Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:42:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081915.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_SRR3081915 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081915.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:42:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081915.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,763,553
Mapped reads	2,550,000 / 92.27%
Unmapped reads	213,553 / 7.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,391 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	92,797 / 3.36%
Duplication rate	2.64%
Clipped reads	988,368 / 35.76%

2.2. ACGT Content

Number/percentage of A's	49,100,162 / 28.22%
Number/percentage of C's	32,880,513 / 18.9%
Number/percentage of T's	54,077,085 / 31.08%
Number/percentage of G's	37,956,321 / 21.81%
Number/percentage of N's	2,097 / 0%
GC Percentage	40.71%

2.3. Coverage

Mean	0.0562

Standard Deviation	0.4635

2.4. Mapping Quality

Mean Mapping Quality	46.15

2.5. Mismatches and indels

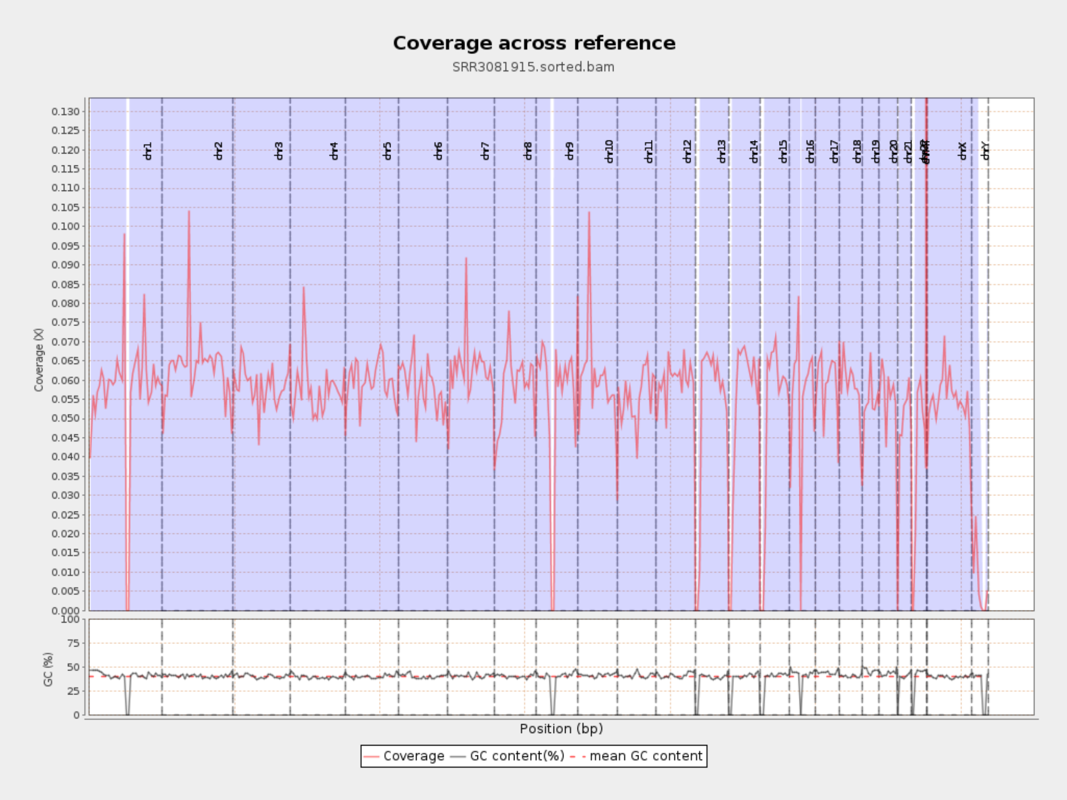
General error rate	0.88%
Mismatches	1,496,594
Insertions	14,450
Mapped reads with at least one insertion	0.56%
Deletions	41,177
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47.08%

2.6. Chromosome stats

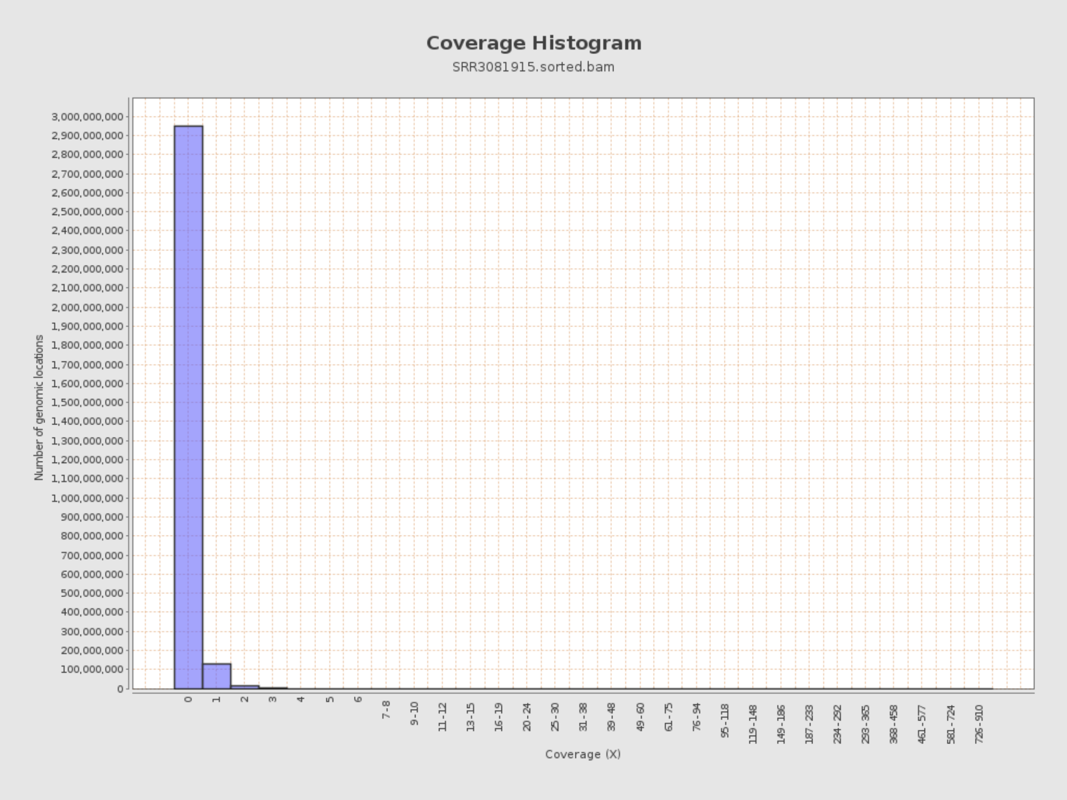
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14272373	0.0573	0.8759
chr2	243199373	15491700	0.0637	0.5491
chr3	198022430	11586105	0.0585	0.277
chr4	191154276	11001776	0.0576	0.3025
chr5	180915260	10835710	0.0599	0.2771
chr6	171115067	10004069	0.0585	0.3158
chr7	159138663	10076591	0.0633	0.6001

chr8	146364022	8467659	0.0579	0.5805
chr9	141213431	7692395	0.0545	0.4483
chr10	135534747	8231136	0.0607	0.4952
chr11	135006516	7485549	0.0554	0.3532
chr12	133851895	7975257	0.0596	0.2782
chr13	115169878	5910206	0.0513	0.2534
chr14	107349540	5645312	0.0526	0.2802
chr15	102531392	5198693	0.0507	0.2718
chr16	90354753	4986126	0.0552	0.3215
chr17	81195210	4767710	0.0587	0.3013
chr18	78077248	4630448	0.0593	0.8162
chr19	59128983	3206356	0.0542	0.6124
chr20	63025520	3519285	0.0558	0.2755
chr21	48129895	2247921	0.0467	0.2688
chr22	51304566	1898354	0.037	0.2161
chrMT	16571	14412	0.8697	1.038
chrX	155270560	8508771	0.0548	0.3034
chrY	59373566	430592	0.0073	0.1827

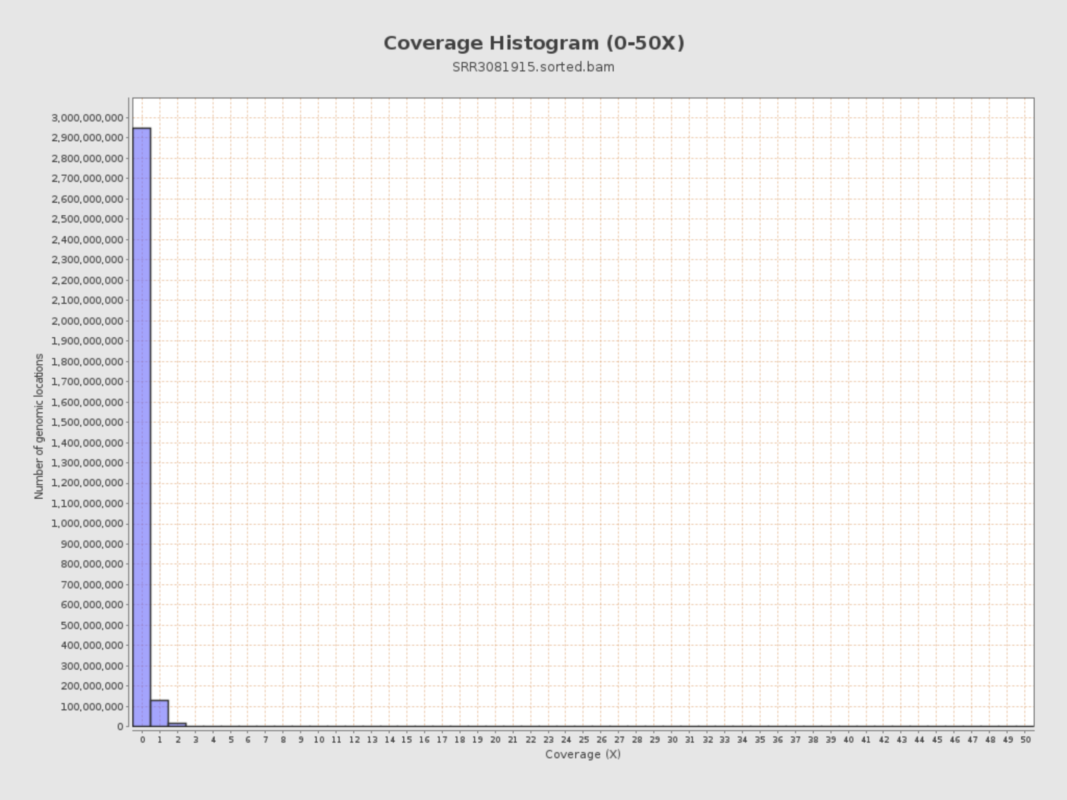
3. Results : Coverage across reference



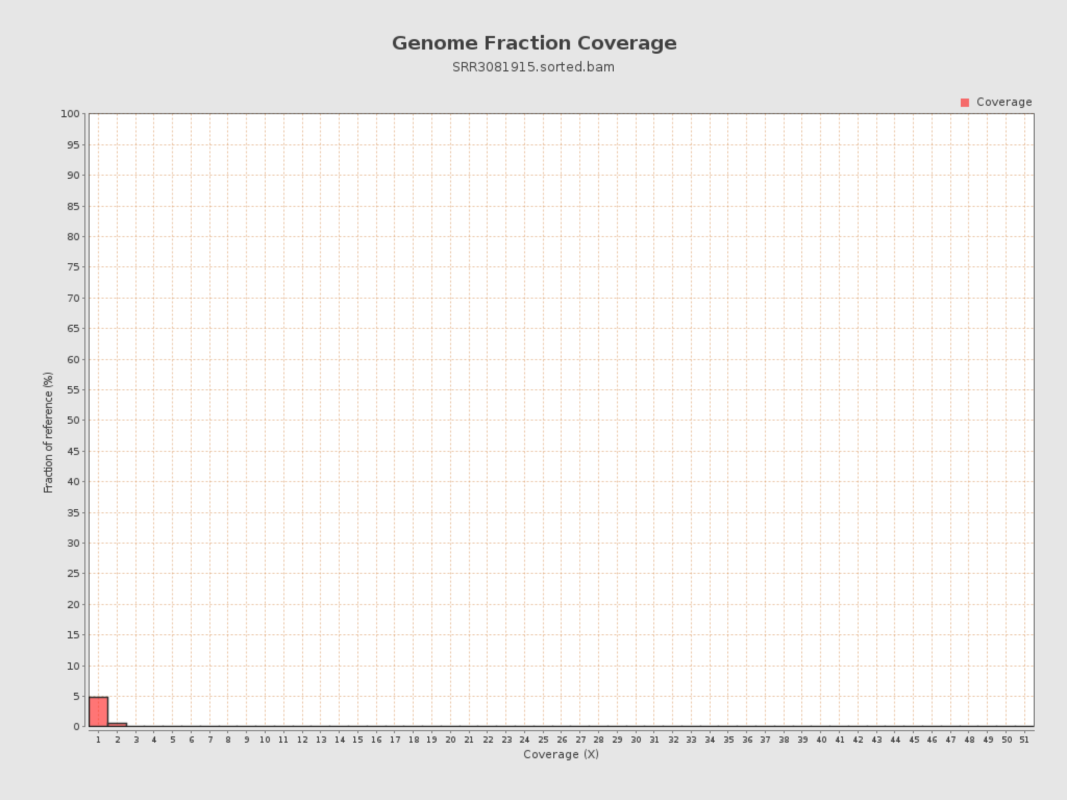
4. Results : Coverage Histogram



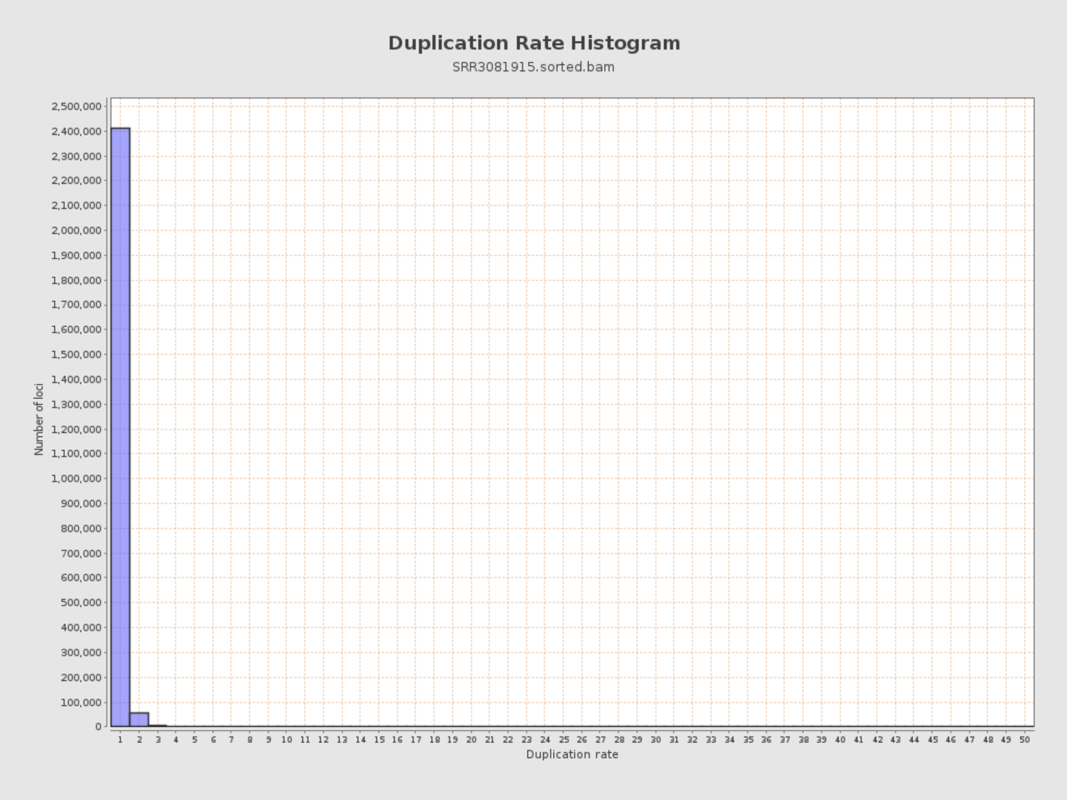
5. Results : Coverage Histogram (0-50X)



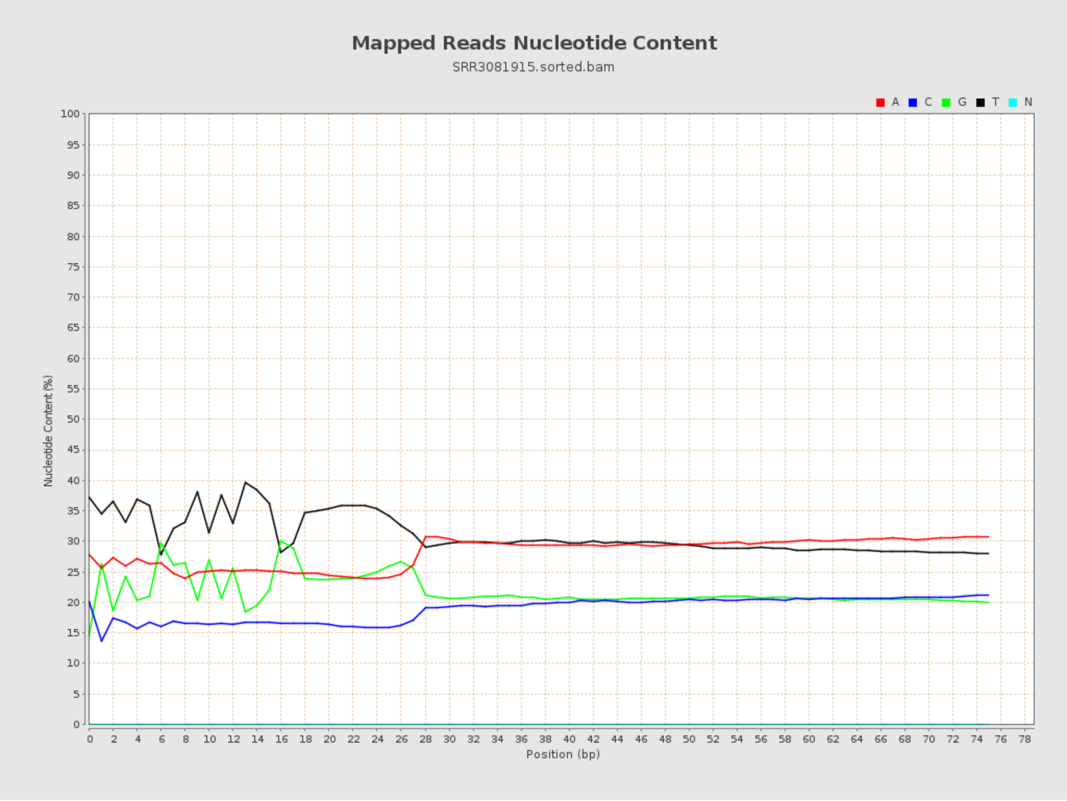
6. Results : Genome Fraction Coverage



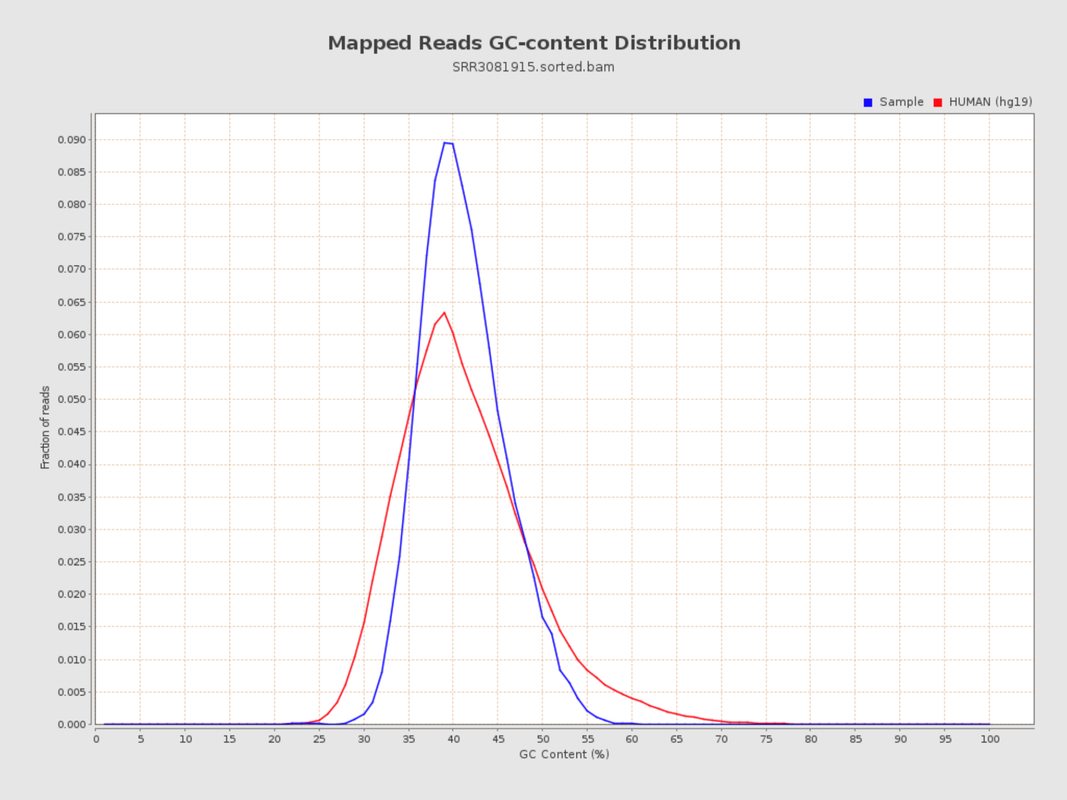
7. Results : Duplication Rate Histogram



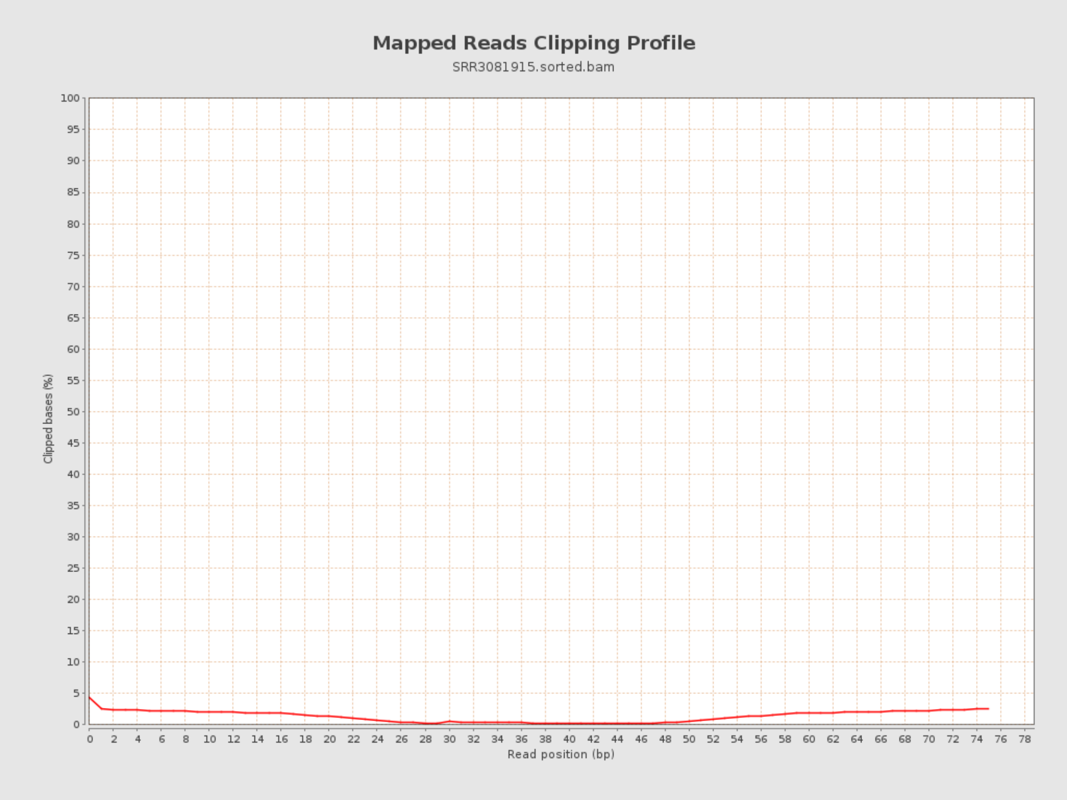
8. Results : Mapped Reads Nucleotide Content



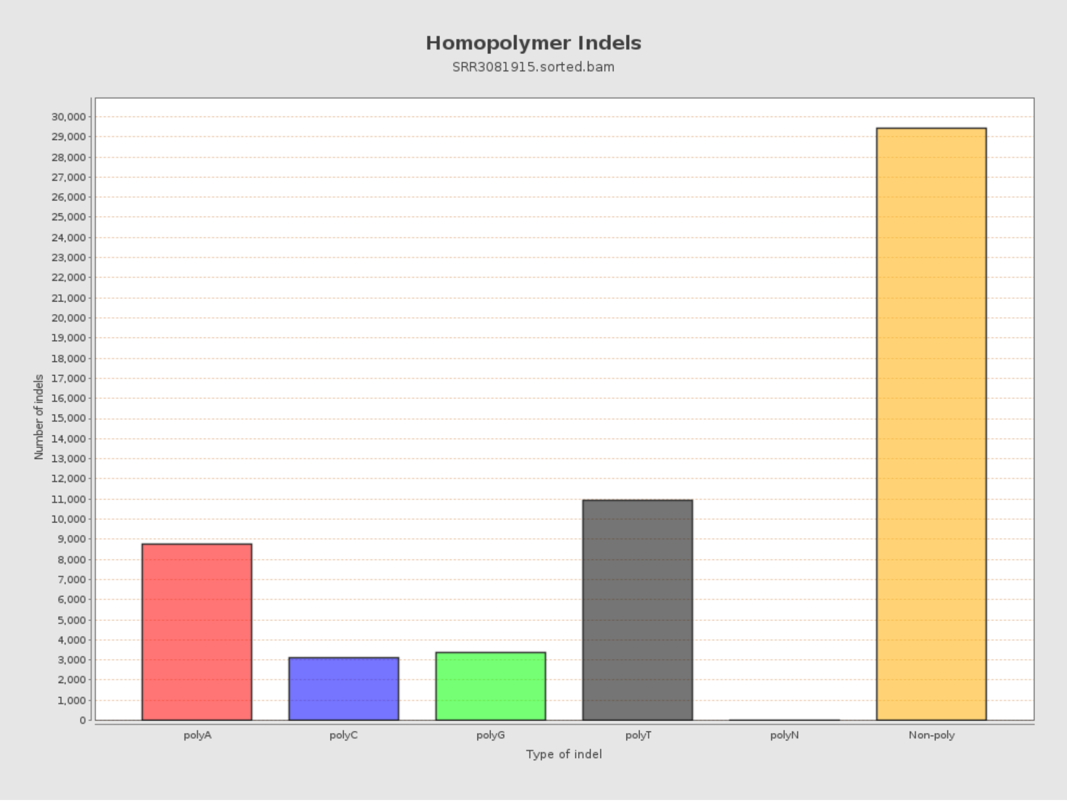
9. Results : Mapped Reads GC-content Distribution



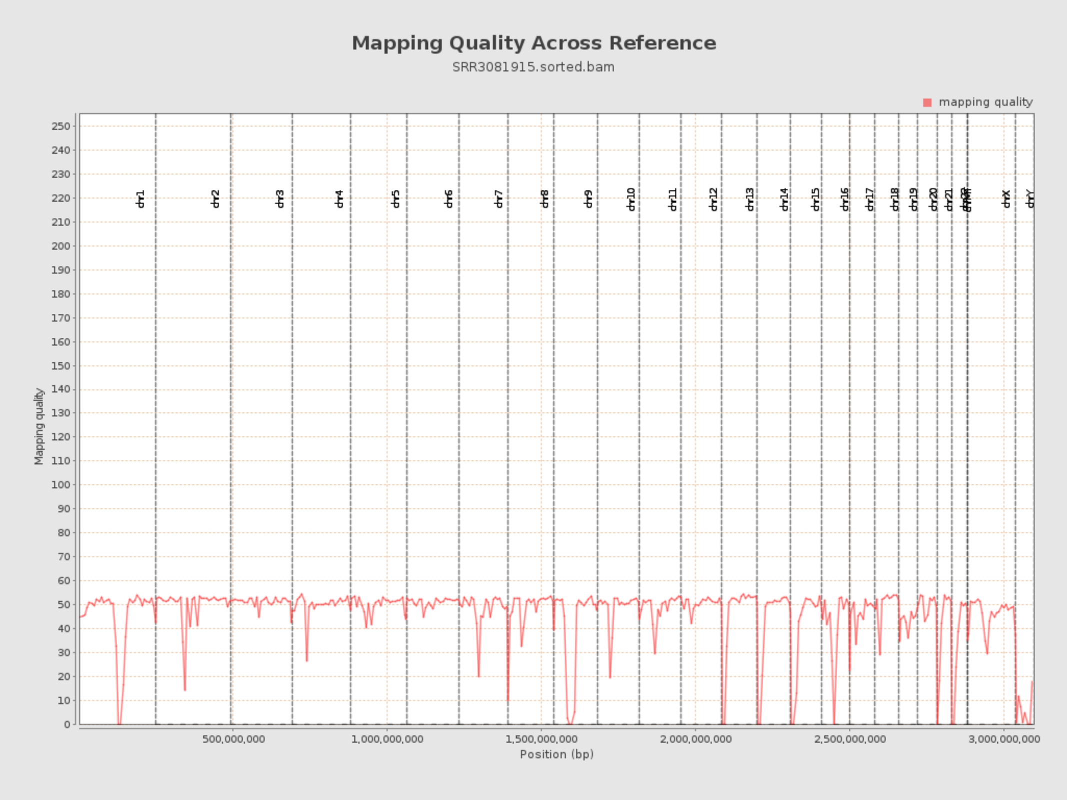
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram