Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:05:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085019.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_SRR3085019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:05:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,190,204
Mapped reads	1,862,490 / 85.04%
Unmapped reads	327,714 / 14.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,907 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	58,863 / 2.69%
Duplication rate	2.6%
Clipped reads	1,022,630 / 46.69%

2.2. ACGT Content

Number/percentage of A's	33,149,194 / 27.53%
Number/percentage of C's	23,330,606 / 19.38%
Number/percentage of T's	36,314,325 / 30.16%
Number/percentage of G's	27,597,216 / 22.92%
Number/percentage of N's	12,366 / 0.01%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0389

Standard Deviation	0.2887

2.4. Mapping Quality

Mean Mapping Quality	43.07

2.5. Mismatches and indels

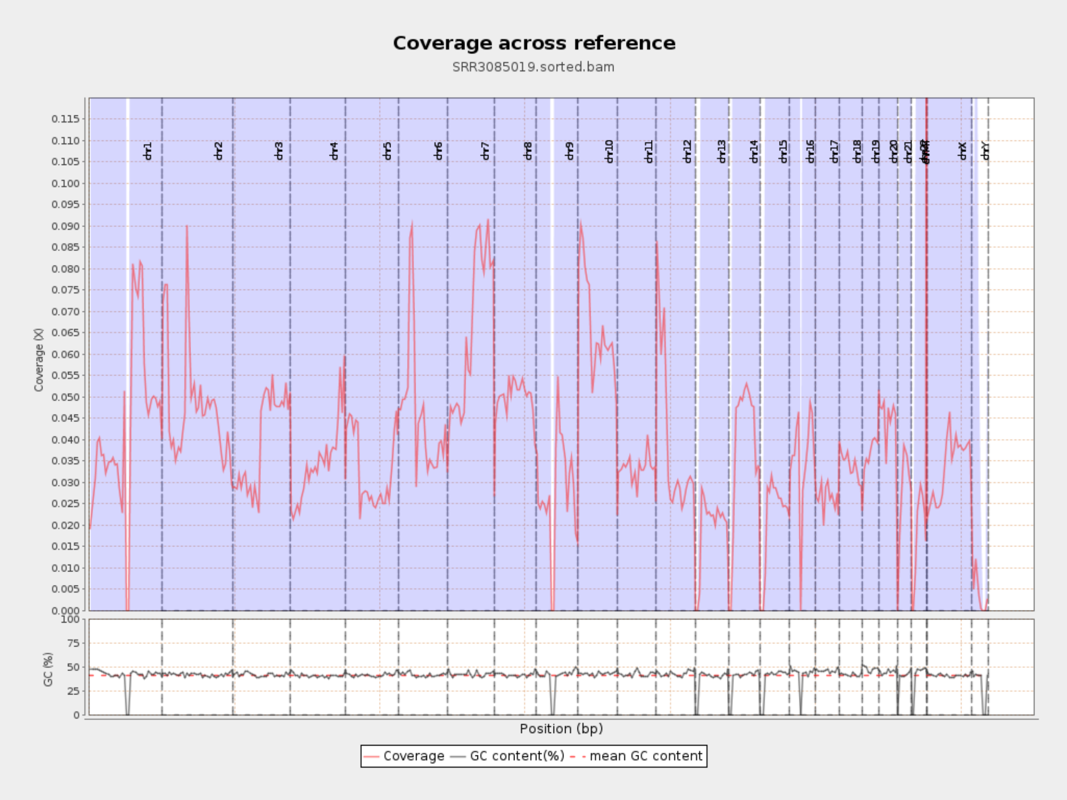
General error rate	0.9%
Mismatches	1,069,954
Insertions	8,649
Mapped reads with at least one insertion	0.46%
Deletions	25,662
Mapped reads with at least one deletion	1.36%
Homopolymer indels	45.68%

2.6. Chromosome stats

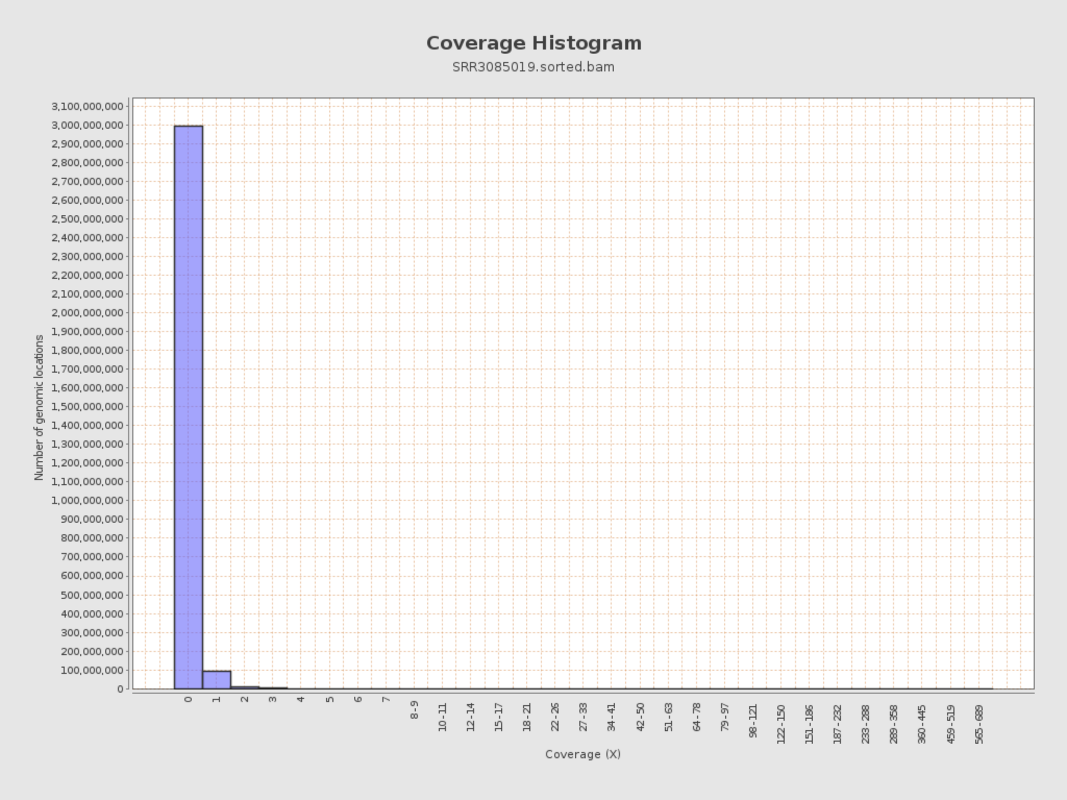
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10698778	0.0429	0.3544
chr2	243199373	11733686	0.0482	0.3816
chr3	198022430	7780393	0.0393	0.2242
chr4	191154276	6613474	0.0346	0.2125
chr5	180915260	5932759	0.0328	0.2034
chr6	171115067	7909480	0.0462	0.2787
chr7	159138663	10515191	0.0661	0.3871

chr8	146364022	7332784	0.0501	0.4788
chr9	141213431	3911577	0.0277	0.2497
chr10	135534747	9099066	0.0671	0.3973
chr11	135006516	4471949	0.0331	0.262
chr12	133851895	5261124	0.0393	0.2271
chr13	115169878	2199508	0.0191	0.1534
chr14	107349540	4112586	0.0383	0.2294
chr15	102531392	2228526	0.0217	0.1875
chr16	90354753	3219363	0.0356	0.2179
chr17	81195210	2143894	0.0264	0.1918
chr18	78077248	2656635	0.034	0.337
chr19	59128983	2191381	0.0371	0.2995
chr20	63025520	2800006	0.0444	0.2395
chr21	48129895	1318295	0.0274	0.1892
chr22	51304566	893651	0.0174	0.147
chrMT	16571	5455	0.3292	0.693
chrX	155270560	5174450	0.0333	0.2189
chrY	59373566	245054	0.0041	0.0851

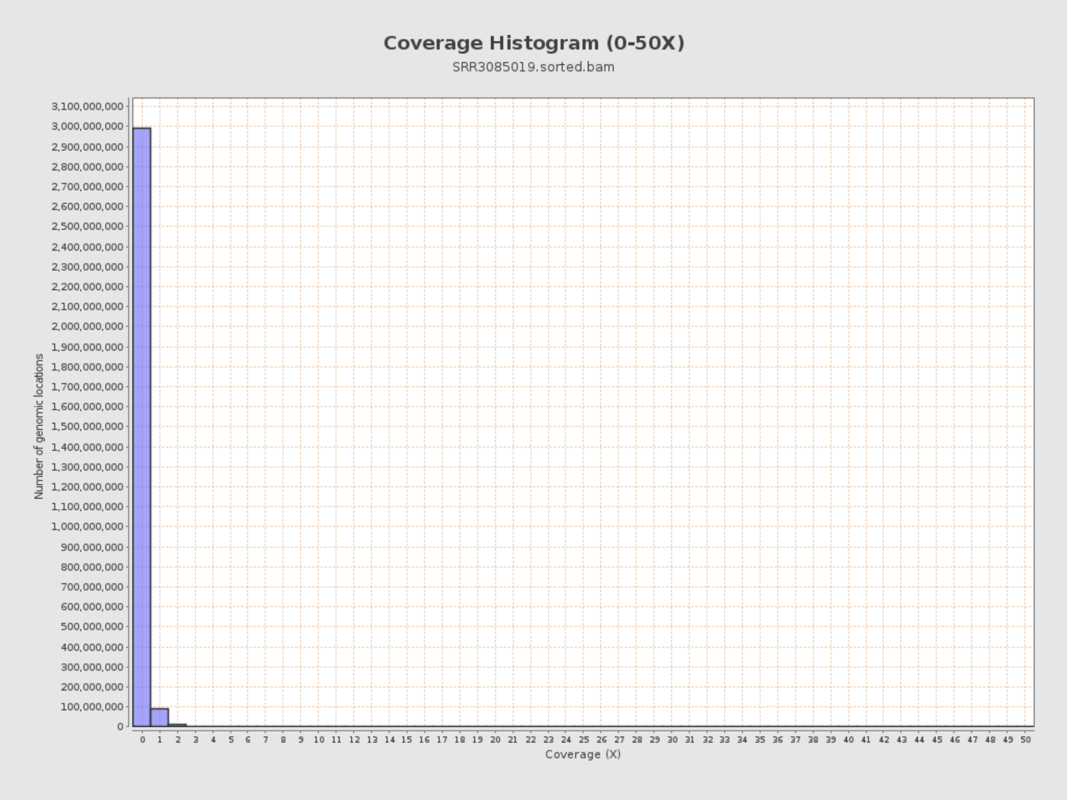
3. Results : Coverage across reference



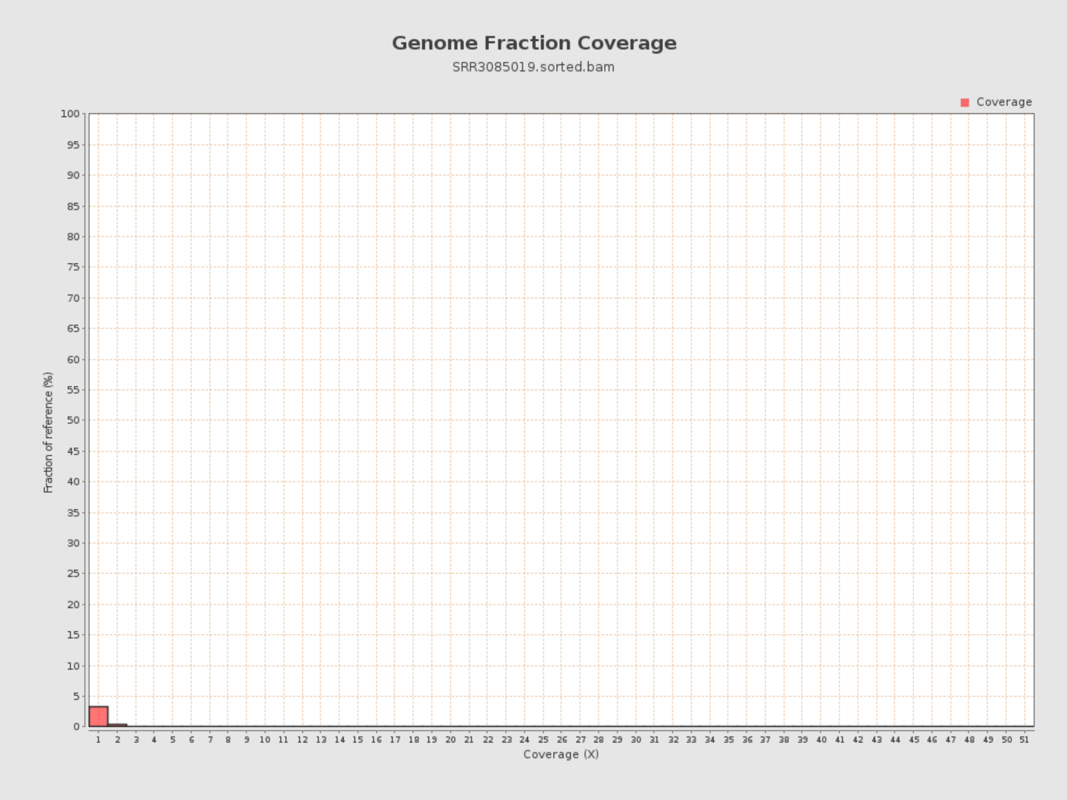
4. Results : Coverage Histogram



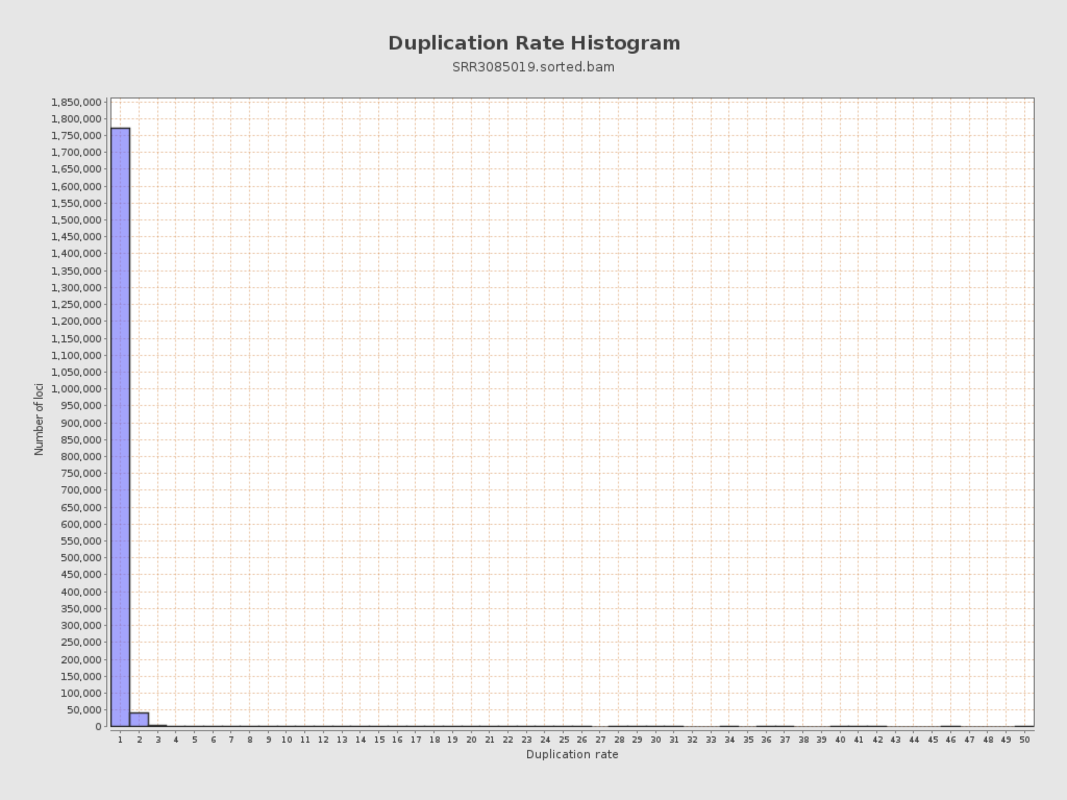
5. Results : Coverage Histogram (0-50X)



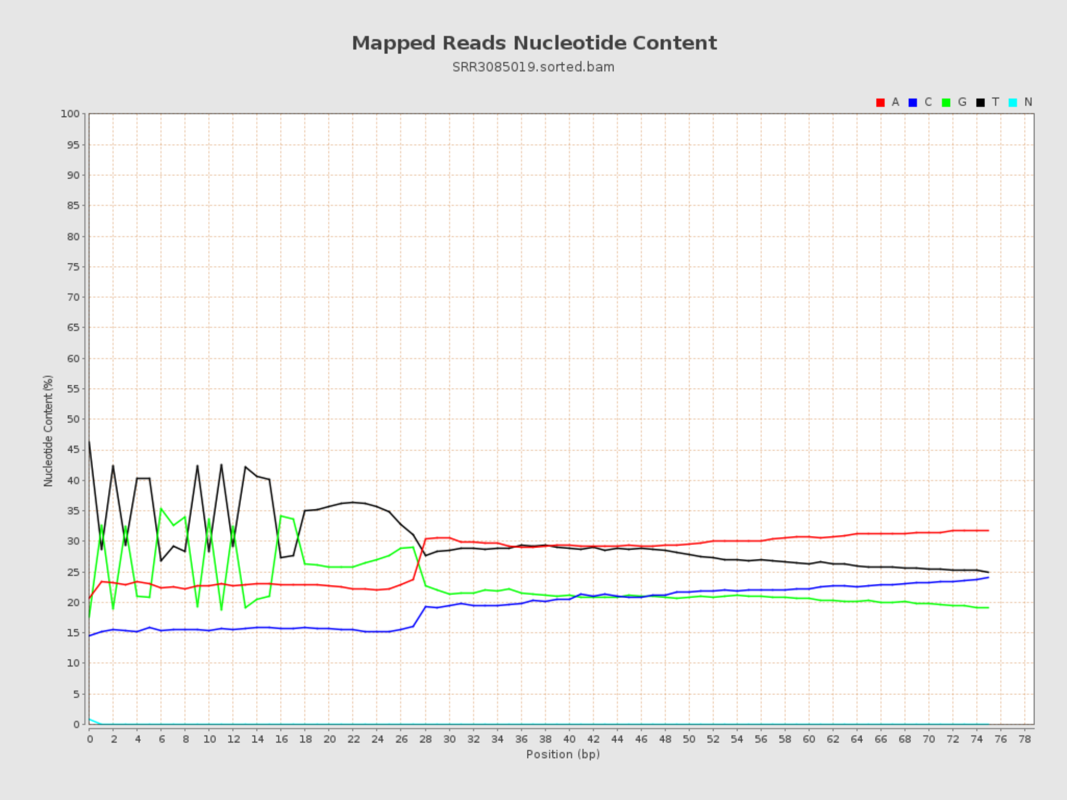
6. Results : Genome Fraction Coverage



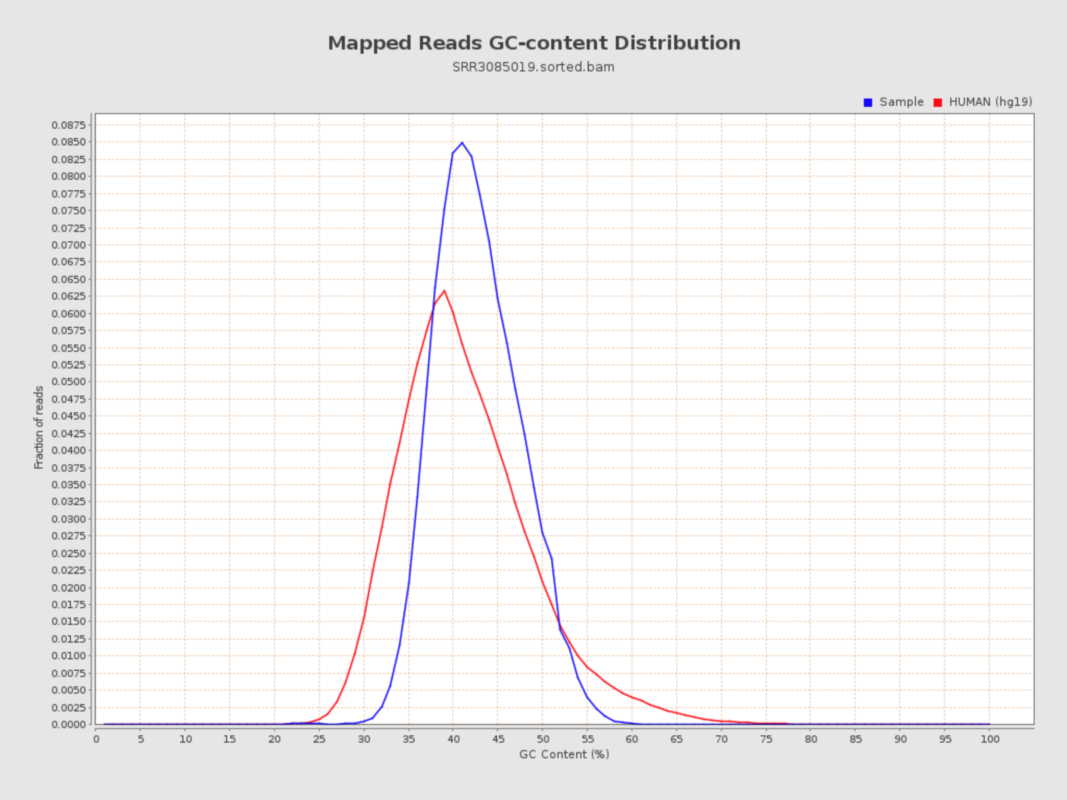
7. Results : Duplication Rate Histogram



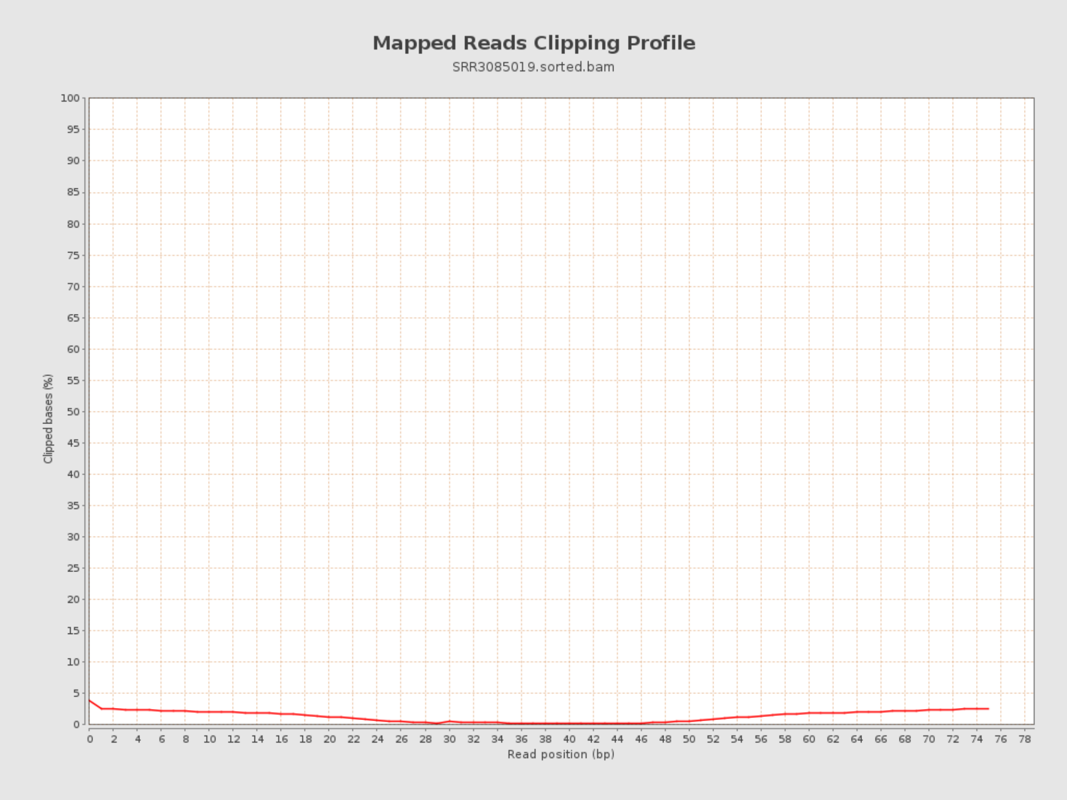
8. Results : Mapped Reads Nucleotide Content



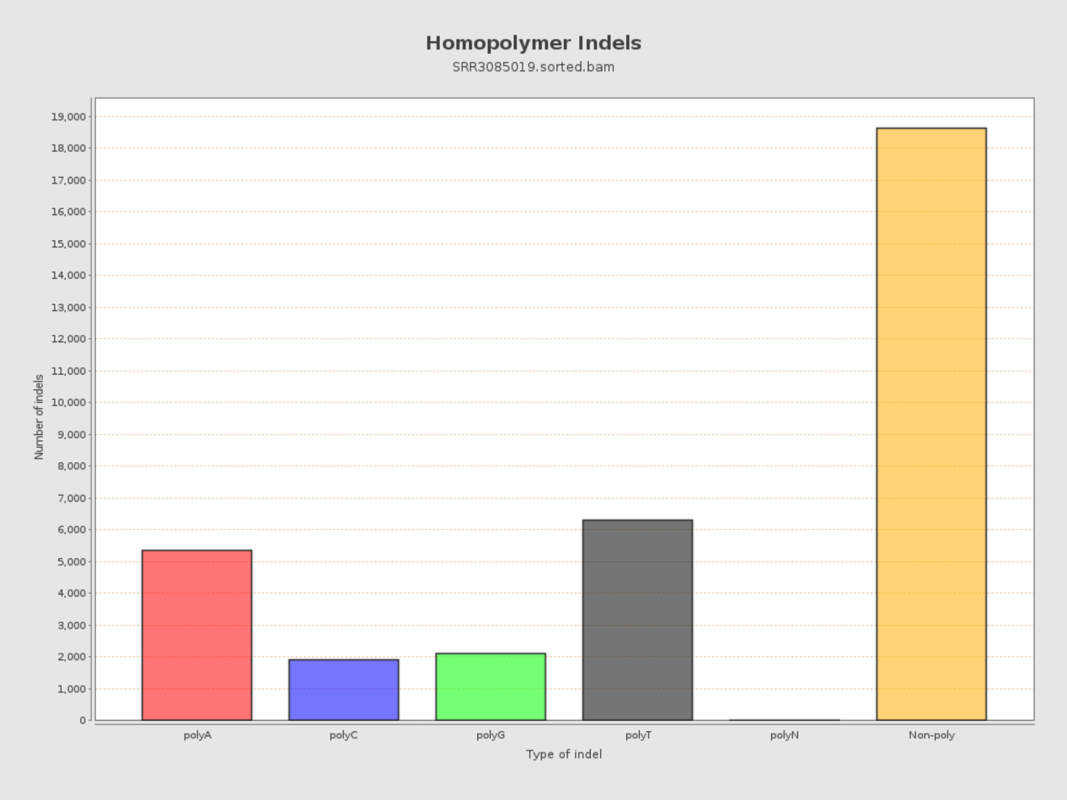
9. Results : Mapped Reads GC-content Distribution



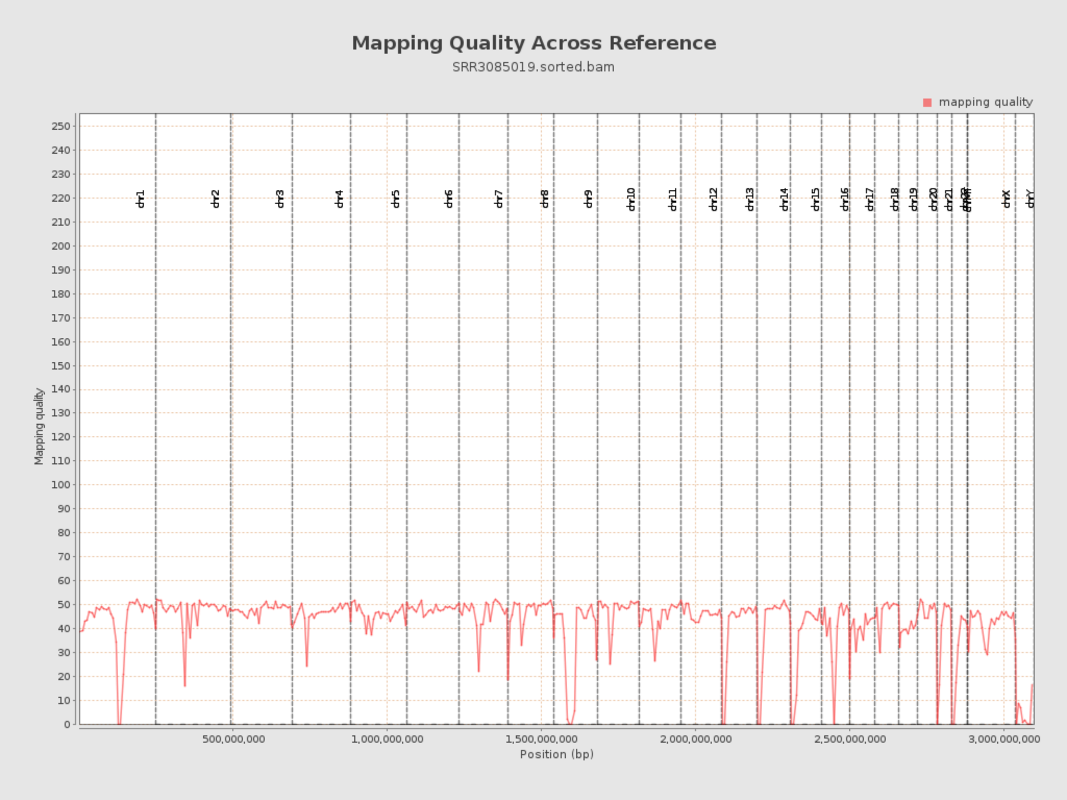
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram