Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:55:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085115.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_SRR3085115 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085115.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:55:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,209,741
Mapped reads	1,872,007 / 84.72%
Unmapped reads	337,734 / 15.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,208 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	56,590 / 2.56%
Duplication rate	2.58%
Clipped reads	1,377,778 / 62.35%

2.2. ACGT Content

Number/percentage of A's	33,058,061 / 29.8%
Number/percentage of C's	22,183,120 / 20%
Number/percentage of T's	32,076,651 / 28.92%
Number/percentage of G's	23,596,850 / 21.27%
Number/percentage of N's	2,311 / 0%
GC Percentage	41.27%

2.3. Coverage

Mean	0.0358

Standard Deviation	0.2649

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

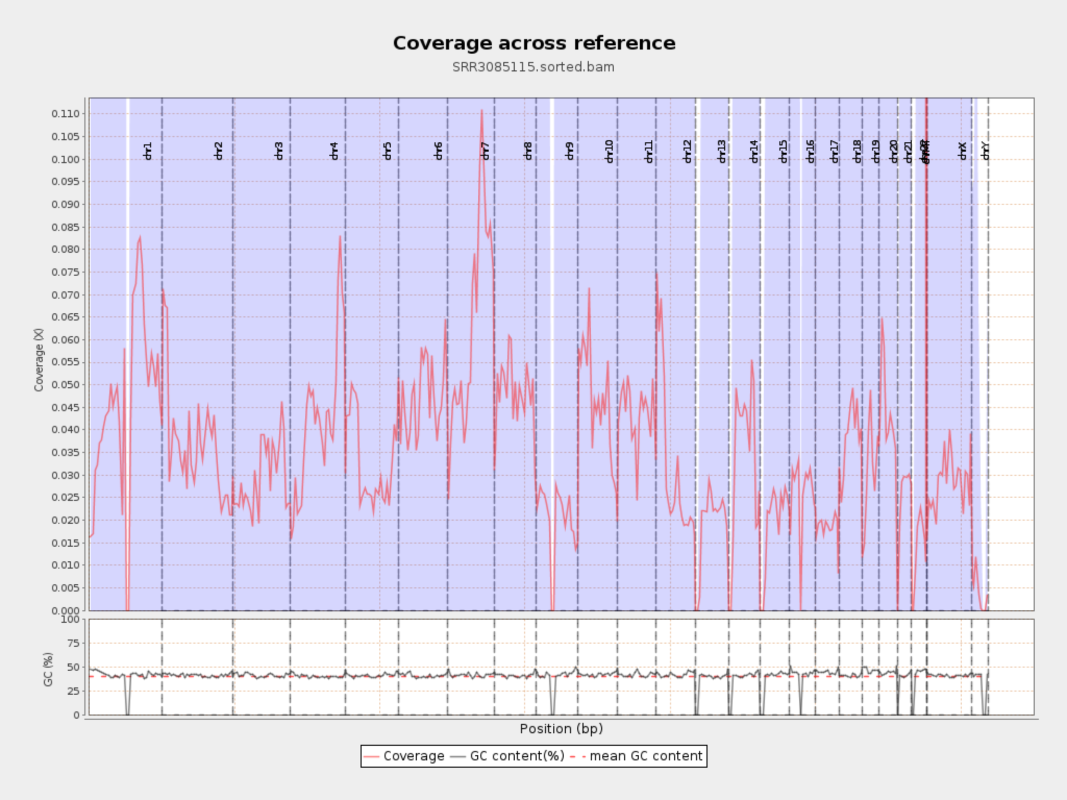
General error rate	0.82%
Mismatches	897,331
Insertions	7,645
Mapped reads with at least one insertion	0.41%
Deletions	20,956
Mapped reads with at least one deletion	1.11%
Homopolymer indels	45.32%

2.6. Chromosome stats

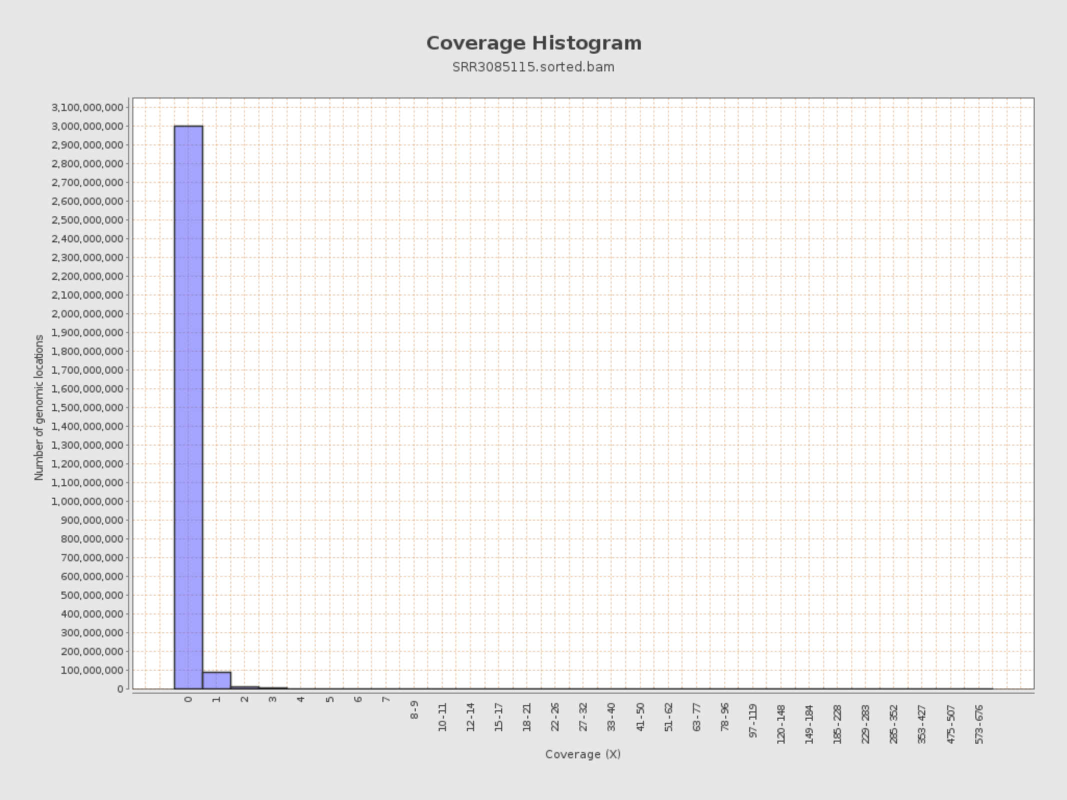
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11464783	0.046	0.3947
chr2	243199373	8945647	0.0368	0.2599
chr3	198022430	5861454	0.0296	0.1946
chr4	191154276	8156112	0.0427	0.232
chr5	180915260	5909804	0.0327	0.1996
chr6	171115067	8122616	0.0475	0.2736
chr7	159138663	10210401	0.0642	0.3083

chr8	146364022	7073056	0.0483	0.4481
chr9	141213431	2864830	0.0203	0.1914
chr10	135534747	6371492	0.047	0.3762
chr11	135006516	5849916	0.0433	0.2641
chr12	133851895	4277916	0.032	0.1989
chr13	115169878	2192555	0.019	0.1506
chr14	107349540	3623823	0.0338	0.2082
chr15	102531392	1968276	0.0192	0.1526
chr16	90354753	2359146	0.0261	0.1886
chr17	81195210	1490753	0.0184	0.1568
chr18	78077248	3032648	0.0388	0.3255
chr19	59128983	1860955	0.0315	0.2693
chr20	63025520	2760974	0.0438	0.234
chr21	48129895	1197116	0.0249	0.1799
chr22	51304566	678025	0.0132	0.1255
chrMT	16571	46637	2.8144	2.2782
chrX	155270560	4403858	0.0284	0.2001
chrY	59373566	227417	0.0038	0.0783

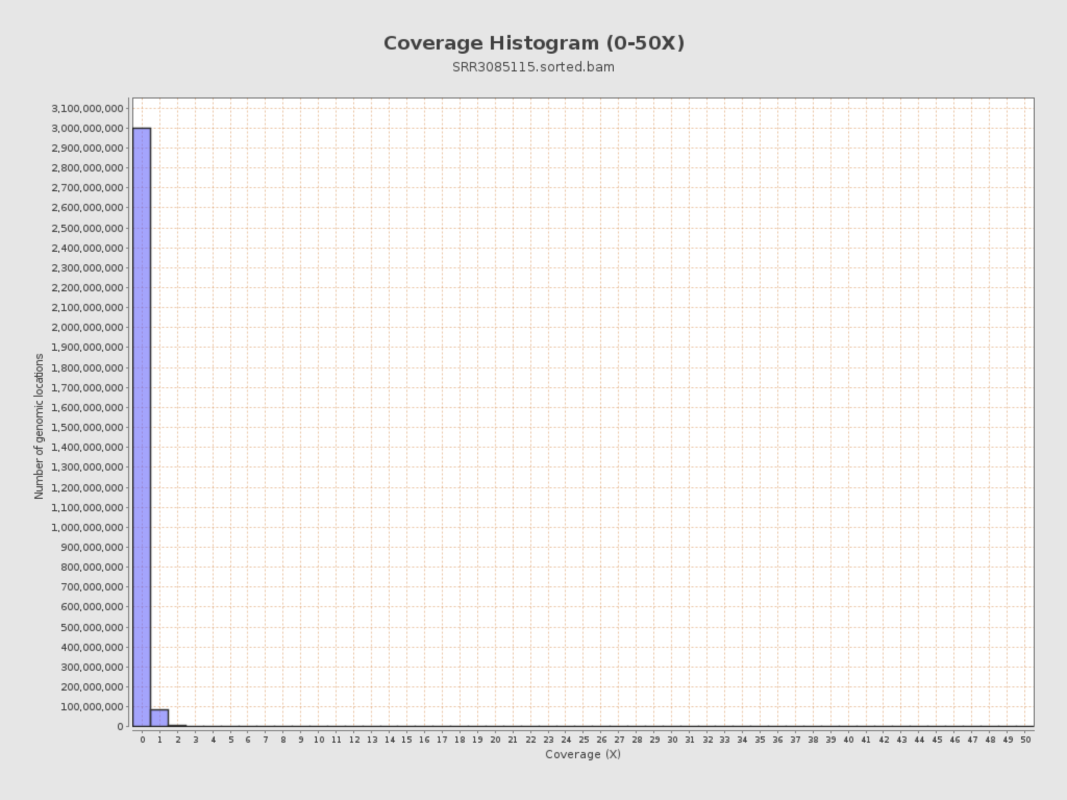
3. Results : Coverage across reference



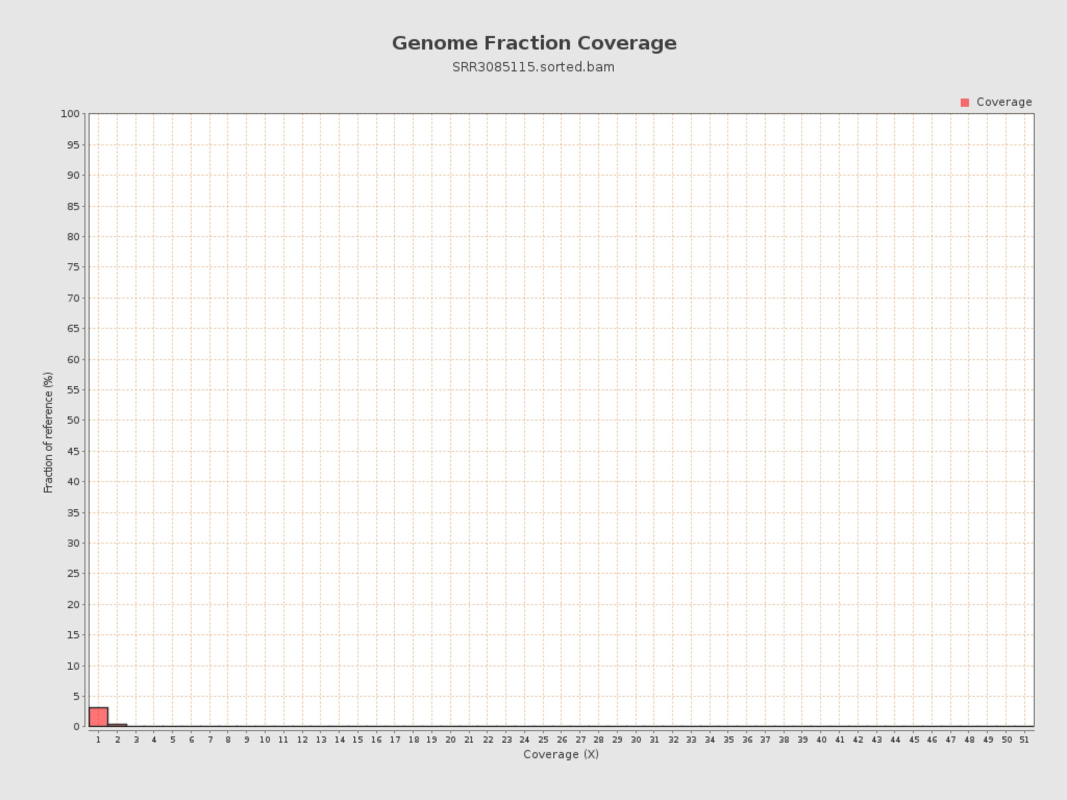
4. Results : Coverage Histogram



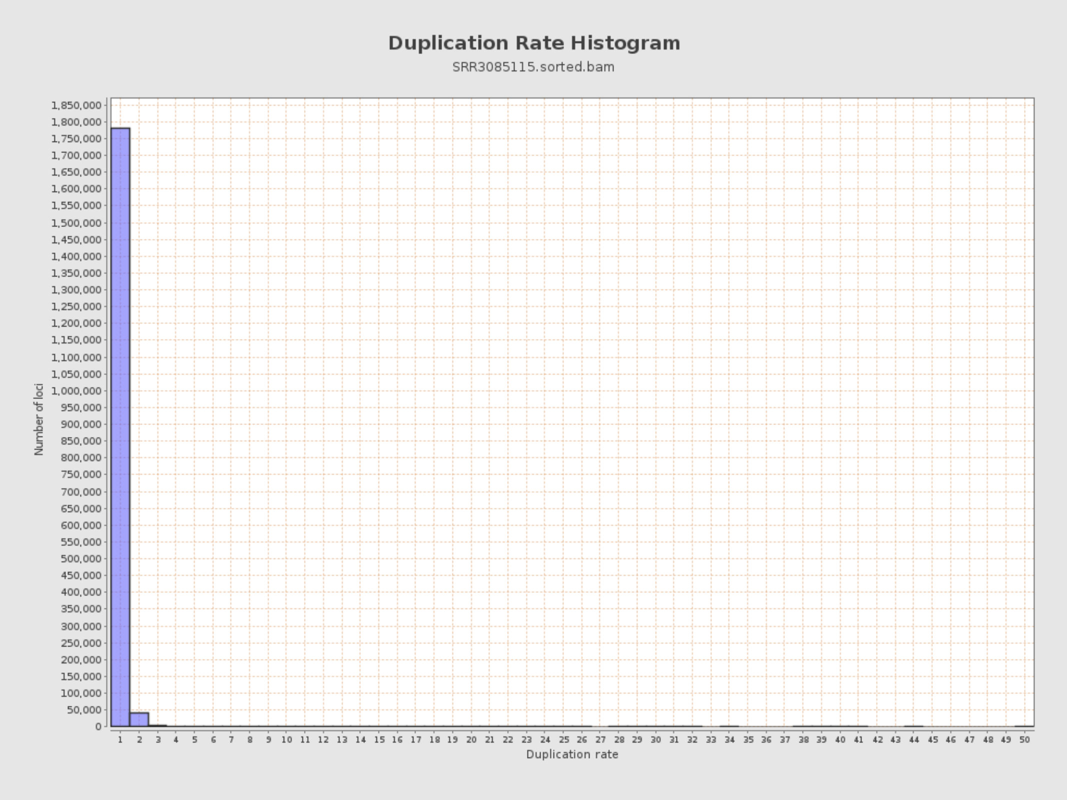
5. Results : Coverage Histogram (0-50X)



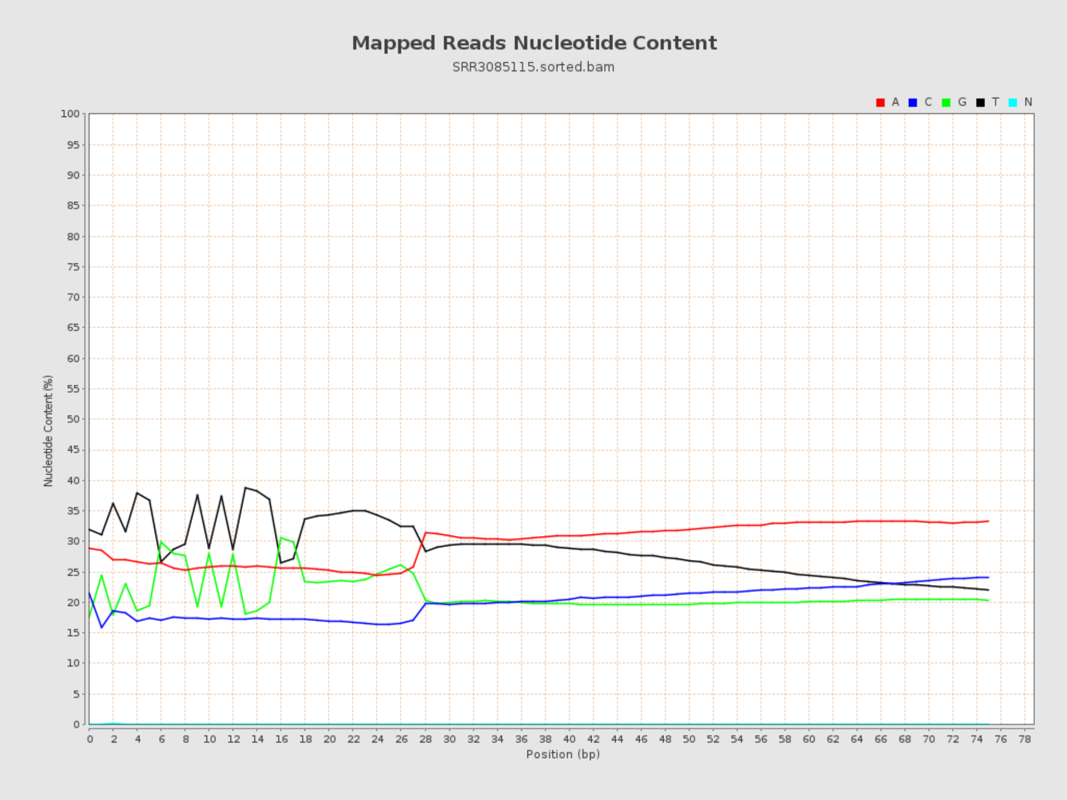
6. Results : Genome Fraction Coverage



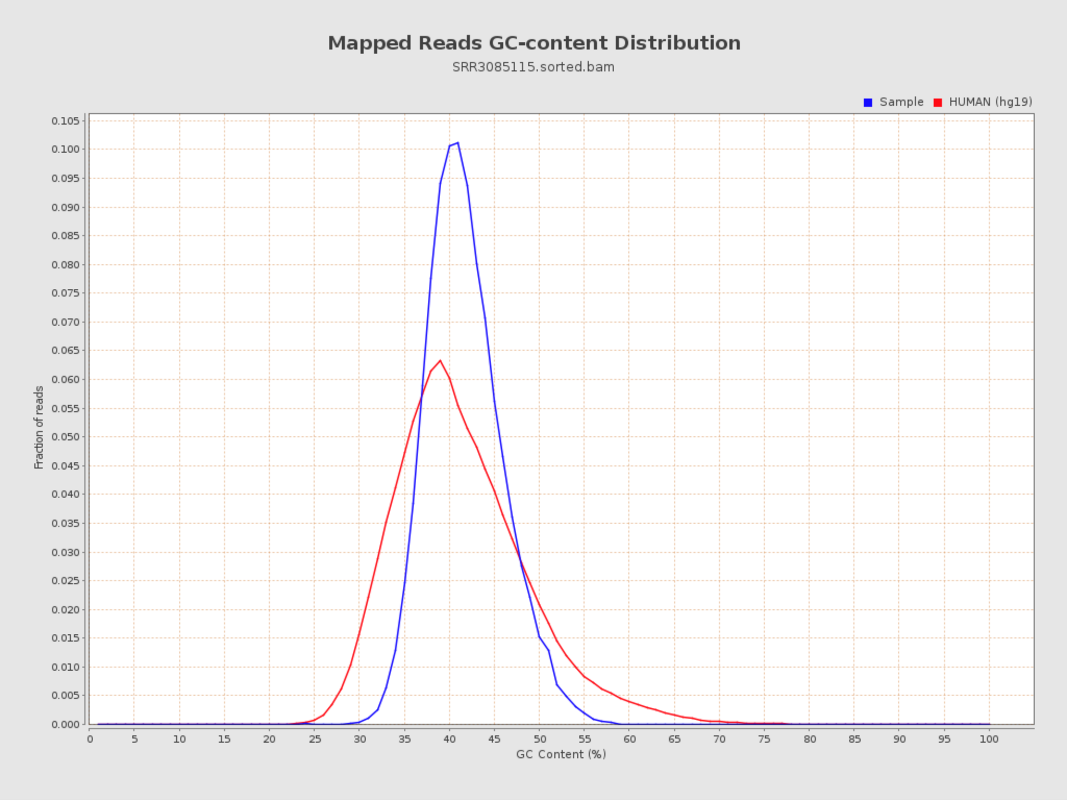
7. Results : Duplication Rate Histogram



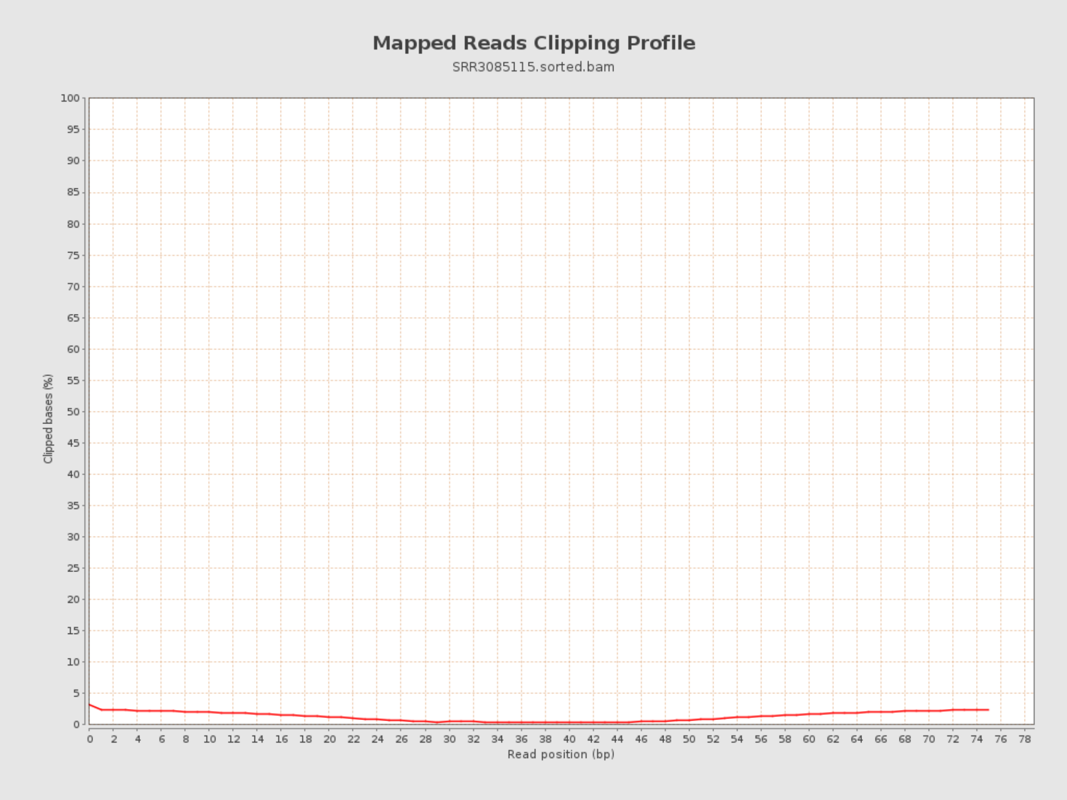
8. Results : Mapped Reads Nucleotide Content



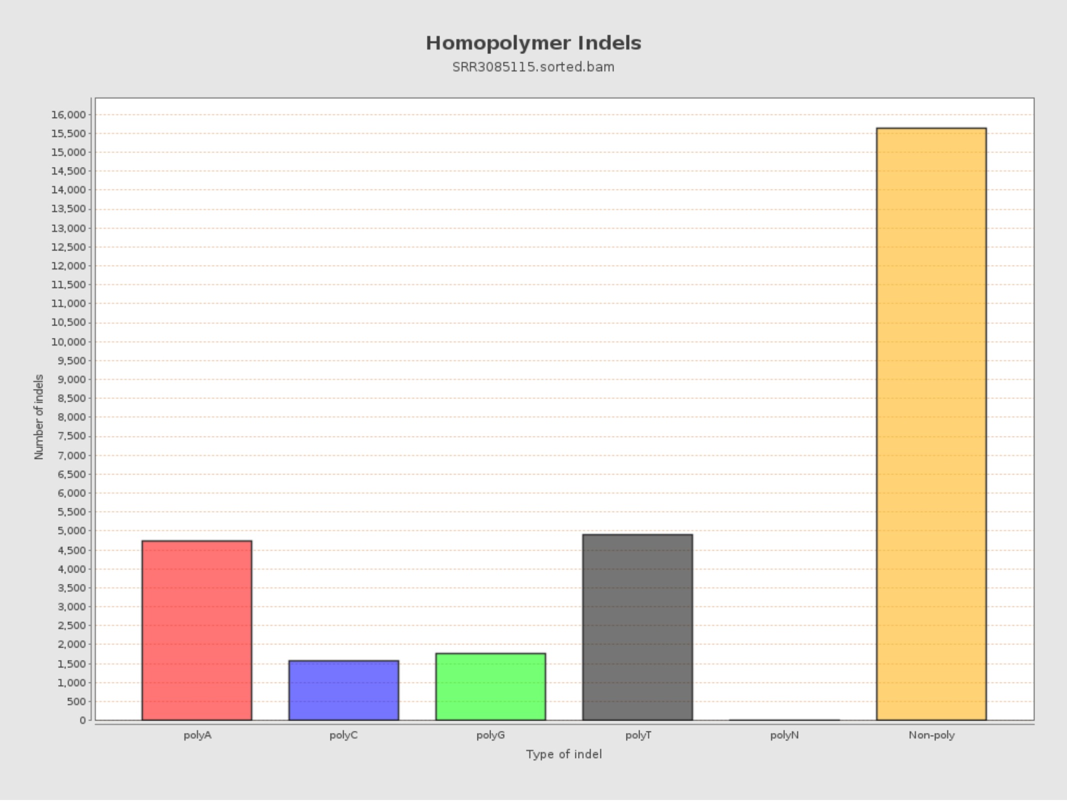
9. Results : Mapped Reads GC-content Distribution



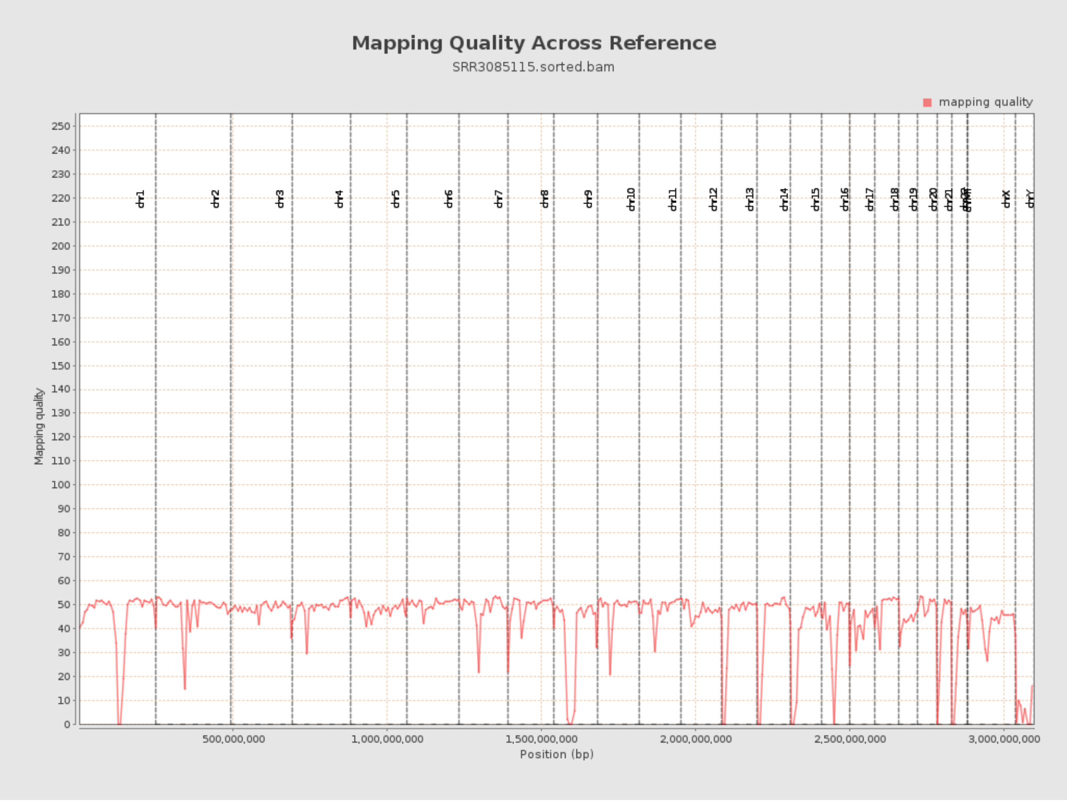
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram