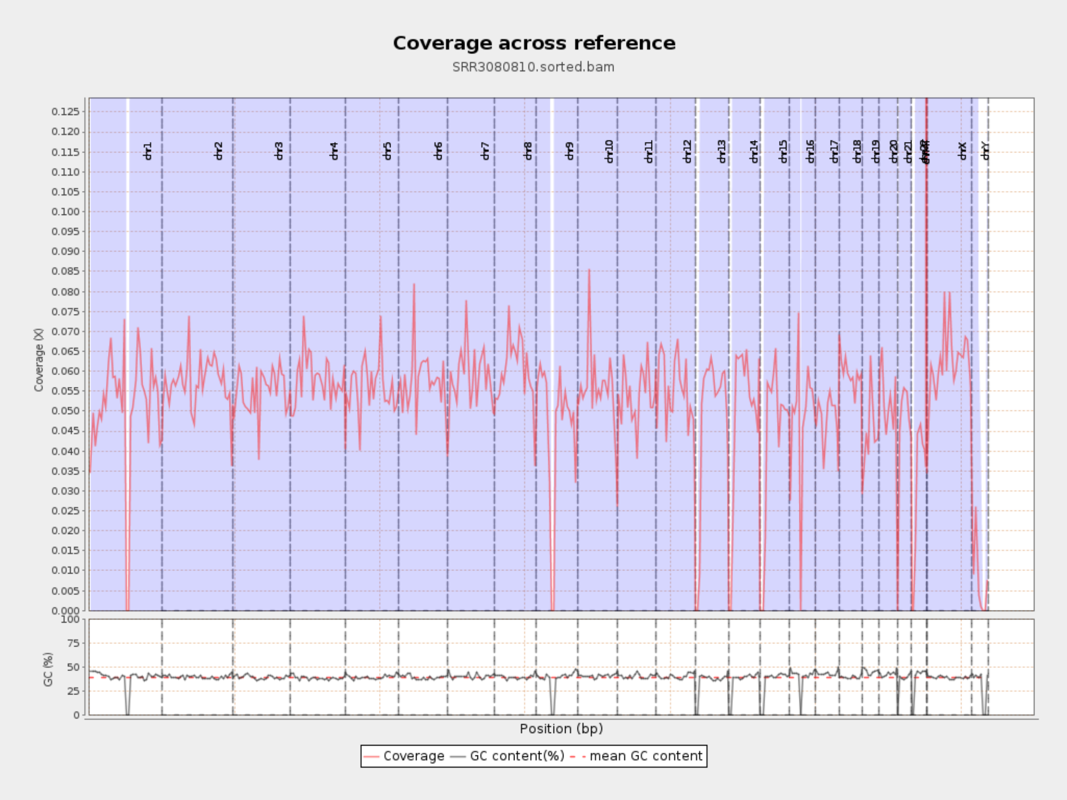
General error rate	0.83%
Mismatches	1,324,059
Insertions	12,294
Mapped reads with at least one insertion	0.51%
Deletions	35,743
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.99%

2.6. Chromosome stats

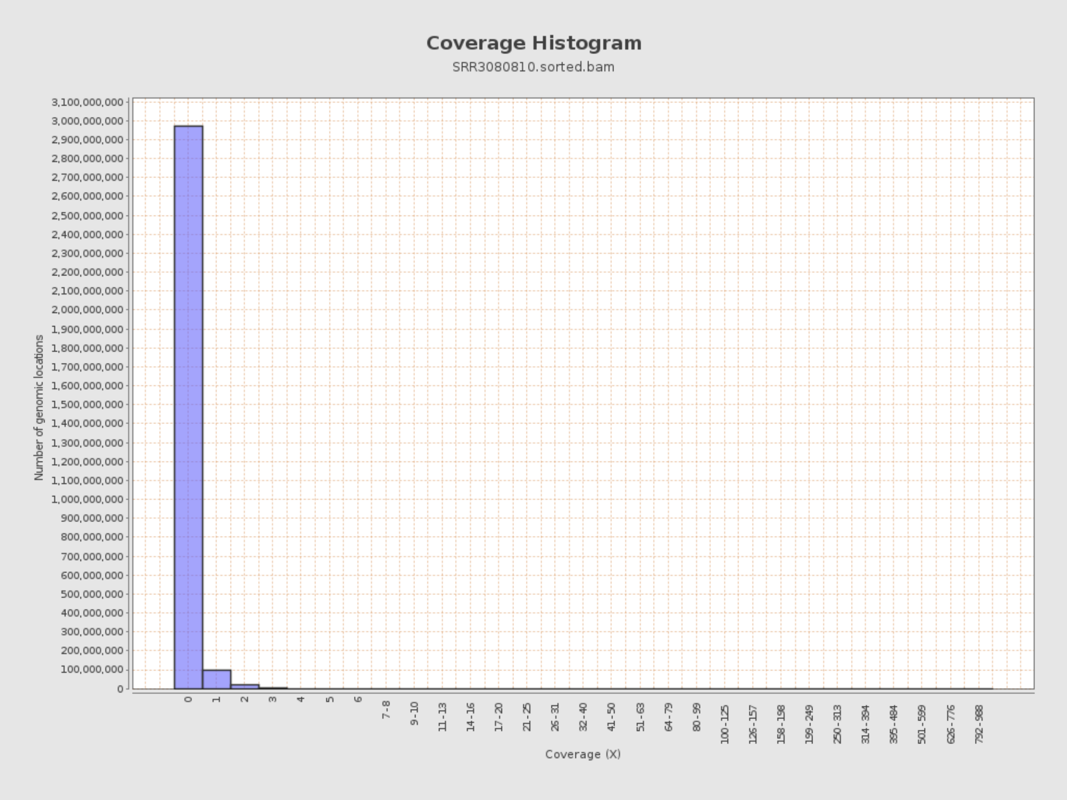
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12722412	0.051	0.5099
chr2	243199373	13984395	0.0575	0.4349
chr3	198022430	10902384	0.0551	0.2894
chr4	191154276	11065932	0.0579	0.3178
chr5	180915260	10151145	0.0561	0.2906
chr6	171115067	9847279	0.0575	0.3678
chr7	159138663	9404327	0.0591	0.5313

chr8	146364022	8794620	0.0601	0.6772
chr9	141213431	6481937	0.0459	0.335
chr10	135534747	7649030	0.0564	0.4384
chr11	135006516	7234698	0.0536	0.3144
chr12	133851895	7379905	0.0551	0.2933
chr13	115169878	5473454	0.0475	0.2683
chr14	107349540	5130684	0.0478	0.2766
chr15	102531392	4445046	0.0434	0.2551
chr16	90354753	4392835	0.0486	0.3029
chr17	81195210	3867744	0.0476	0.2812
chr18	78077248	4640098	0.0594	0.6126
chr19	59128983	2671263	0.0452	0.4396
chr20	63025520	3288394	0.0522	0.2874
chr21	48129895	2197448	0.0457	0.282
chr22	51304566	1532429	0.0299	0.2112
chrMT	16571	9622	0.5807	0.9765
chrX	155270560	9598358	0.0618	0.3233
chrY	59373566	458700	0.0077	0.2076

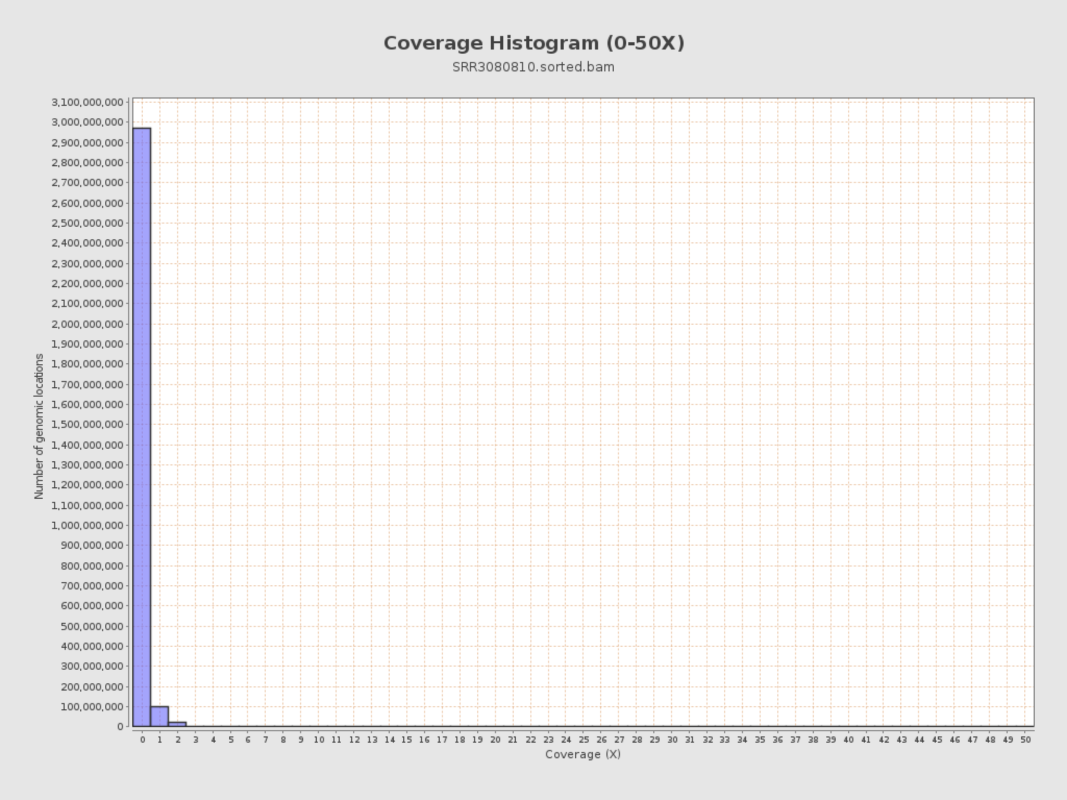
3. Results : Coverage across reference



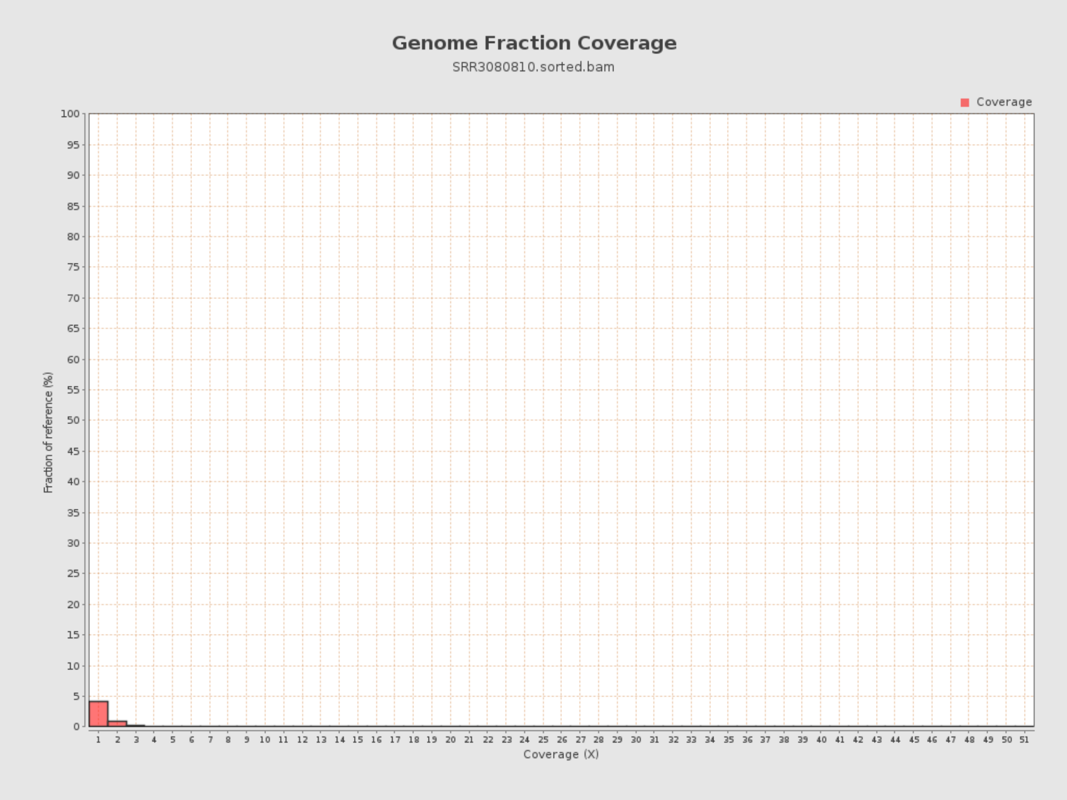
4. Results : Coverage Histogram



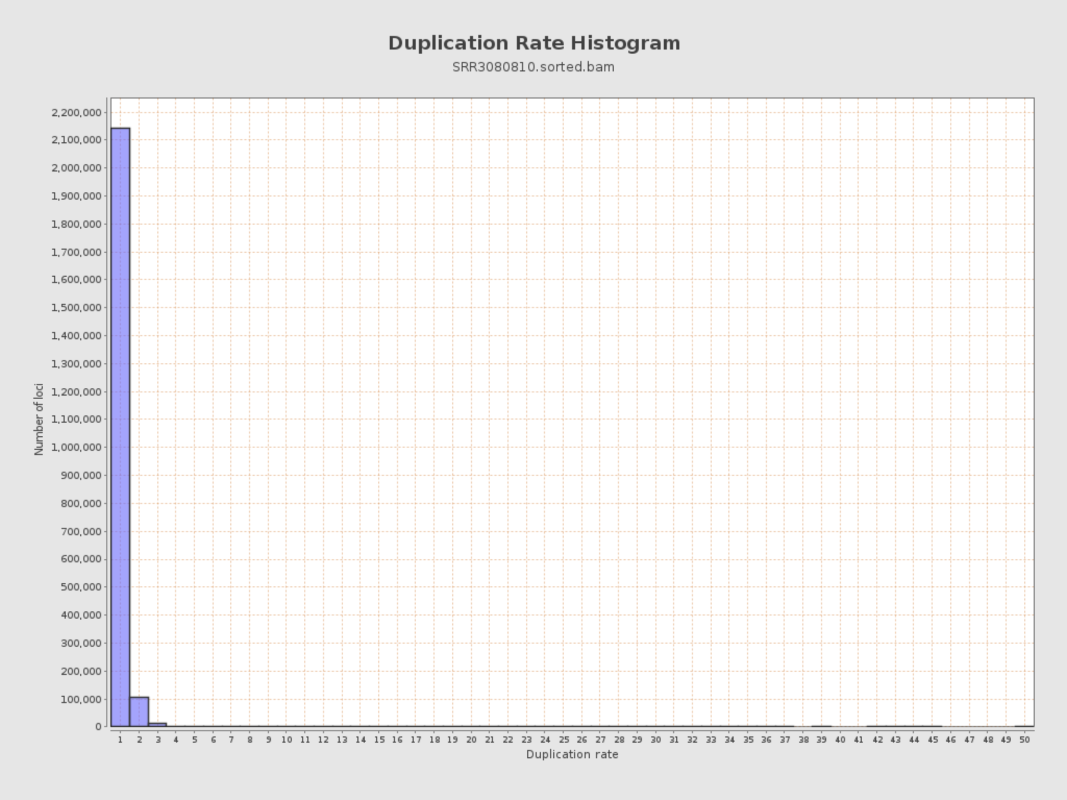
5. Results : Coverage Histogram (0-50X)



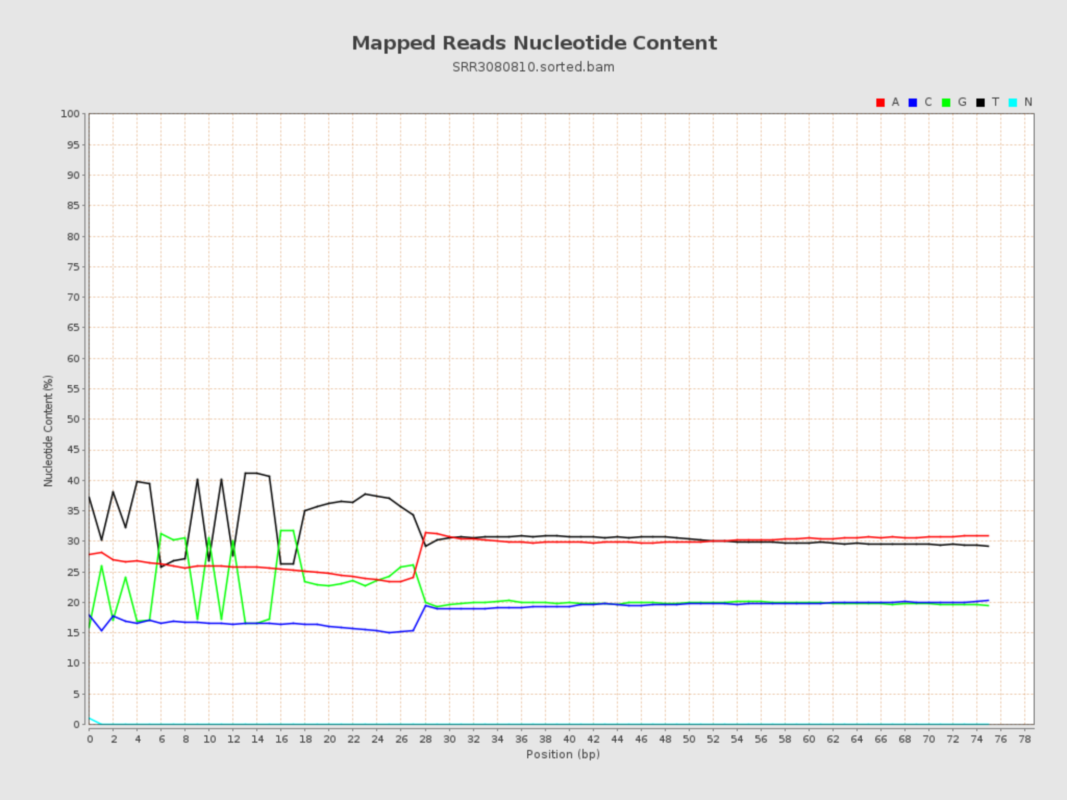
6. Results : Genome Fraction Coverage



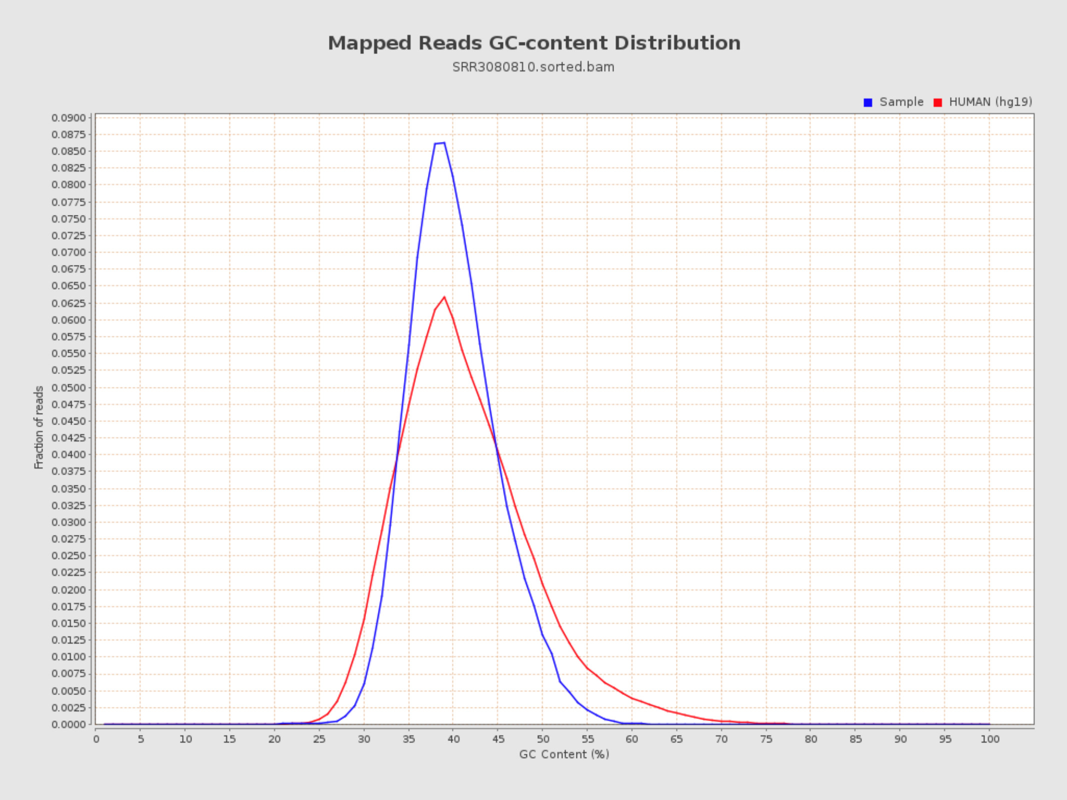
7. Results : Duplication Rate Histogram



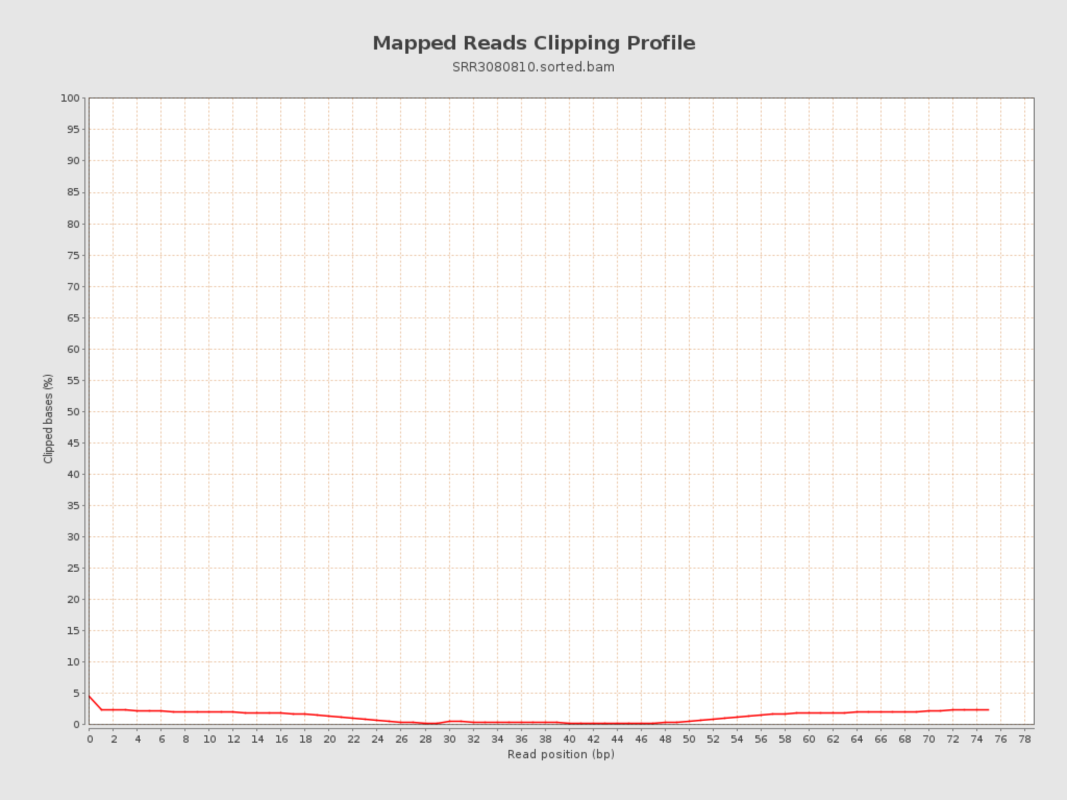
8. Results : Mapped Reads Nucleotide Content



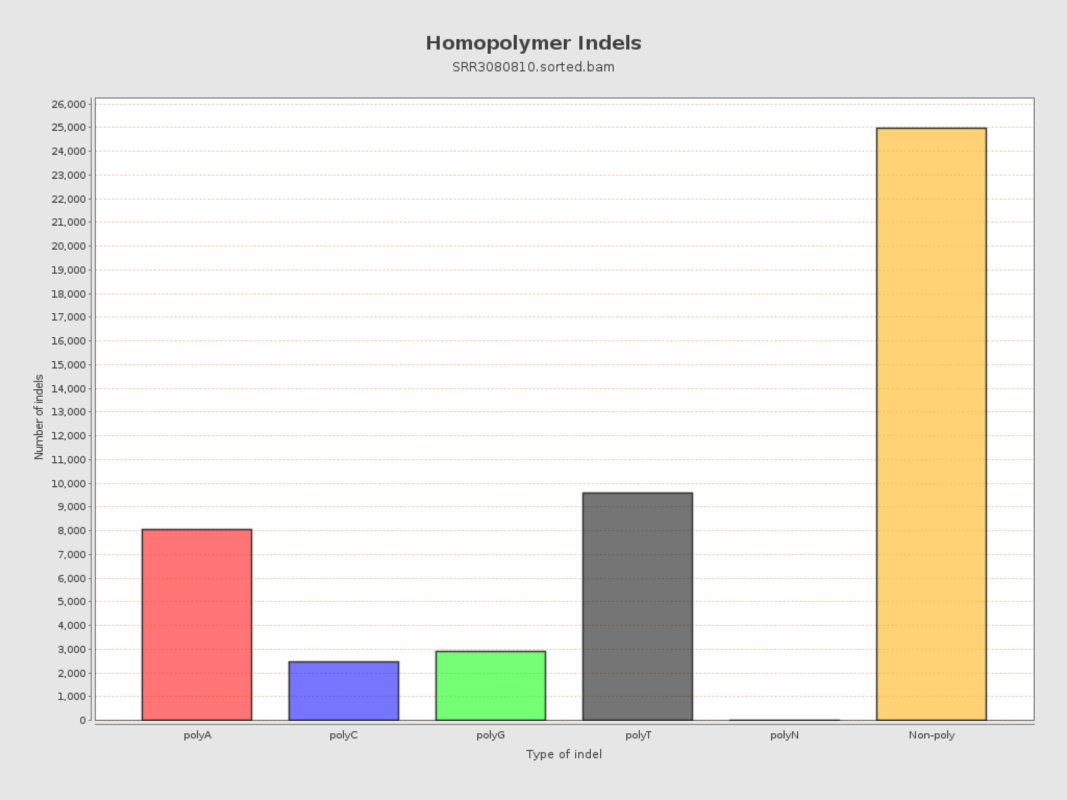
9. Results : Mapped Reads GC-content Distribution



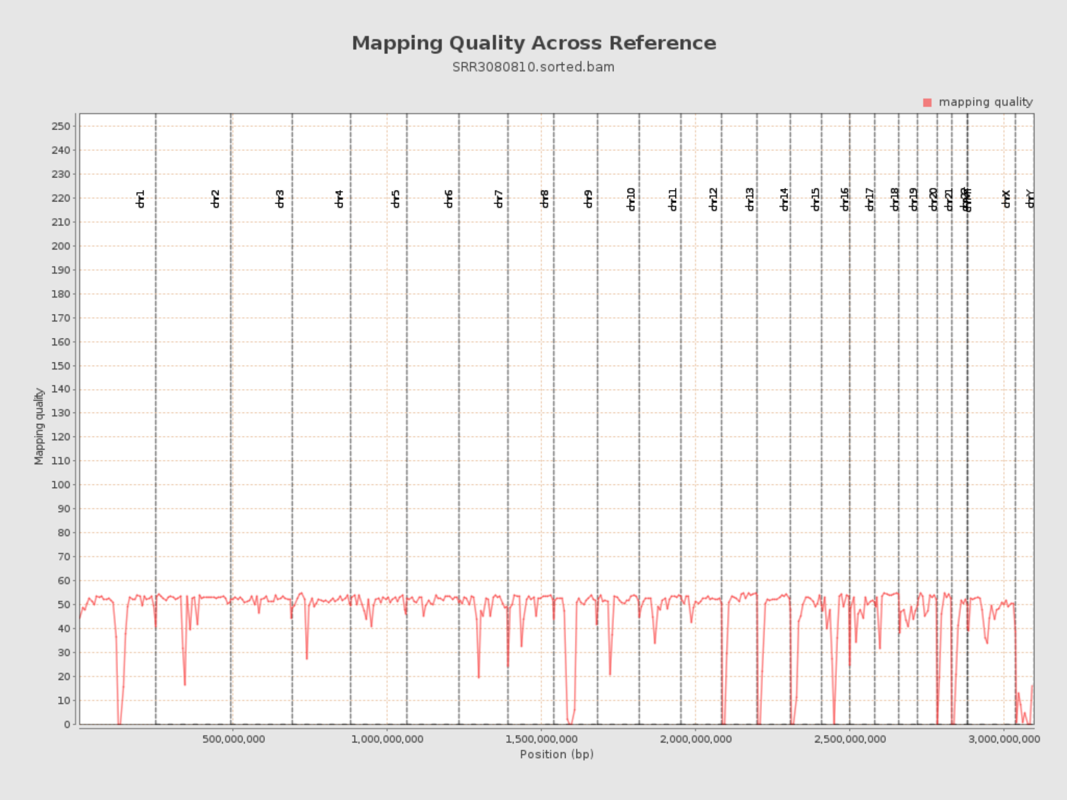
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram