Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:49:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085015.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_SRR3085015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085015.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:49:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,896,266
Mapped reads	1,732,679 / 91.37%
Unmapped reads	163,587 / 8.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,301 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	48,636 / 2.56%
Duplication rate	2.33%
Clipped reads	776,601 / 40.95%

2.2. ACGT Content

Number/percentage of A's	32,843,348 / 28.31%
Number/percentage of C's	22,367,705 / 19.28%
Number/percentage of T's	35,496,947 / 30.6%
Number/percentage of G's	25,289,090 / 21.8%
Number/percentage of N's	12,701 / 0.01%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.2736

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

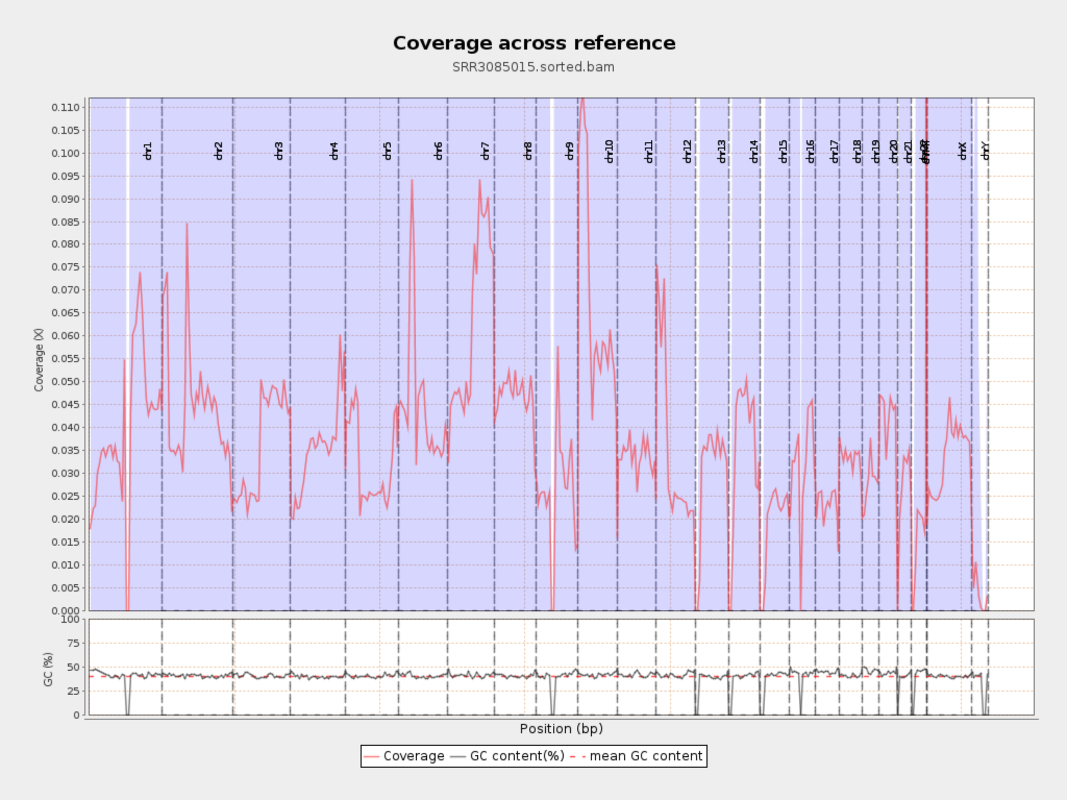
General error rate	0.86%
Mismatches	982,931
Insertions	8,016
Mapped reads with at least one insertion	0.46%
Deletions	22,575
Mapped reads with at least one deletion	1.29%
Homopolymer indels	47.45%

2.6. Chromosome stats

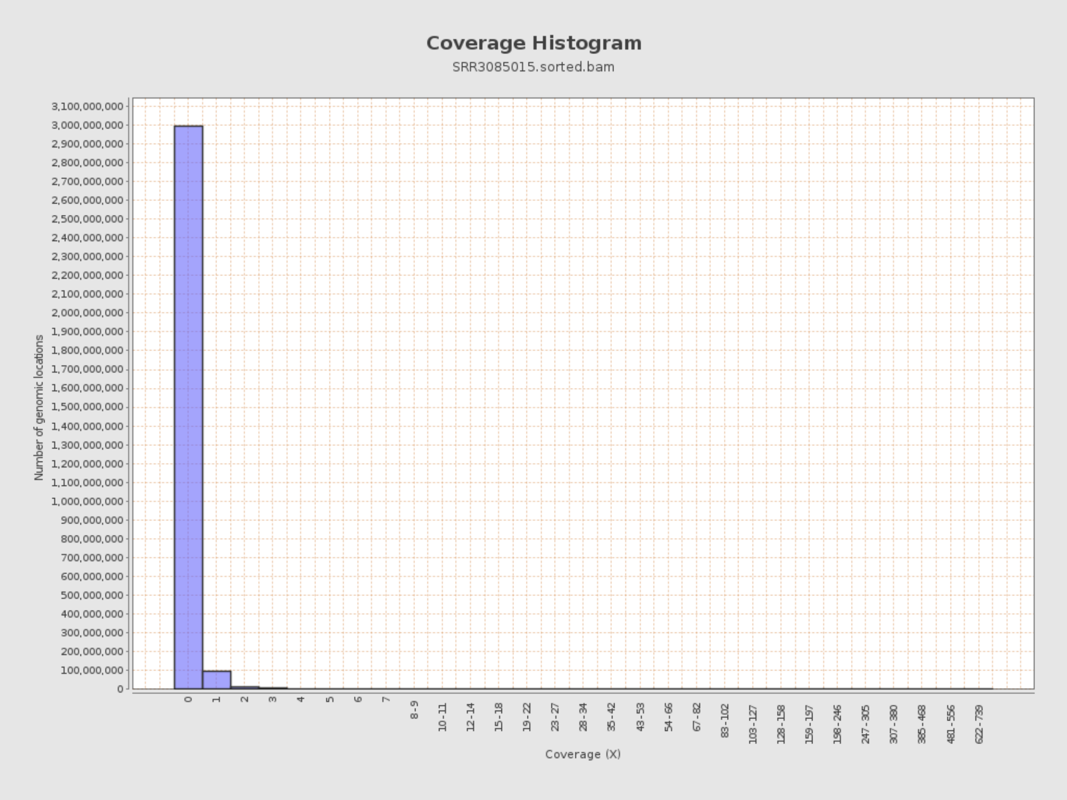
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9817552	0.0394	0.3414
chr2	243199373	10996839	0.0452	0.3307
chr3	198022430	7184459	0.0363	0.2119
chr4	191154276	6783361	0.0355	0.2121
chr5	180915260	5791489	0.032	0.1983
chr6	171115067	7835032	0.0458	0.2837
chr7	159138663	10127742	0.0636	0.3265

chr8	146364022	6861540	0.0469	0.4902
chr9	141213431	3717506	0.0263	0.237
chr10	135534747	9448800	0.0697	0.3542
chr11	135006516	4520058	0.0335	0.2555
chr12	133851895	4677934	0.0349	0.2101
chr13	115169878	3414877	0.0297	0.1912
chr14	107349540	3809600	0.0355	0.2165
chr15	102531392	1948516	0.019	0.1578
chr16	90354753	2924867	0.0324	0.2065
chr17	81195210	1838168	0.0226	0.1779
chr18	78077248	2622113	0.0336	0.3567
chr19	59128983	1670263	0.0282	0.2578
chr20	63025520	2659369	0.0422	0.2292
chr21	48129895	1263127	0.0262	0.1868
chr22	51304566	730730	0.0142	0.1306
chrMT	16571	6537	0.3945	0.6552
chrX	155270560	5174199	0.0333	0.2145
chrY	59373566	224528	0.0038	0.0792

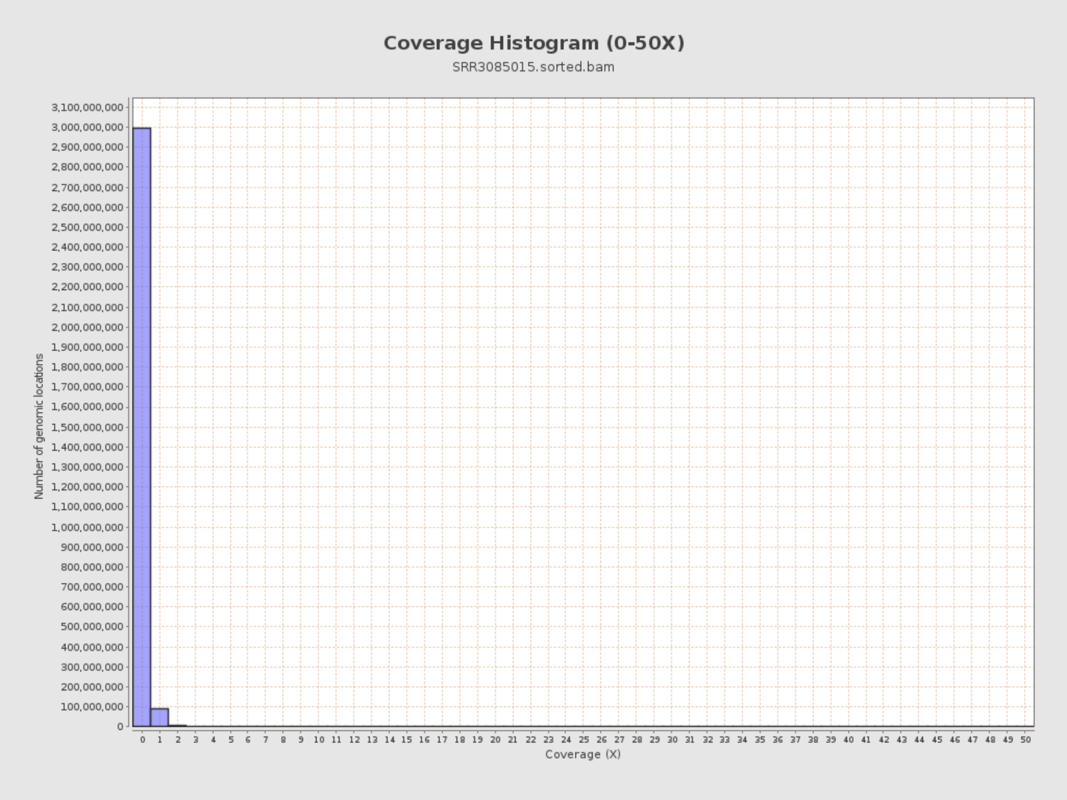
3. Results : Coverage across reference



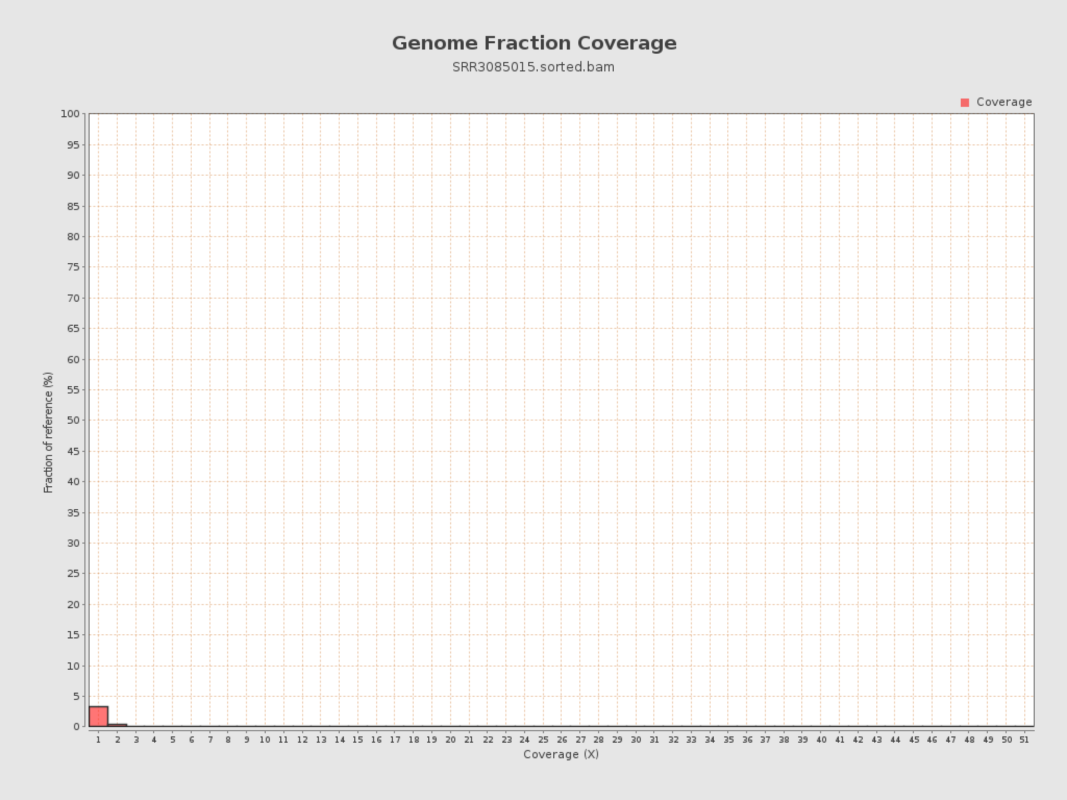
4. Results : Coverage Histogram



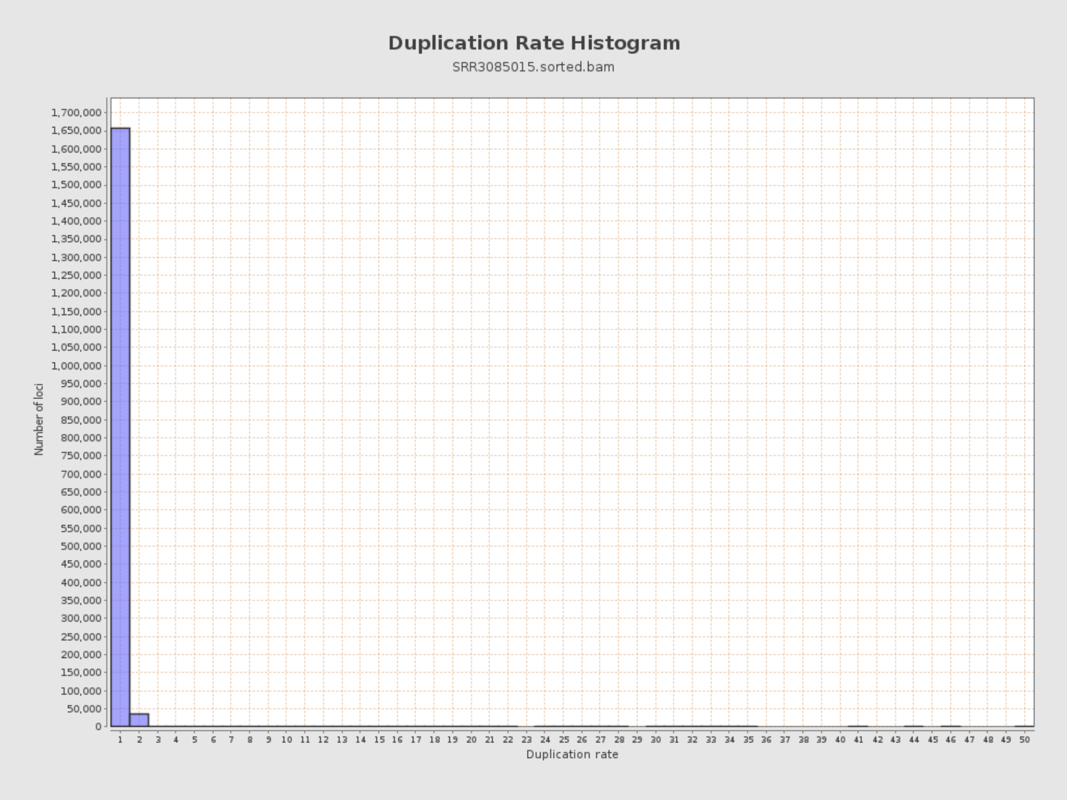
5. Results : Coverage Histogram (0-50X)



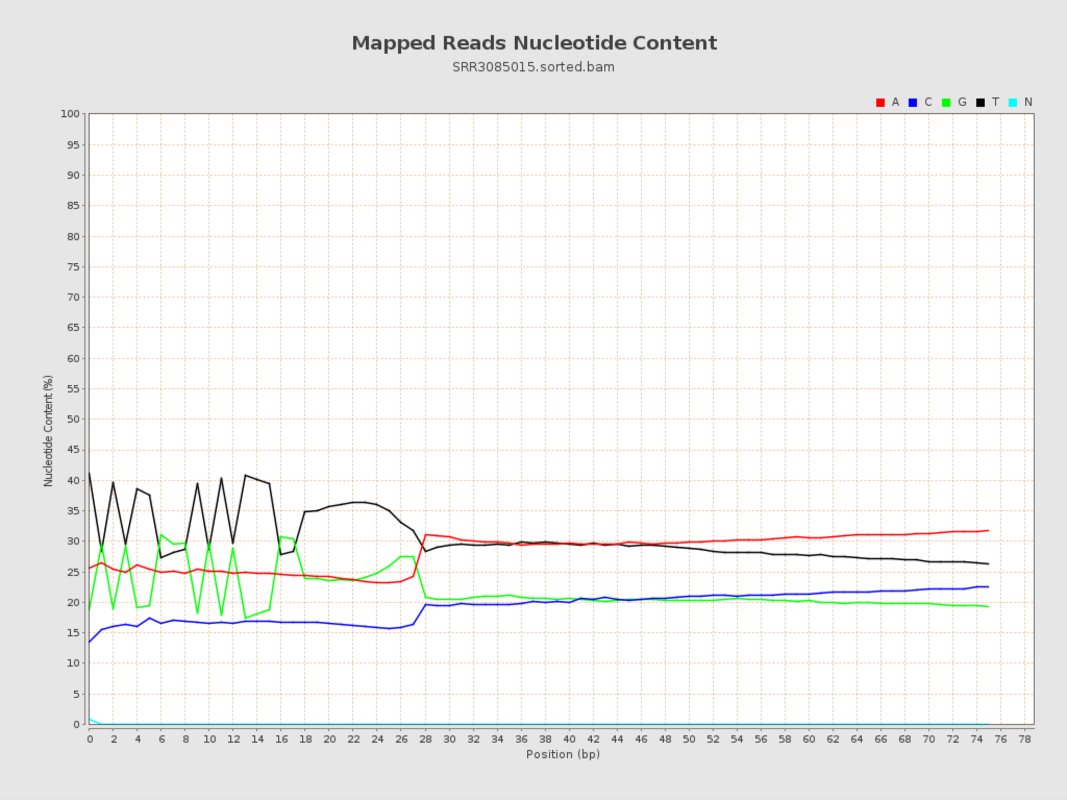
6. Results : Genome Fraction Coverage



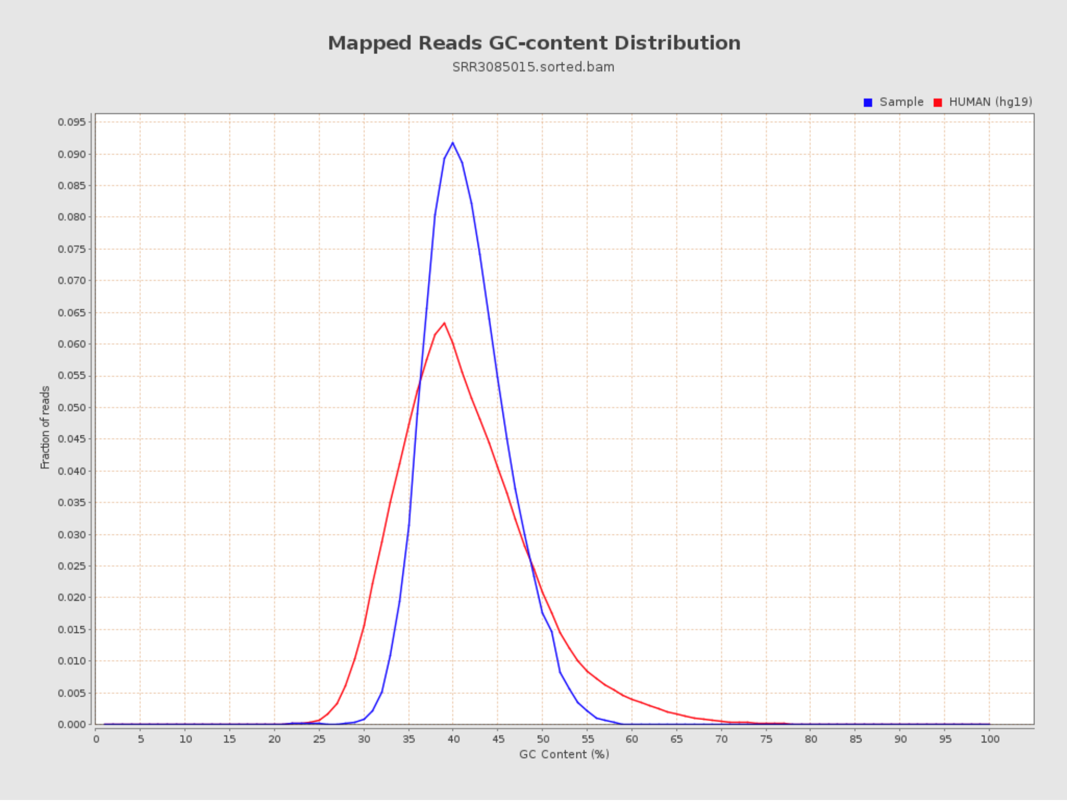
7. Results : Duplication Rate Histogram



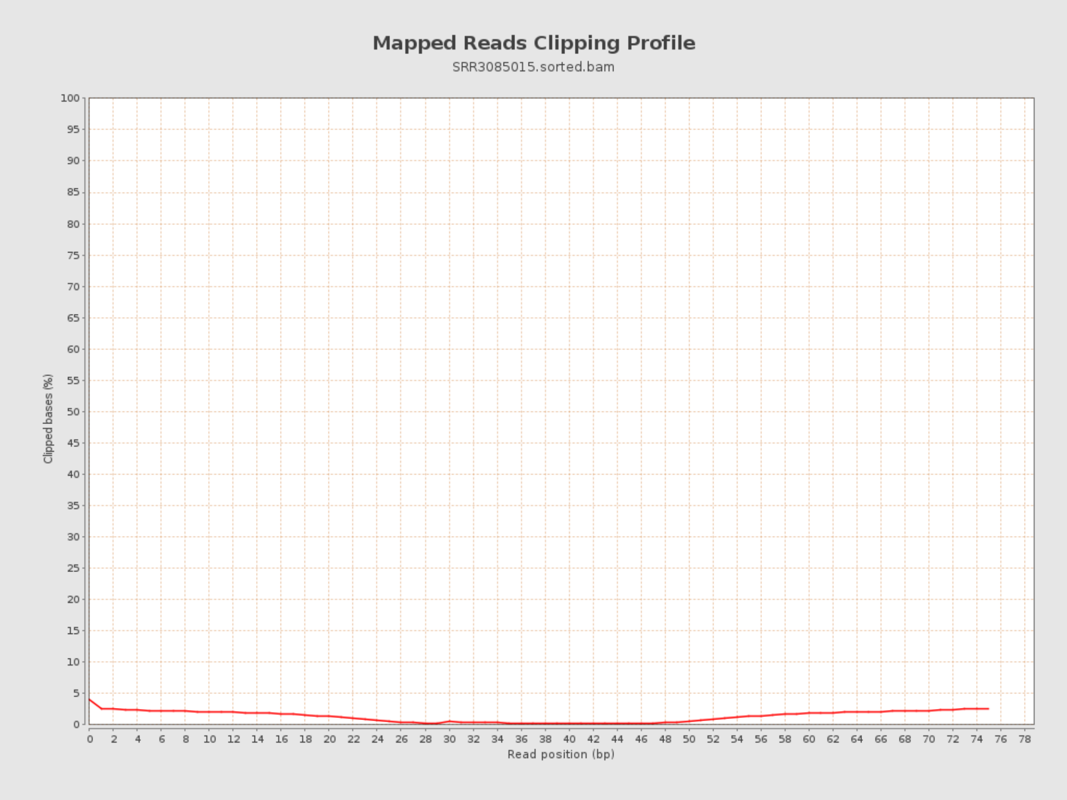
8. Results : Mapped Reads Nucleotide Content



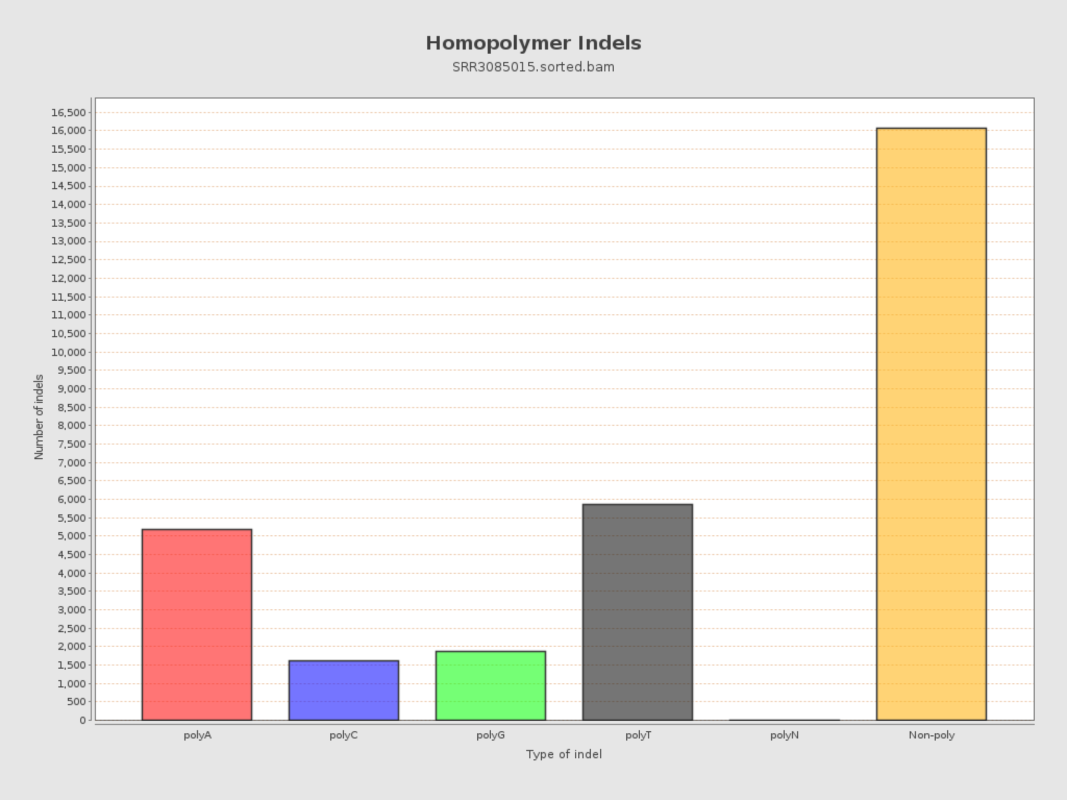
9. Results : Mapped Reads GC-content Distribution



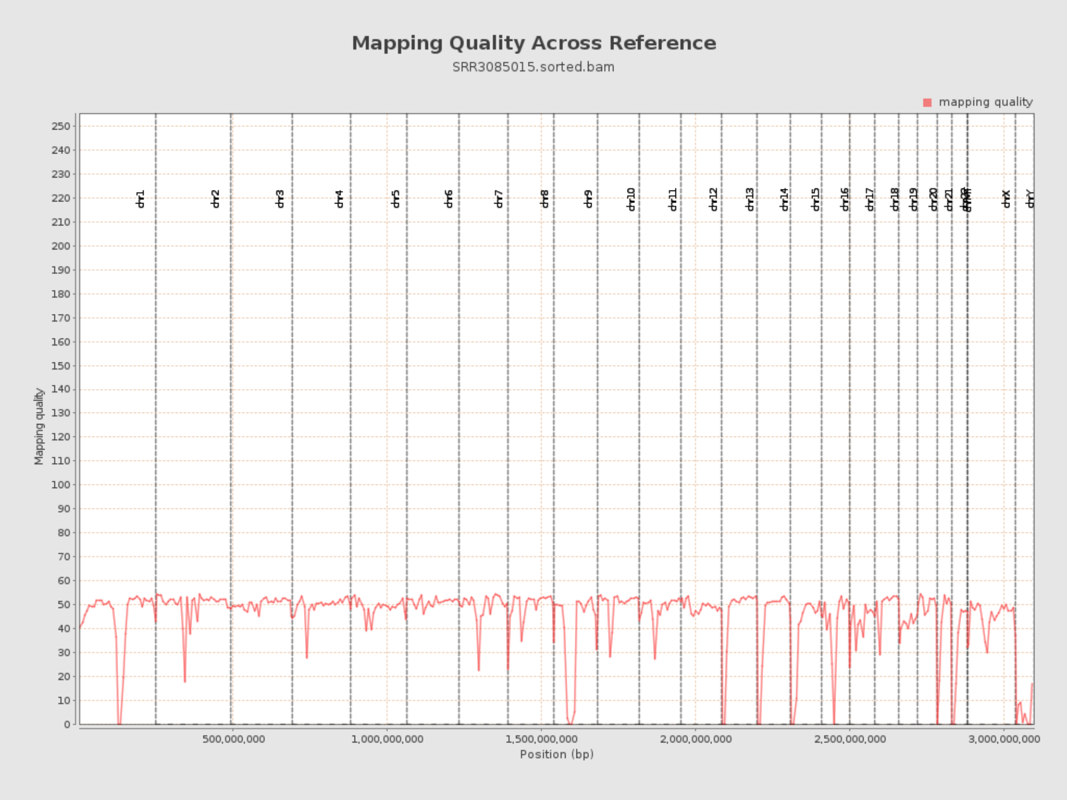
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram