Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:37:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082909.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_SRR3082909 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082909.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:37:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082909.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,660,616
Mapped reads	1,458,334 / 87.82%
Unmapped reads	202,282 / 12.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,469 / 1.17%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	86,491 / 5.21%
Duplication rate	5%
Clipped reads	708,888 / 42.69%

2.2. ACGT Content

Number/percentage of A's	26,081,427 / 27.2%
Number/percentage of C's	17,729,953 / 18.49%
Number/percentage of T's	30,486,573 / 31.79%
Number/percentage of G's	21,589,053 / 22.51%
Number/percentage of N's	4,224 / 0%
GC Percentage	41%

2.3. Coverage

Mean	0.031

Standard Deviation	0.2789

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

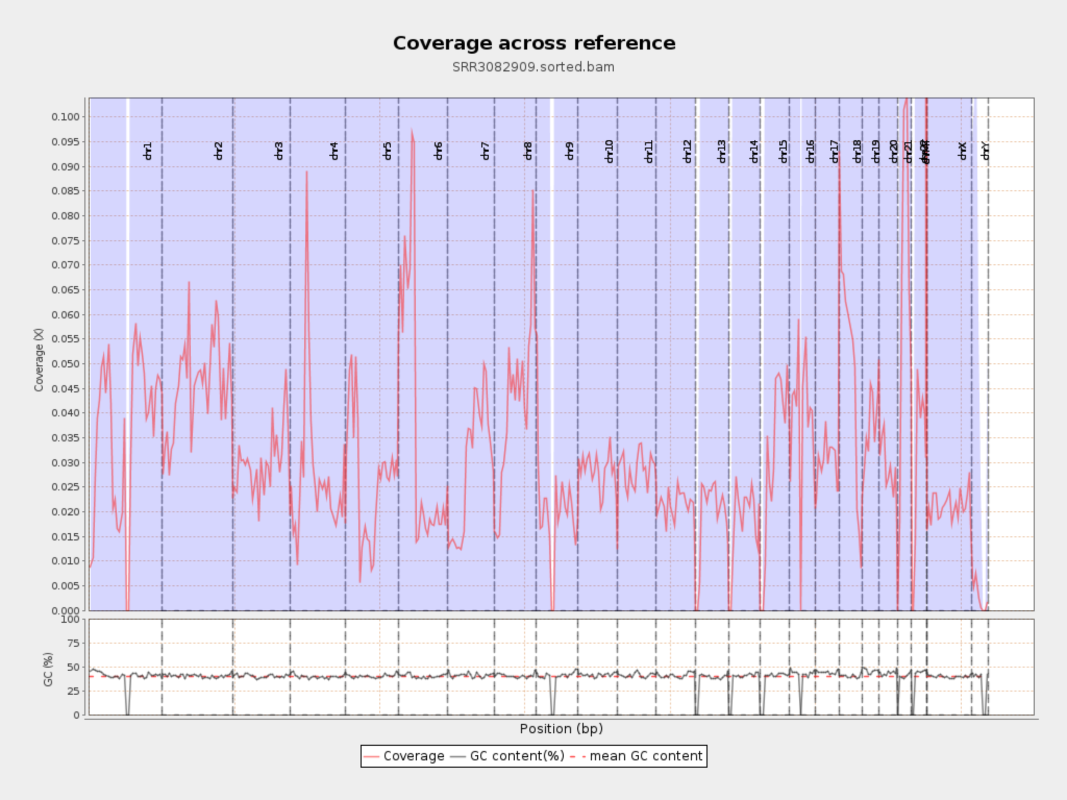
General error rate	0.76%
Mismatches	711,020
Insertions	7,827
Mapped reads with at least one insertion	0.53%
Deletions	22,084
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.84%

2.6. Chromosome stats

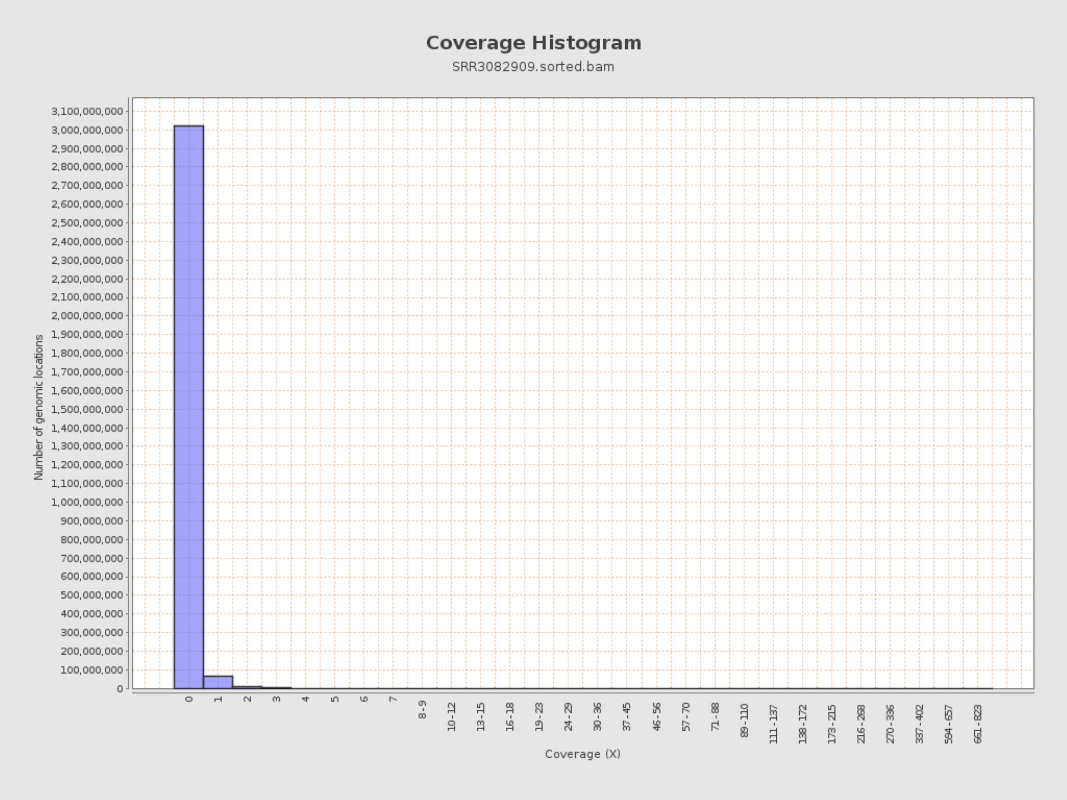
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8954251	0.0359	0.3993
chr2	243199373	11117675	0.0457	0.4743
chr3	198022430	5982813	0.0302	0.2094
chr4	191154276	5277032	0.0276	0.2024
chr5	180915260	4841673	0.0268	0.1986
chr6	171115067	6399928	0.0374	0.282
chr7	159138663	4704363	0.0296	0.239

chr8	146364022	6166612	0.0421	0.297
chr9	141213431	2659097	0.0188	0.2279
chr10	135534747	3865421	0.0285	0.2183
chr11	135006516	3848137	0.0285	0.2338
chr12	133851895	2874135	0.0215	0.1801
chr13	115169878	2202494	0.0191	0.1671
chr14	107349540	1879386	0.0175	0.1669
chr15	102531392	3154471	0.0308	0.2133
chr16	90354753	3498739	0.0387	0.2451
chr17	81195210	2441096	0.0301	0.2147
chr18	78077248	3913455	0.0501	0.4713
chr19	59128983	2215805	0.0375	0.3325
chr20	63025520	1844690	0.0293	0.2185
chr21	48129895	2993858	0.0622	0.3067
chr22	51304566	1493562	0.0291	0.2051
chrMT	16571	143256	8.645	6.1555
chrX	155270560	3290873	0.0212	0.189
chrY	59373566	164222	0.0028	0.0663

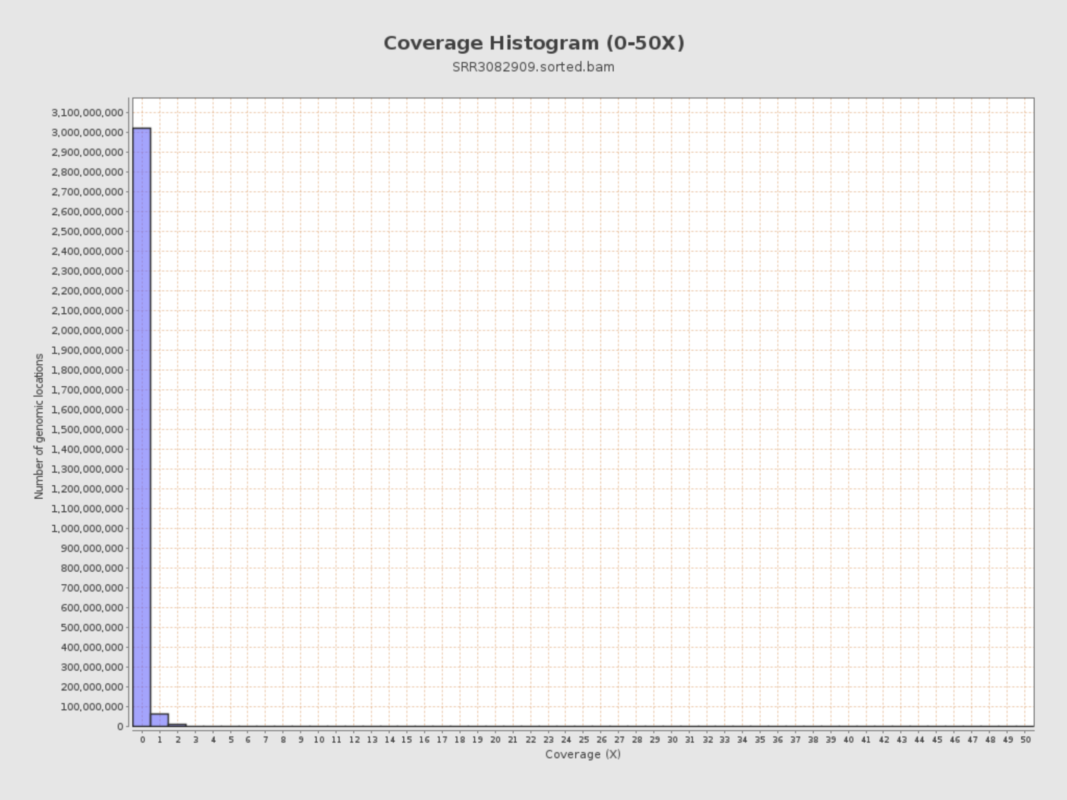
3. Results : Coverage across reference



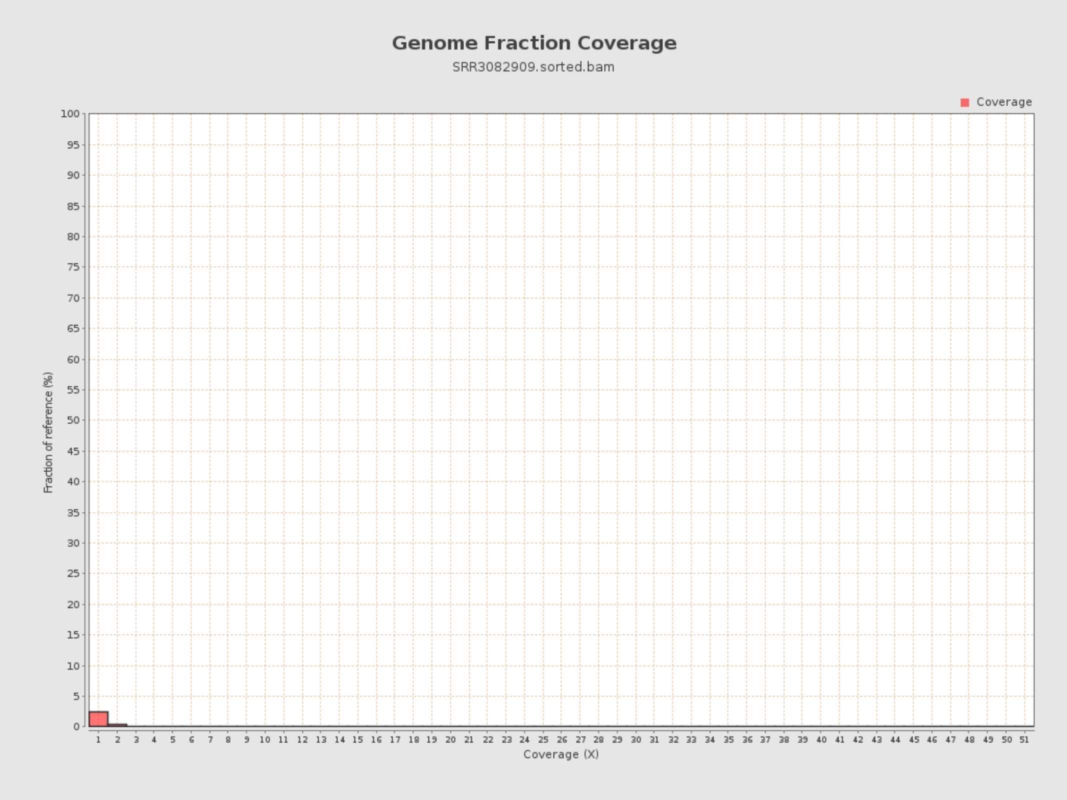
4. Results : Coverage Histogram



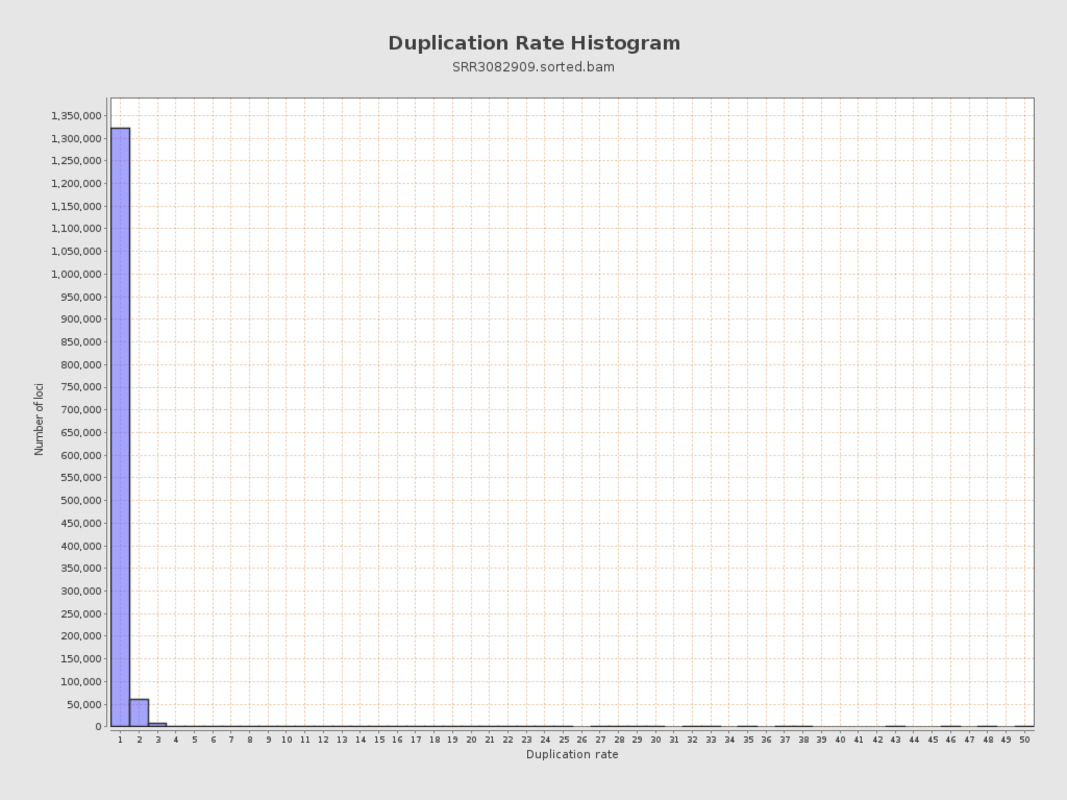
5. Results : Coverage Histogram (0-50X)



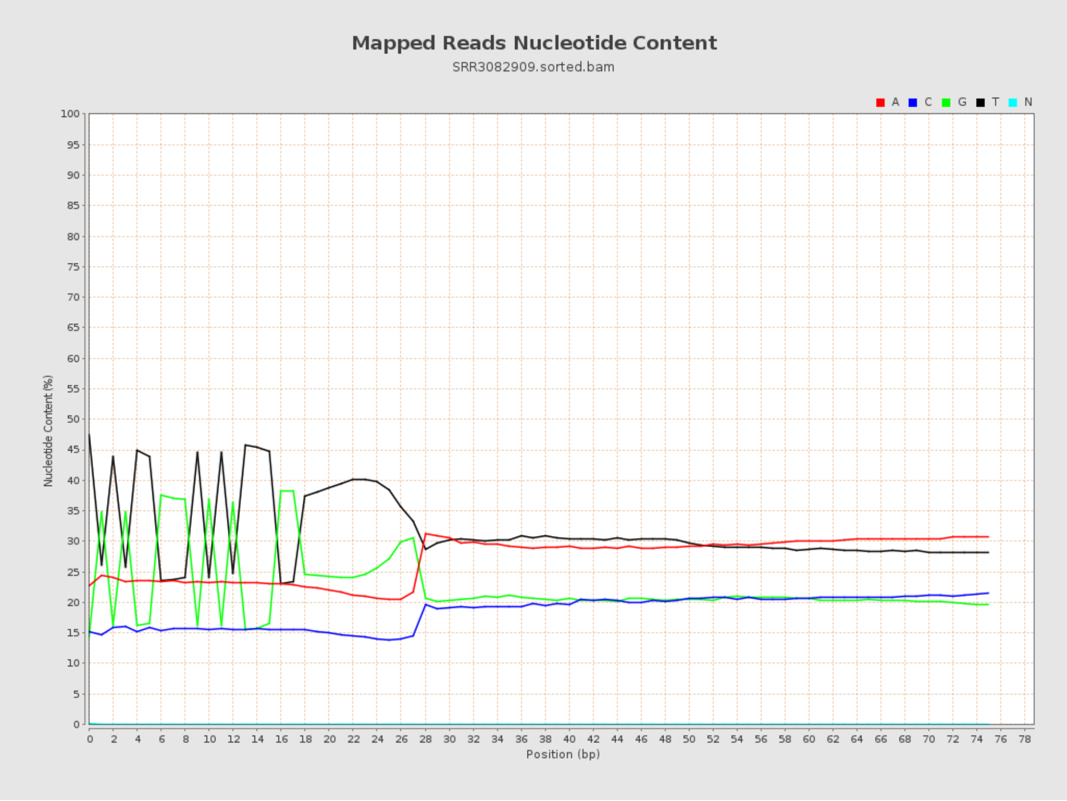
6. Results : Genome Fraction Coverage



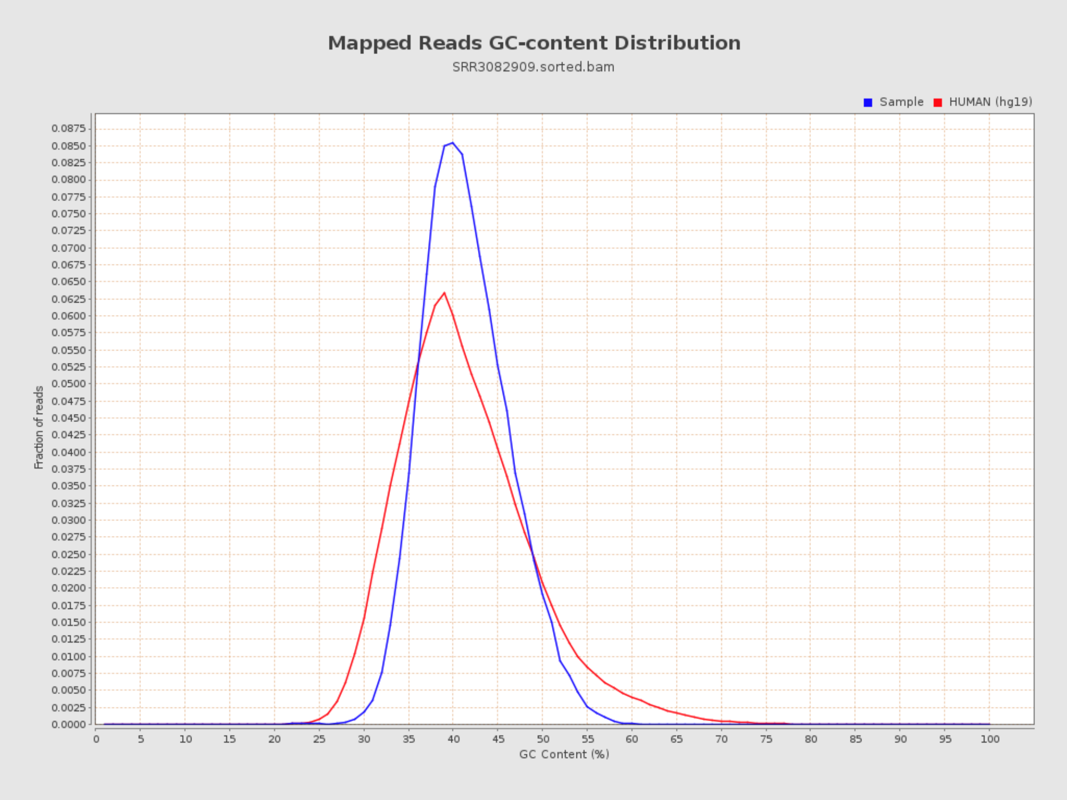
7. Results : Duplication Rate Histogram



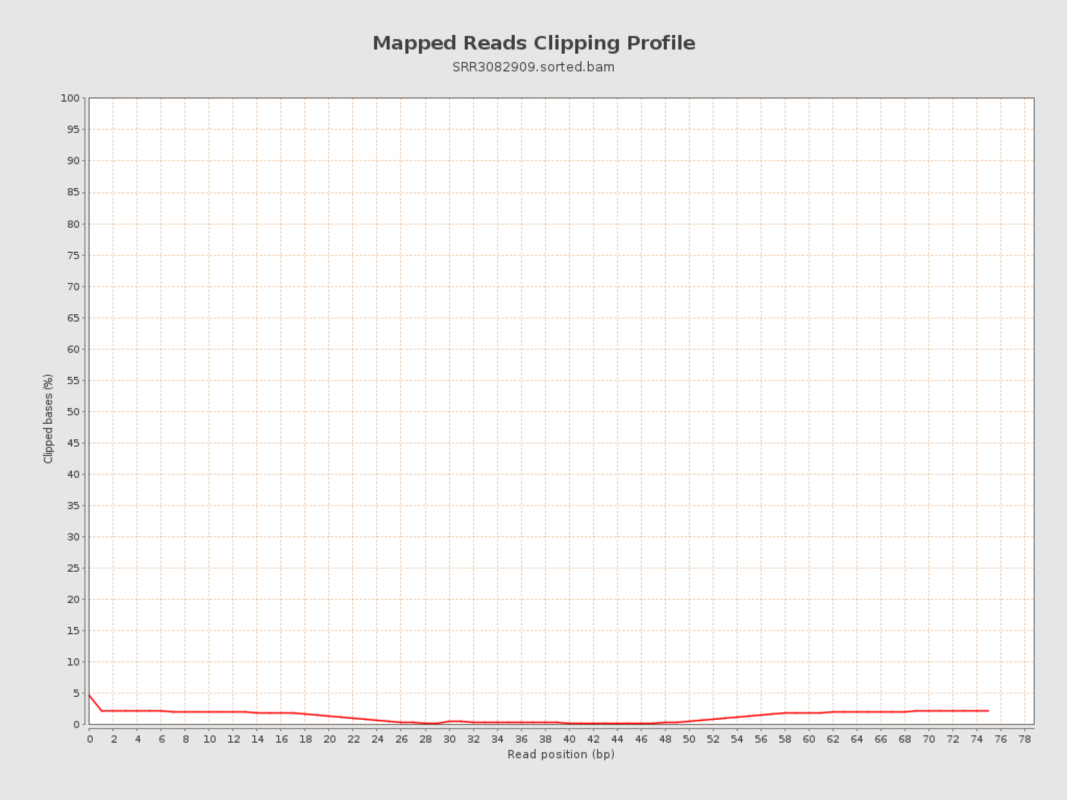
8. Results : Mapped Reads Nucleotide Content



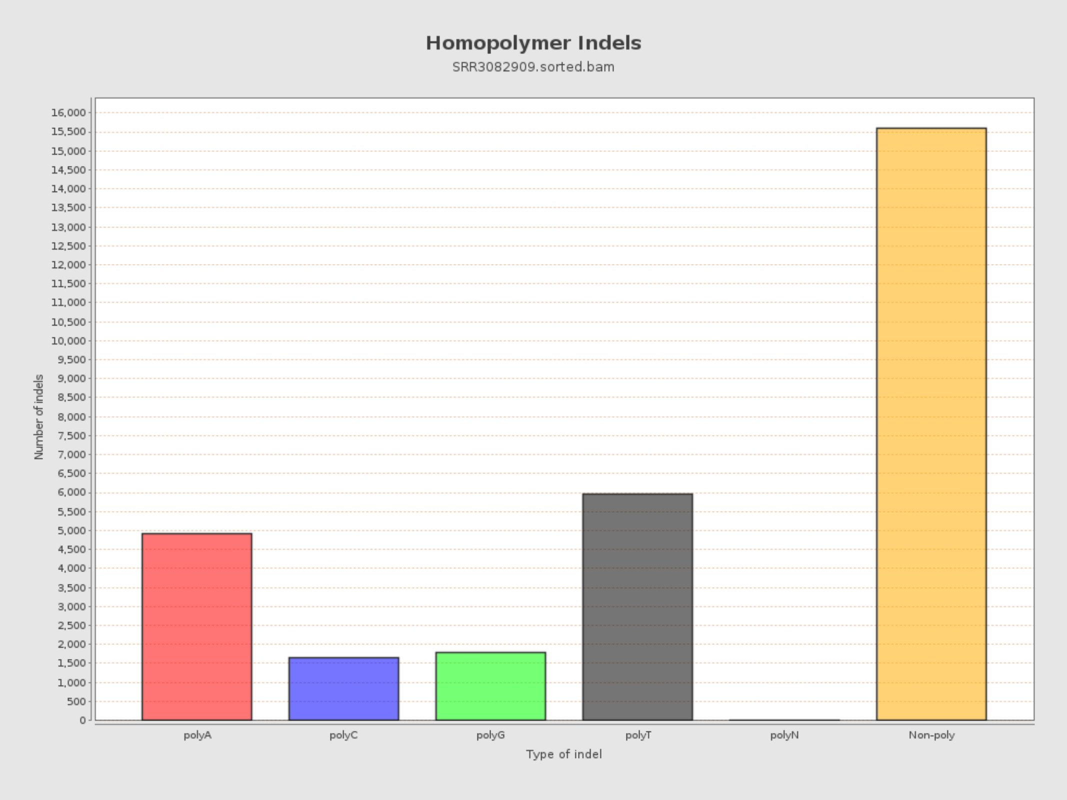
9. Results : Mapped Reads GC-content Distribution



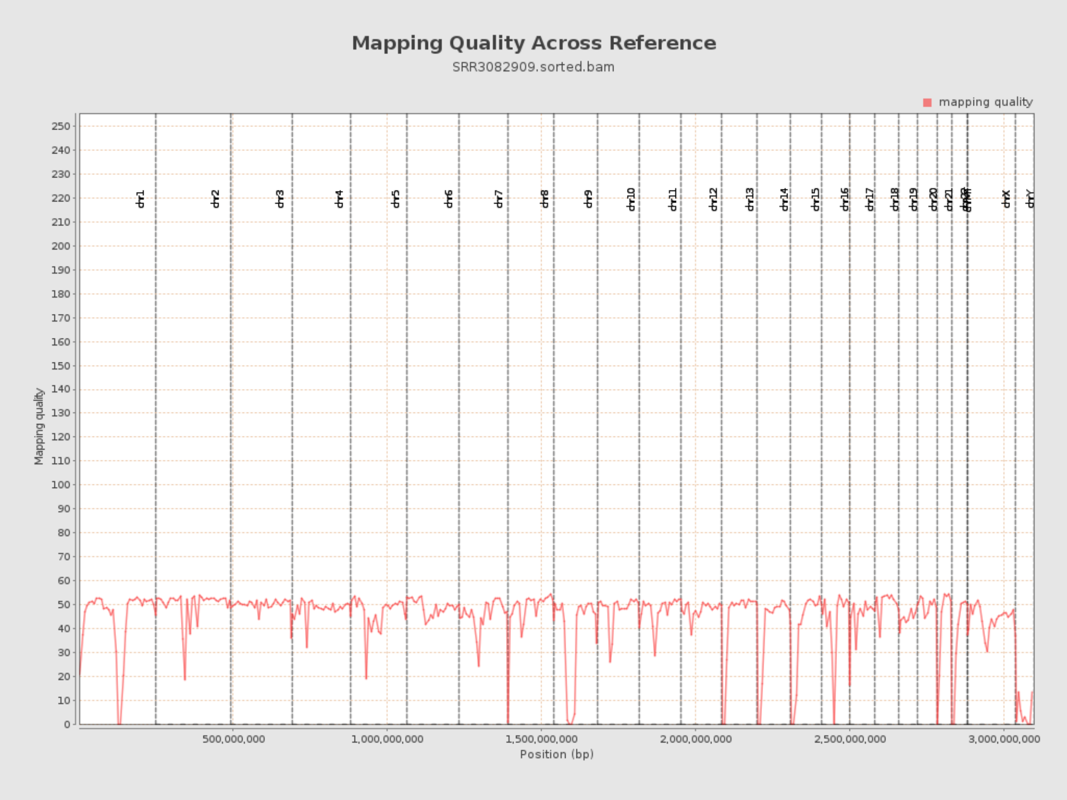
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram