Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:18:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084909.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_SRR3084909 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084909.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:18:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084909.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,793,725
Mapped reads	1,622,523 / 90.46%
Unmapped reads	171,202 / 9.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,668 / 1.04%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	67,875 / 3.78%
Duplication rate	3.63%
Clipped reads	717,418 / 40%

2.2. ACGT Content

Number/percentage of A's	29,605,013 / 27.27%
Number/percentage of C's	20,497,036 / 18.88%
Number/percentage of T's	33,883,086 / 31.21%
Number/percentage of G's	24,548,426 / 22.62%
Number/percentage of N's	15,314 / 0.01%
GC Percentage	41.5%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.26

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

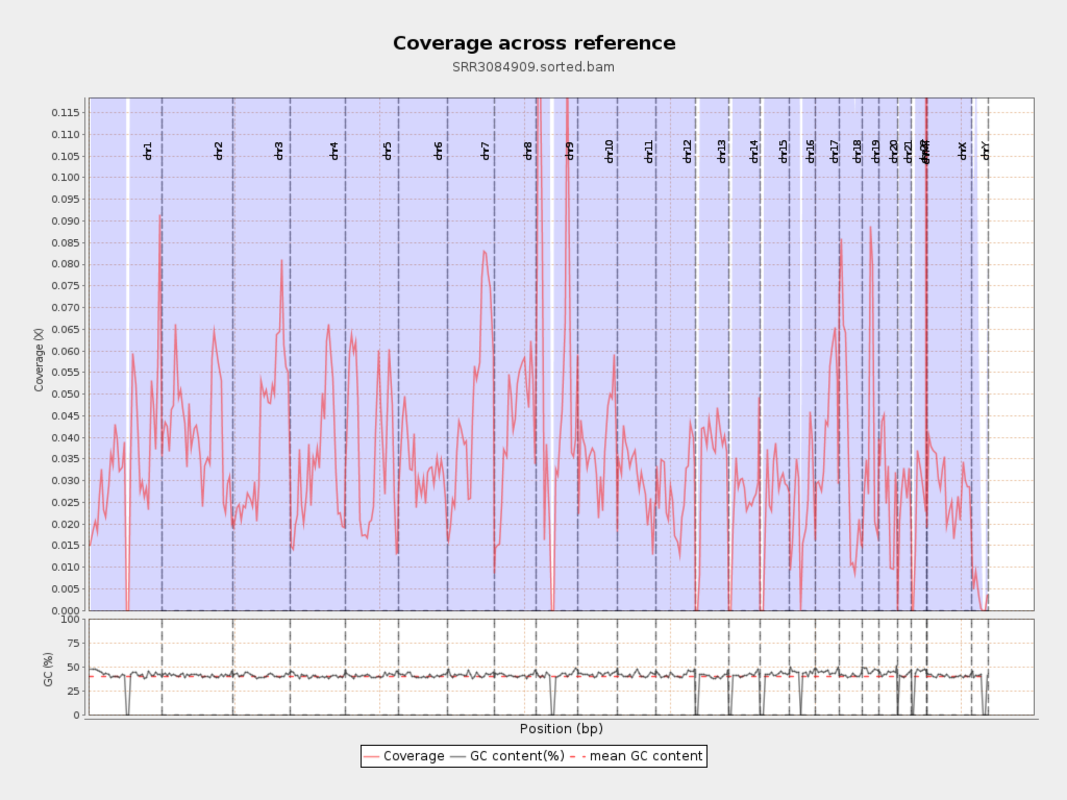
General error rate	0.76%
Mismatches	808,699
Insertions	8,534
Mapped reads with at least one insertion	0.52%
Deletions	25,073
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.33%

2.6. Chromosome stats

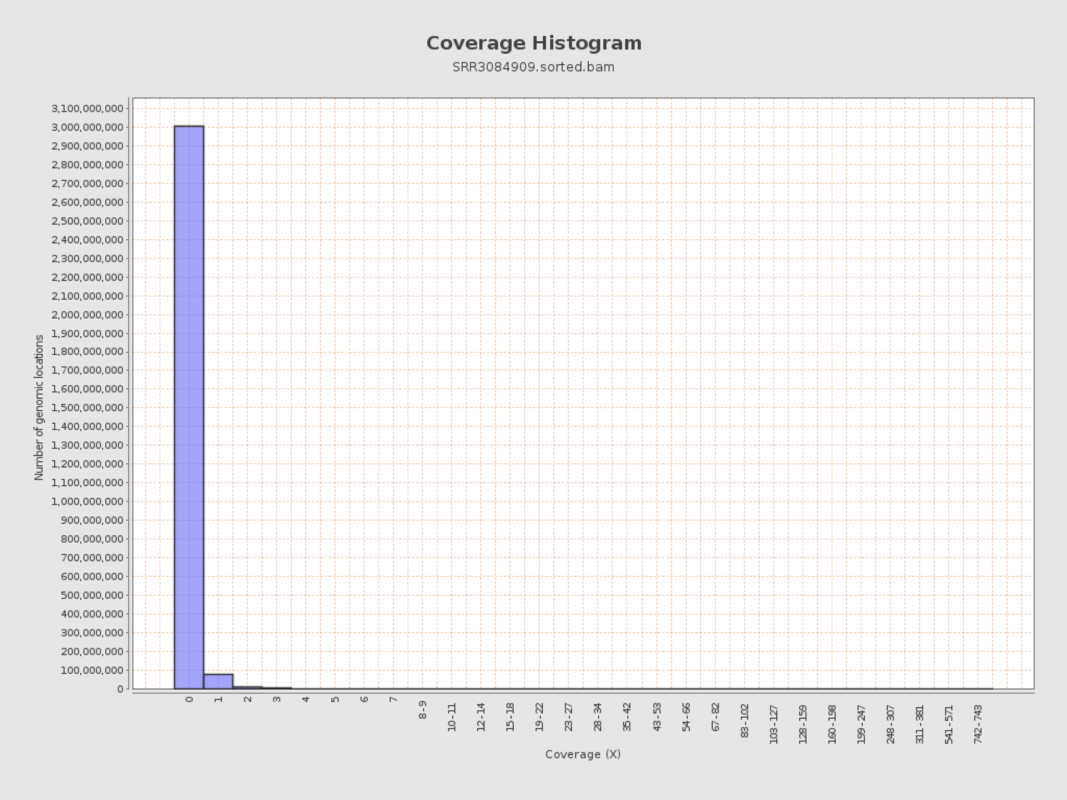
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8340301	0.0335	0.3309
chr2	243199373	10235859	0.0421	0.4064
chr3	198022430	8057193	0.0407	0.2318
chr4	191154276	6416475	0.0336	0.2123
chr5	180915260	6816840	0.0377	0.2263
chr6	171115067	5609374	0.0328	0.2224
chr7	159138663	7692266	0.0483	0.2744

chr8	146364022	6193586	0.0423	0.2703
chr9	141213431	7542410	0.0534	0.3072
chr10	135534747	5091216	0.0376	0.2309
chr11	135006516	4103787	0.0304	0.2356
chr12	133851895	3679199	0.0275	0.1924
chr13	115169878	3859094	0.0335	0.2123
chr14	107349540	2574950	0.024	0.1789
chr15	102531392	2599404	0.0254	0.1887
chr16	90354753	2185802	0.0242	0.1829
chr17	81195210	3526560	0.0434	0.2465
chr18	78077248	2877487	0.0369	0.389
chr19	59128983	2413257	0.0408	0.2841
chr20	63025520	1810000	0.0287	0.1976
chr21	48129895	1179877	0.0245	0.1827
chr22	51304566	1108378	0.0216	0.1683
chrMT	16571	19629	1.1845	1.2774
chrX	155270560	4444962	0.0286	0.2006
chrY	59373566	212644	0.0036	0.0742

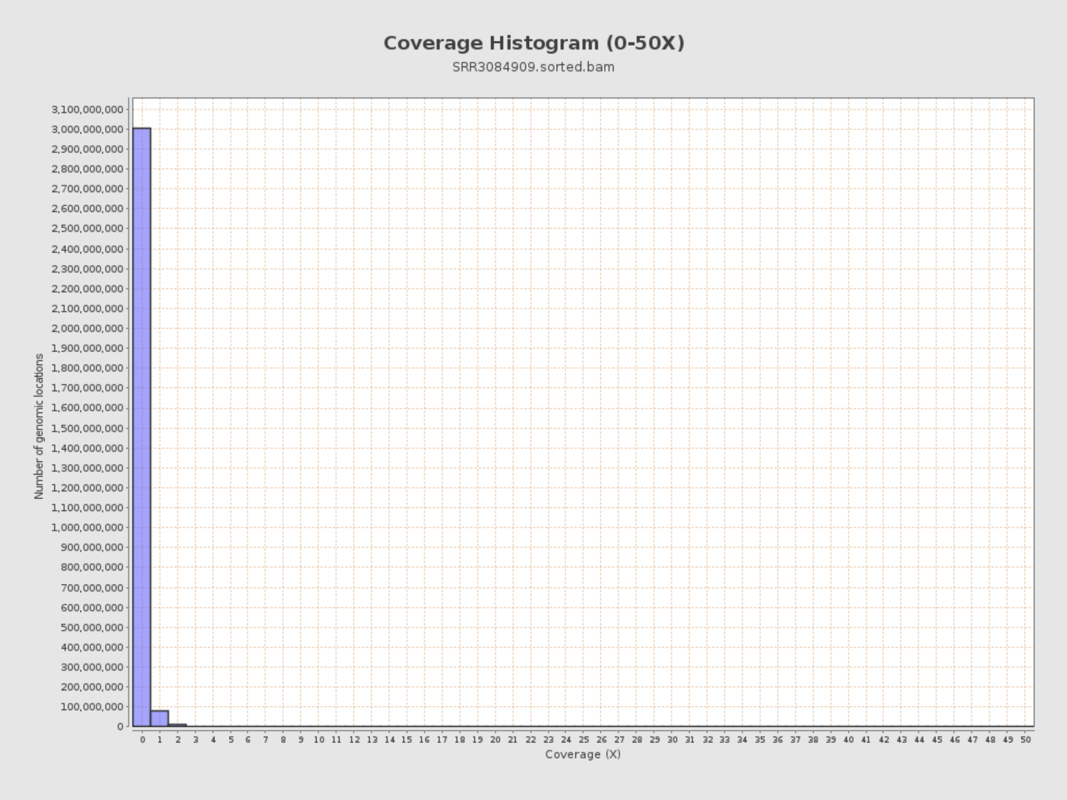
3. Results : Coverage across reference



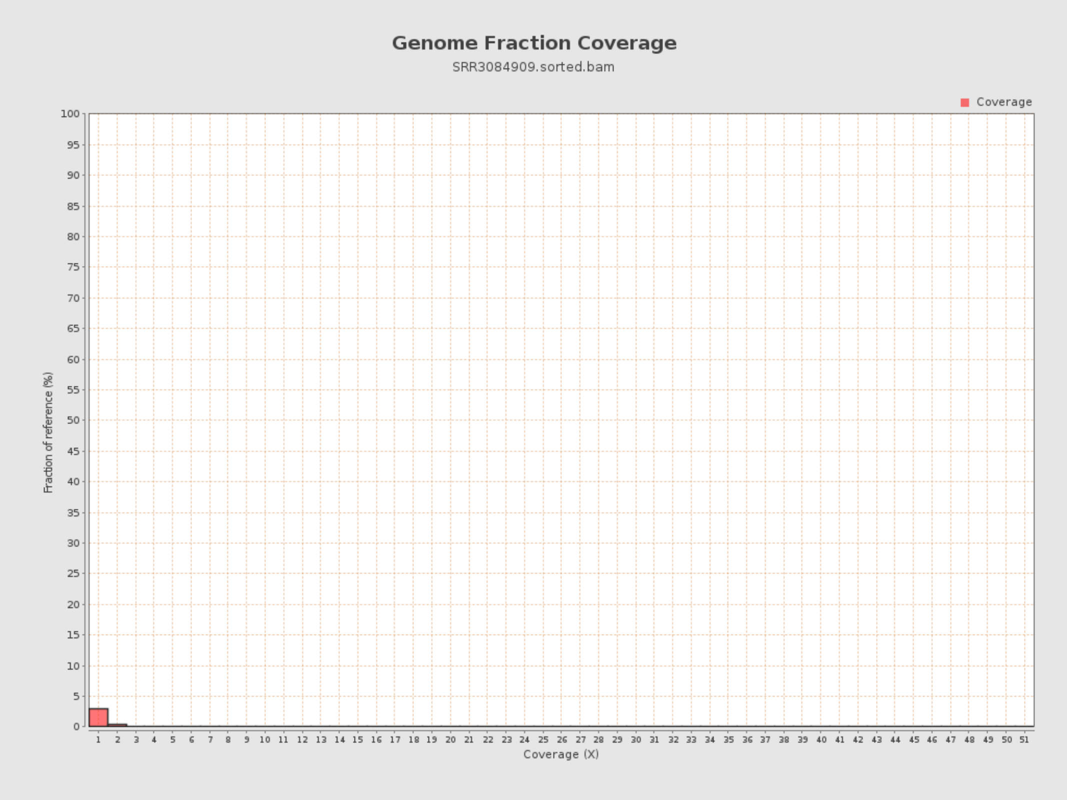
4. Results : Coverage Histogram



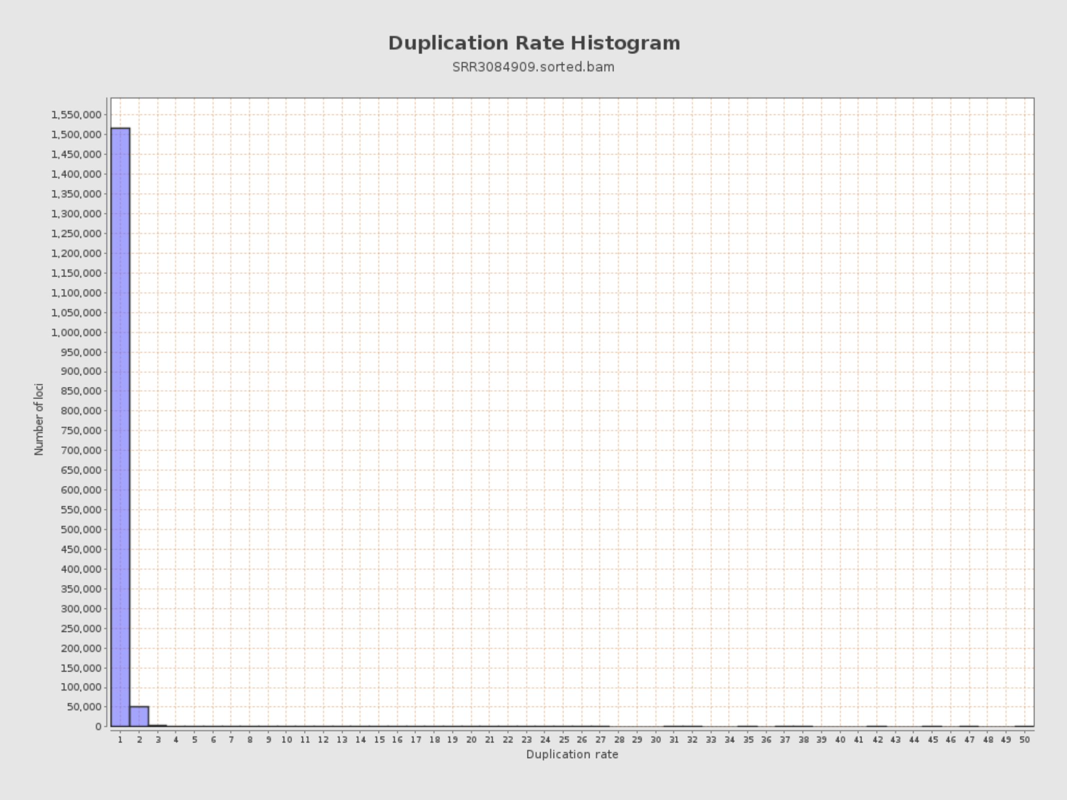
5. Results : Coverage Histogram (0-50X)



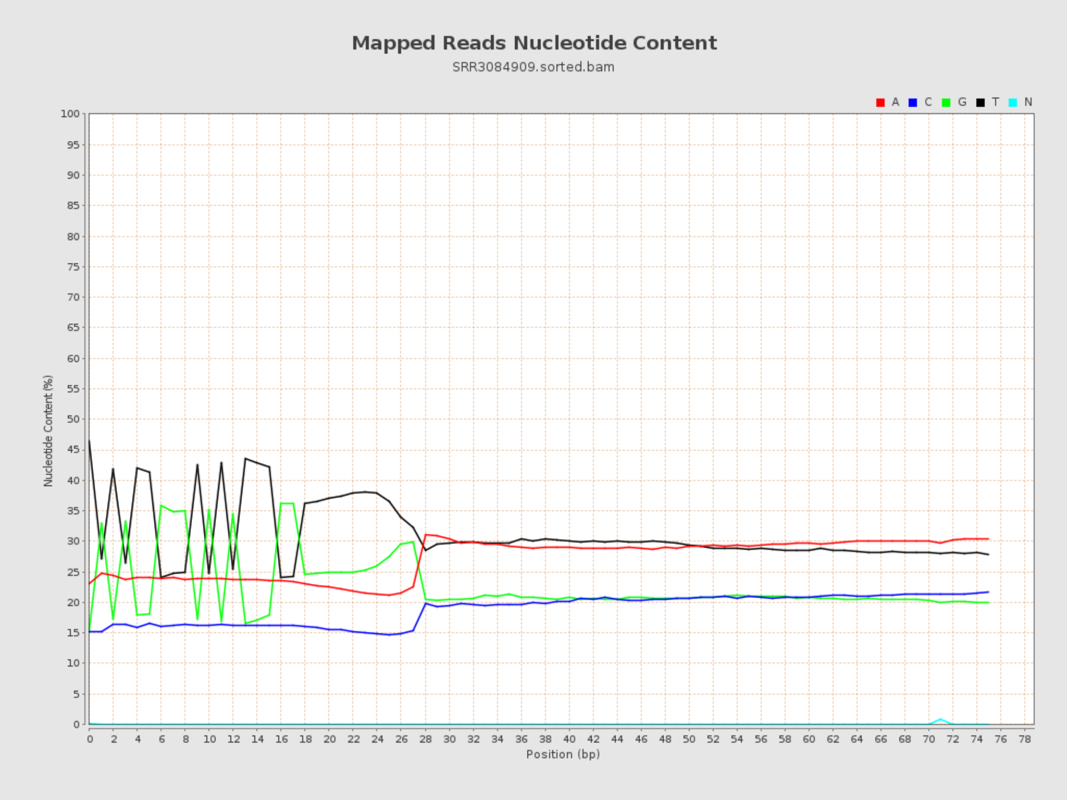
6. Results : Genome Fraction Coverage



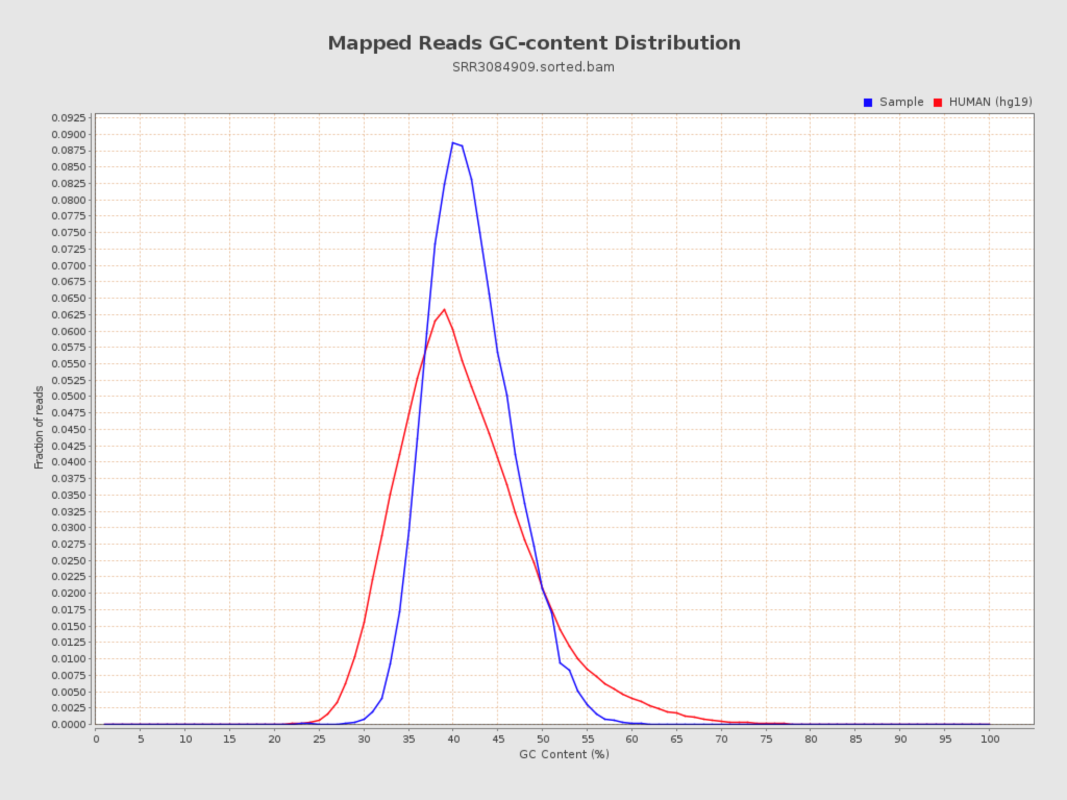
7. Results : Duplication Rate Histogram



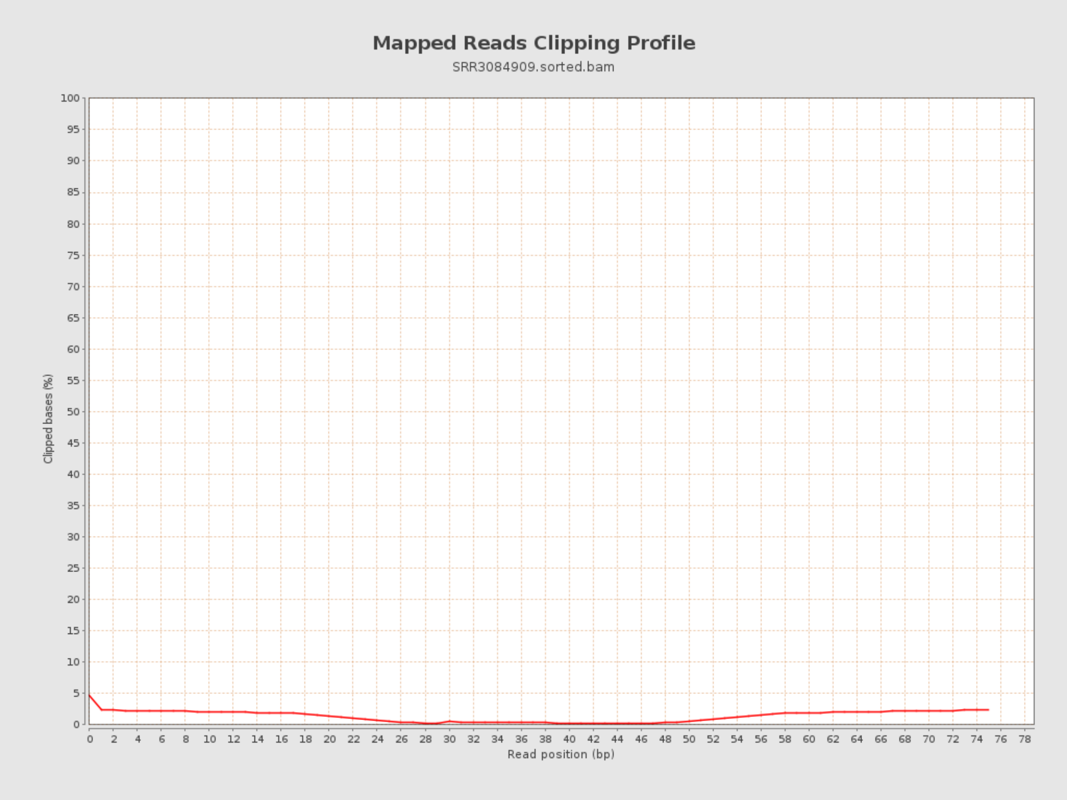
8. Results : Mapped Reads Nucleotide Content



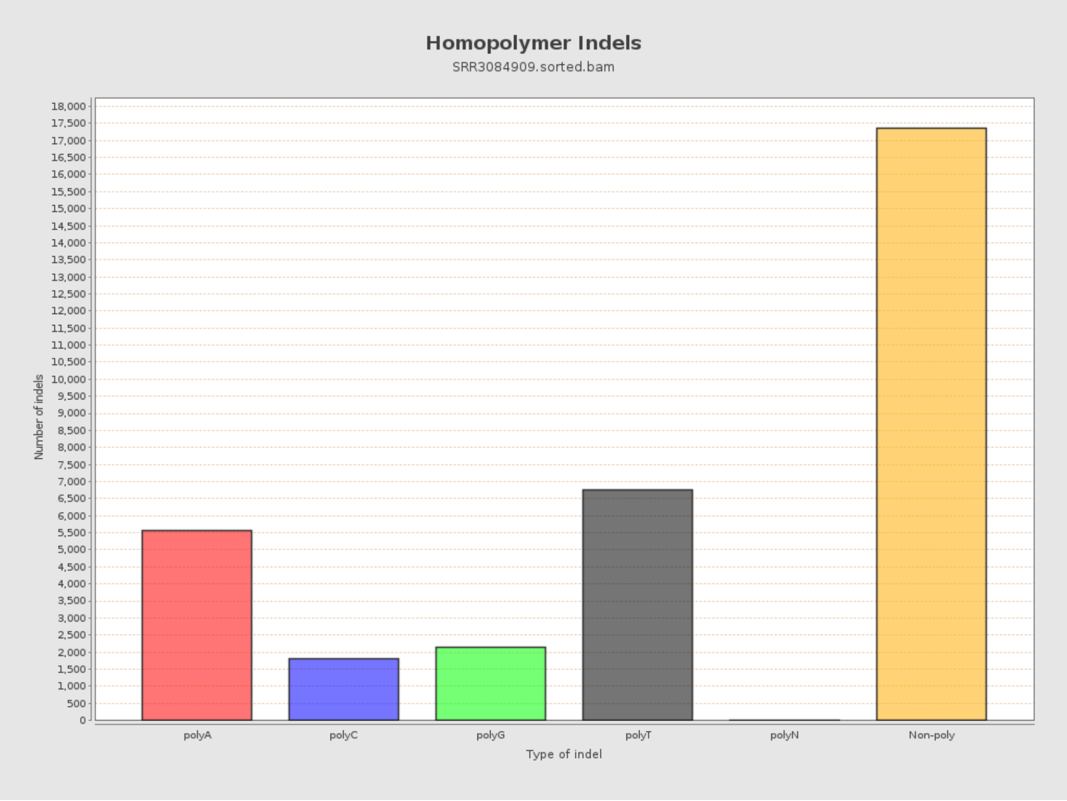
9. Results : Mapped Reads GC-content Distribution



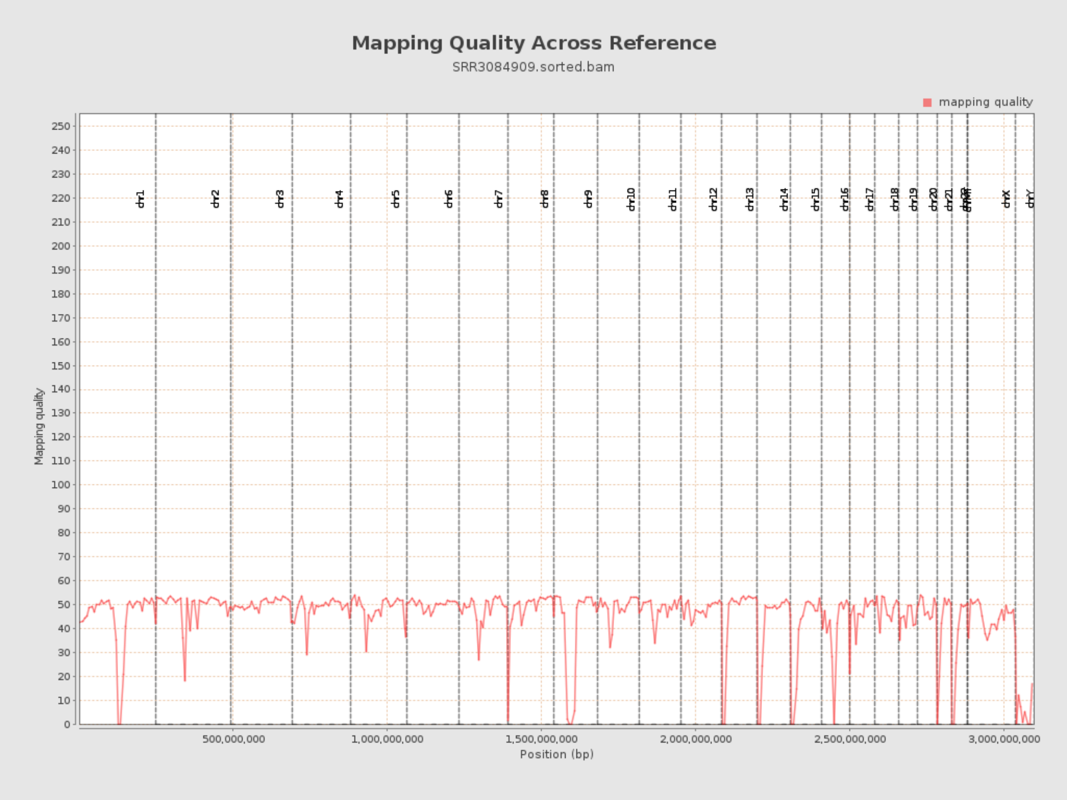
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram