Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:40:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082498.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_SRR3082498 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082498.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:40:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082498.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,926,882
Mapped reads	2,651,776 / 90.6%
Unmapped reads	275,106 / 9.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,560 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	129,583 / 4.43%
Duplication rate	3.94%
Clipped reads	1,147,007 / 39.19%

2.2. ACGT Content

Number/percentage of A's	50,721,897 / 28.3%
Number/percentage of C's	33,942,379 / 18.94%
Number/percentage of T's	55,655,227 / 31.05%
Number/percentage of G's	38,896,507 / 21.7%
Number/percentage of N's	3,790 / 0%
GC Percentage	40.64%

2.3. Coverage

Mean	0.0579

Standard Deviation	0.4533

2.4. Mapping Quality

Mean Mapping Quality	46.96

2.5. Mismatches and indels

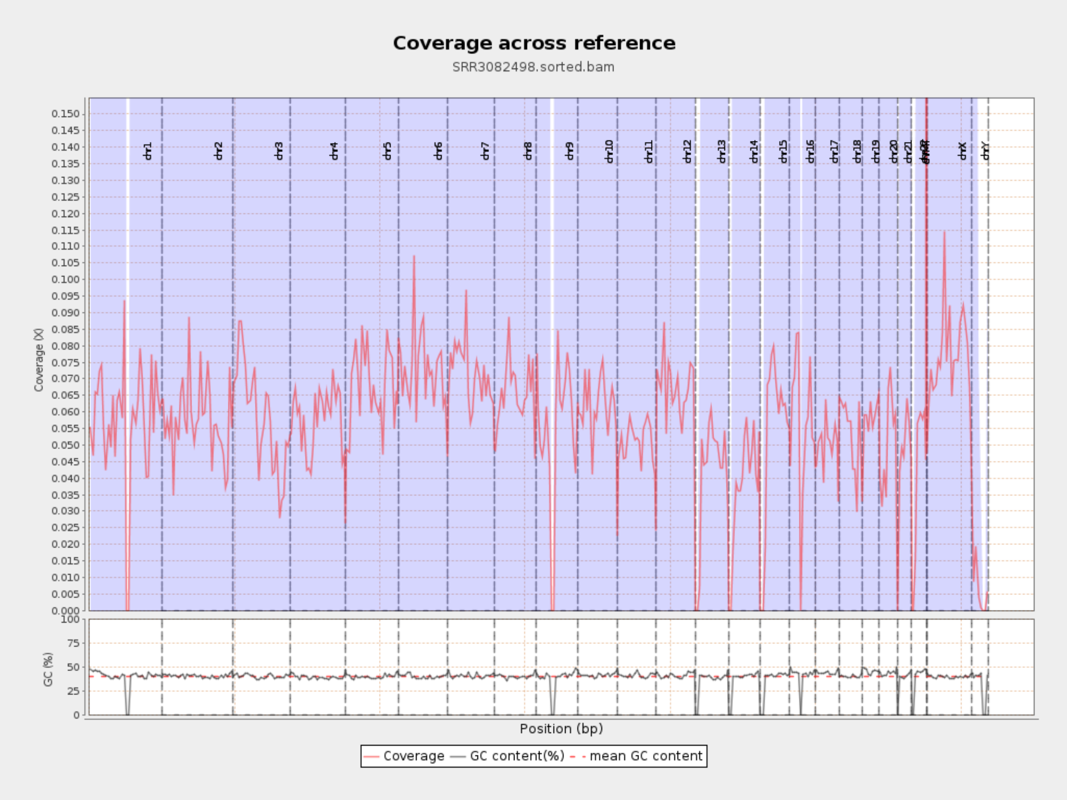
General error rate	0.84%
Mismatches	1,484,777
Insertions	14,131
Mapped reads with at least one insertion	0.53%
Deletions	42,553
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.19%

2.6. Chromosome stats

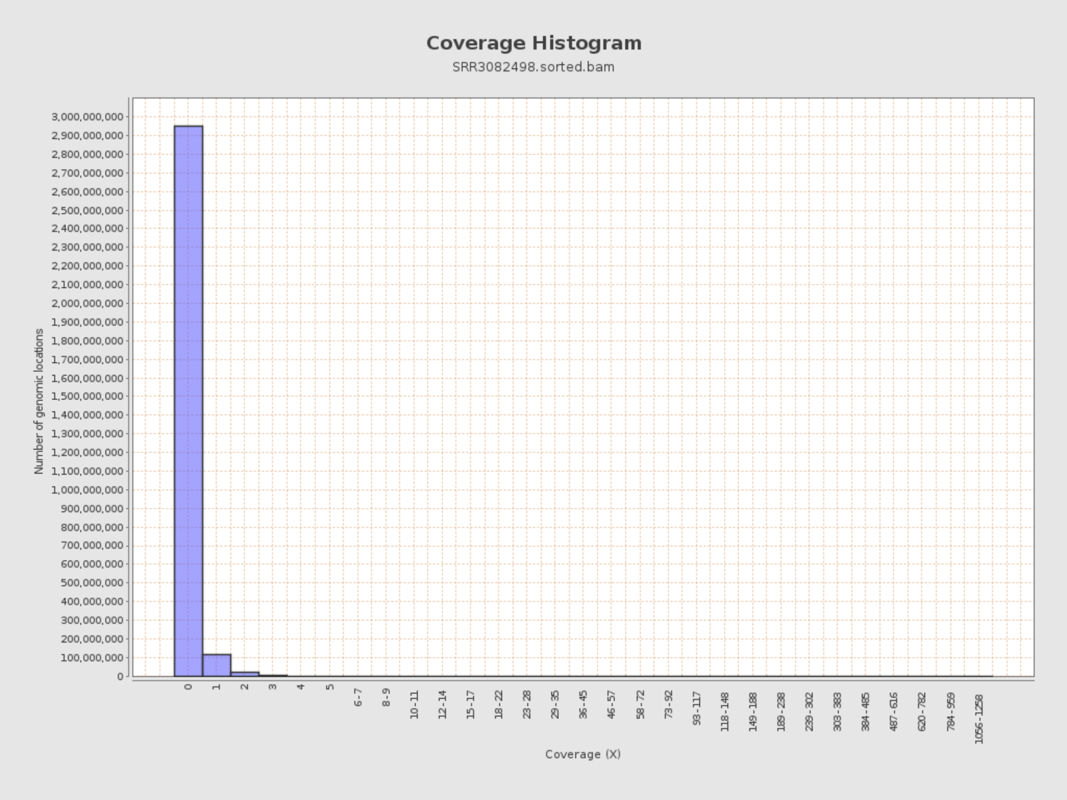
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14246190	0.0572	0.7675
chr2	243199373	14002309	0.0576	0.5066
chr3	198022430	11567350	0.0584	0.2892
chr4	191154276	11074728	0.0579	0.3017
chr5	180915260	12265592	0.0678	0.3112
chr6	171115067	12508539	0.0731	0.4688
chr7	159138663	11435372	0.0719	0.4773

chr8	146364022	9619120	0.0657	0.822
chr9	141213431	7553323	0.0535	0.3684
chr10	135534747	8465914	0.0625	0.3966
chr11	135006516	6797036	0.0503	0.4623
chr12	133851895	8969657	0.067	0.3145
chr13	115169878	4716438	0.041	0.2426
chr14	107349540	3952593	0.0368	0.256
chr15	102531392	5516769	0.0538	0.2833
chr16	90354753	5143559	0.0569	0.2971
chr17	81195210	4060168	0.05	0.3118
chr18	78077248	4173290	0.0535	0.5735
chr19	59128983	3430652	0.058	0.5905
chr20	63025520	3144143	0.0499	0.2741
chr21	48129895	2230818	0.0463	0.2741
chr22	51304566	2023432	0.0394	0.2331
chrMT	16571	11596	0.6998	0.9954
chrX	155270560	11957256	0.077	0.3858
chrY	59373566	422424	0.0071	0.1307

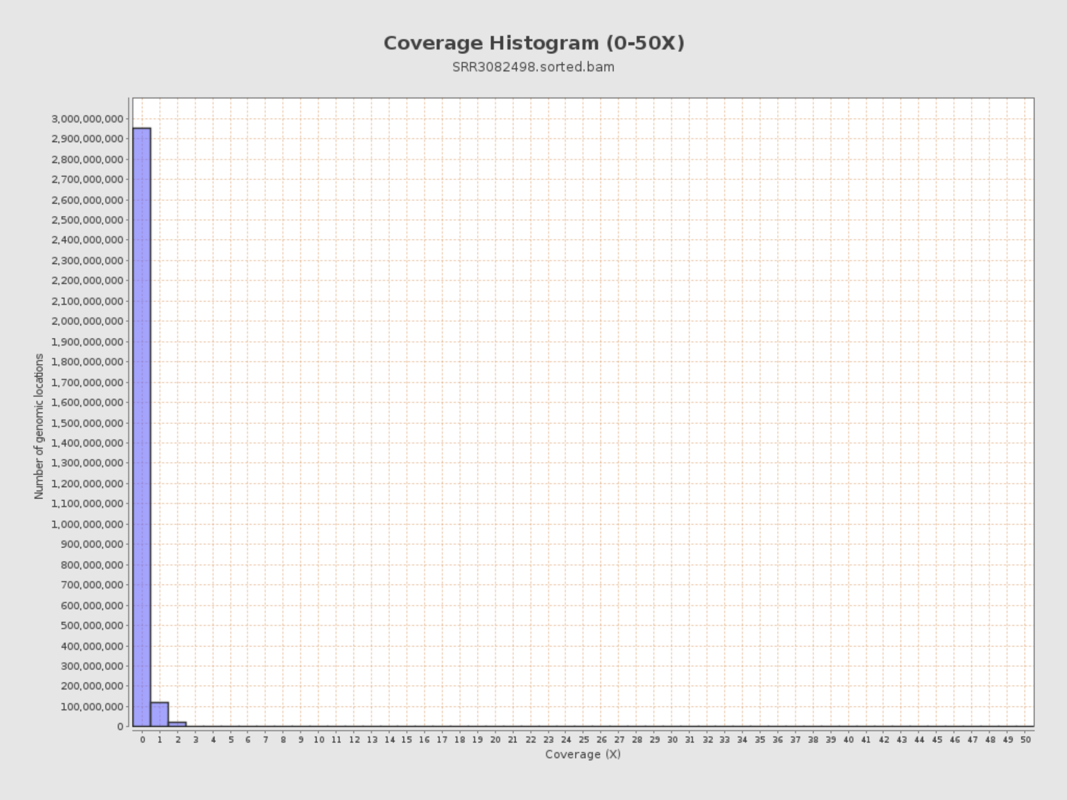
3. Results : Coverage across reference



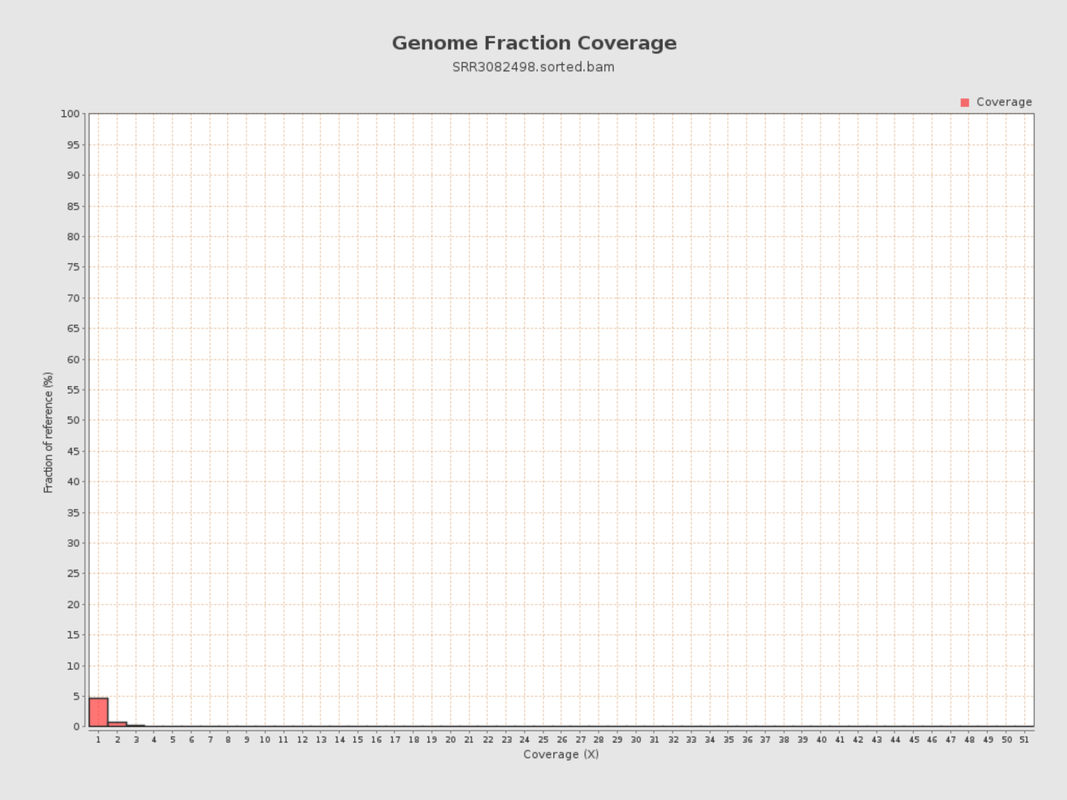
4. Results : Coverage Histogram



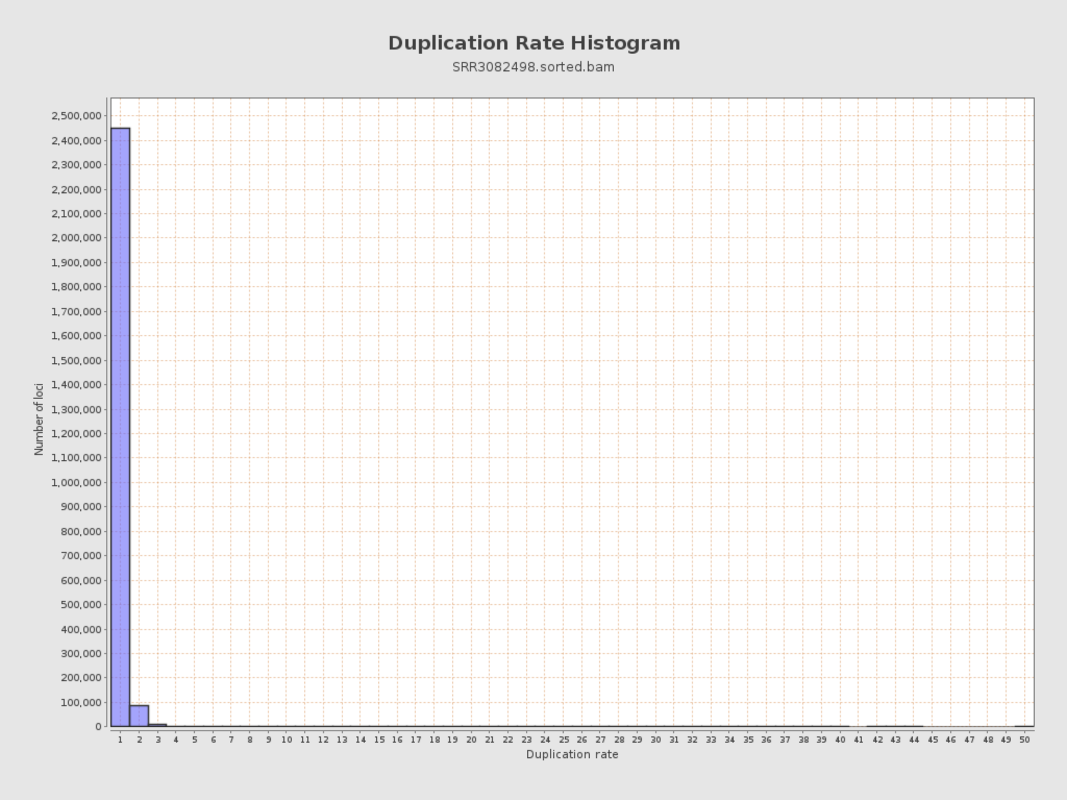
5. Results : Coverage Histogram (0-50X)



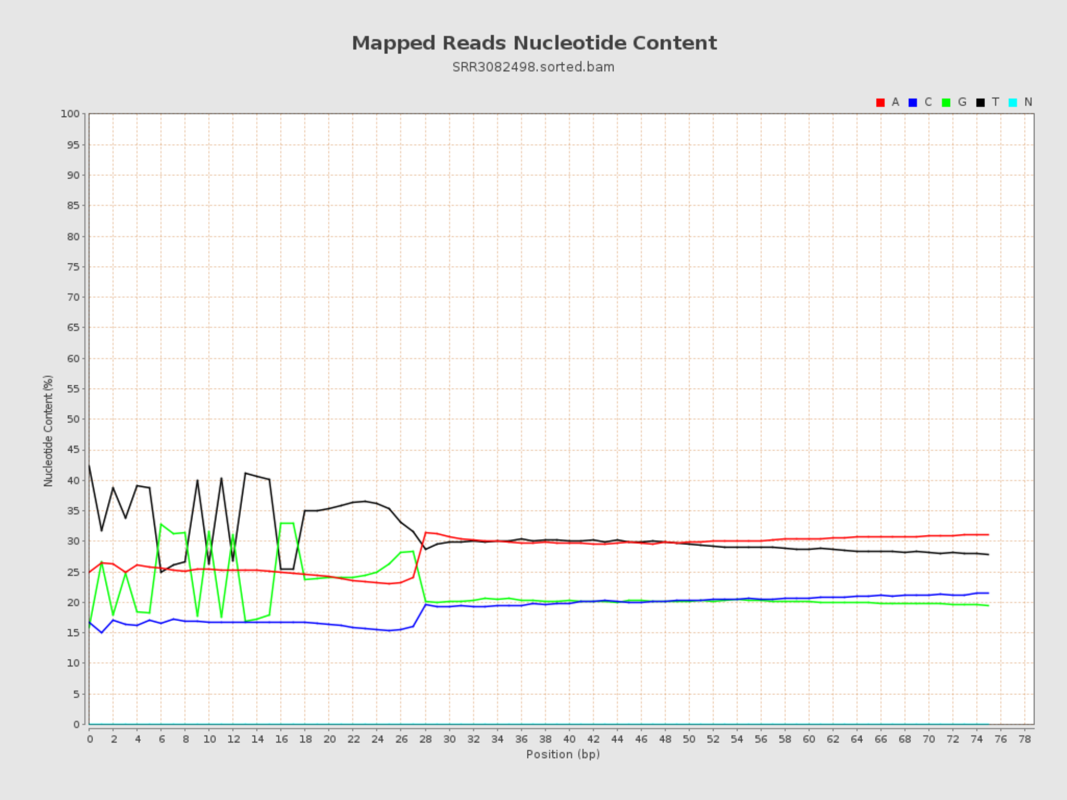
6. Results : Genome Fraction Coverage



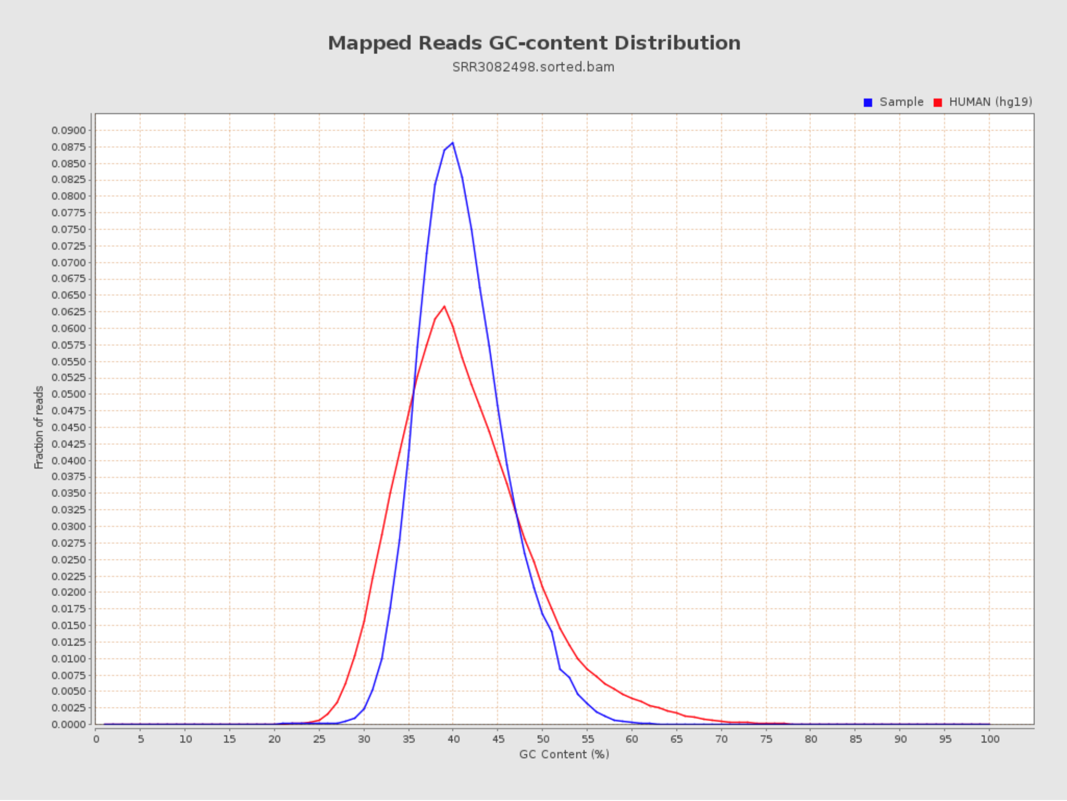
7. Results : Duplication Rate Histogram



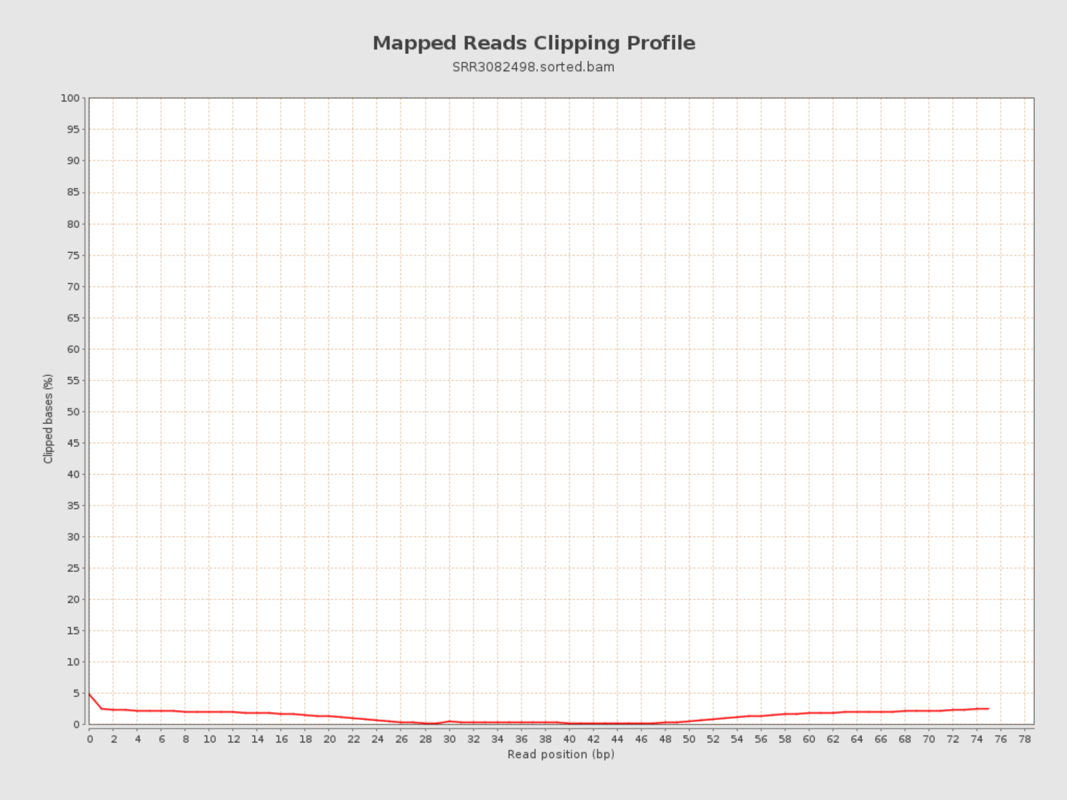
8. Results : Mapped Reads Nucleotide Content



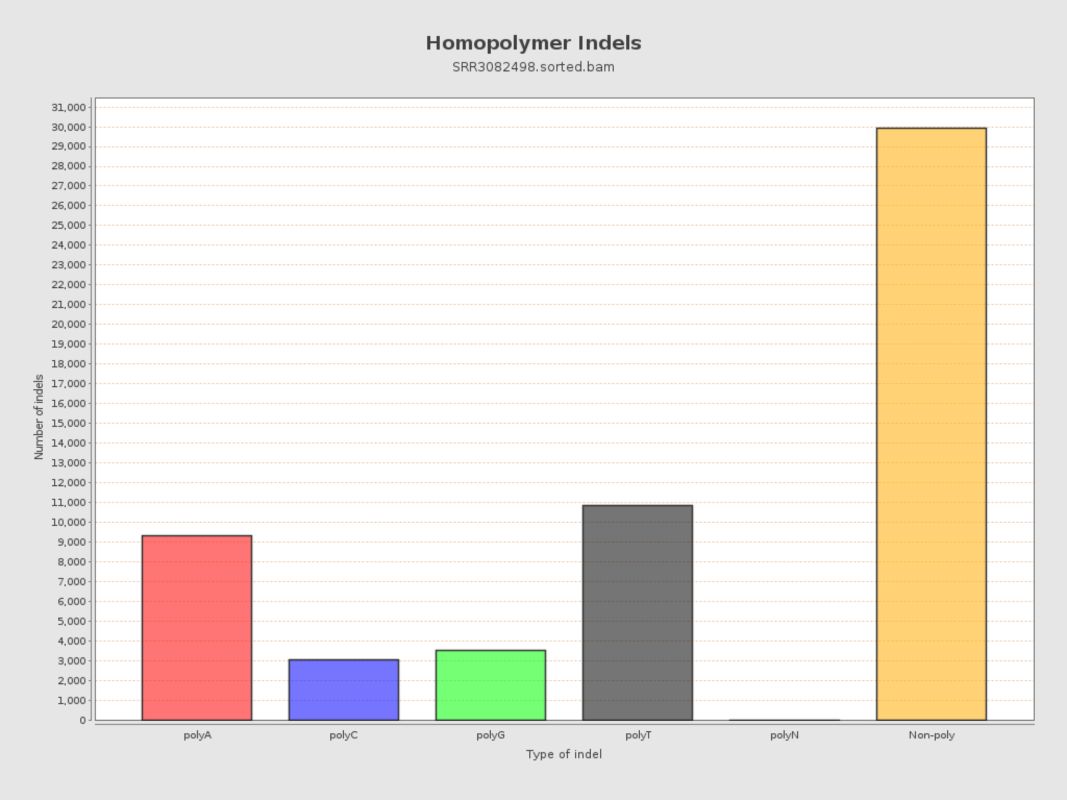
9. Results : Mapped Reads GC-content Distribution



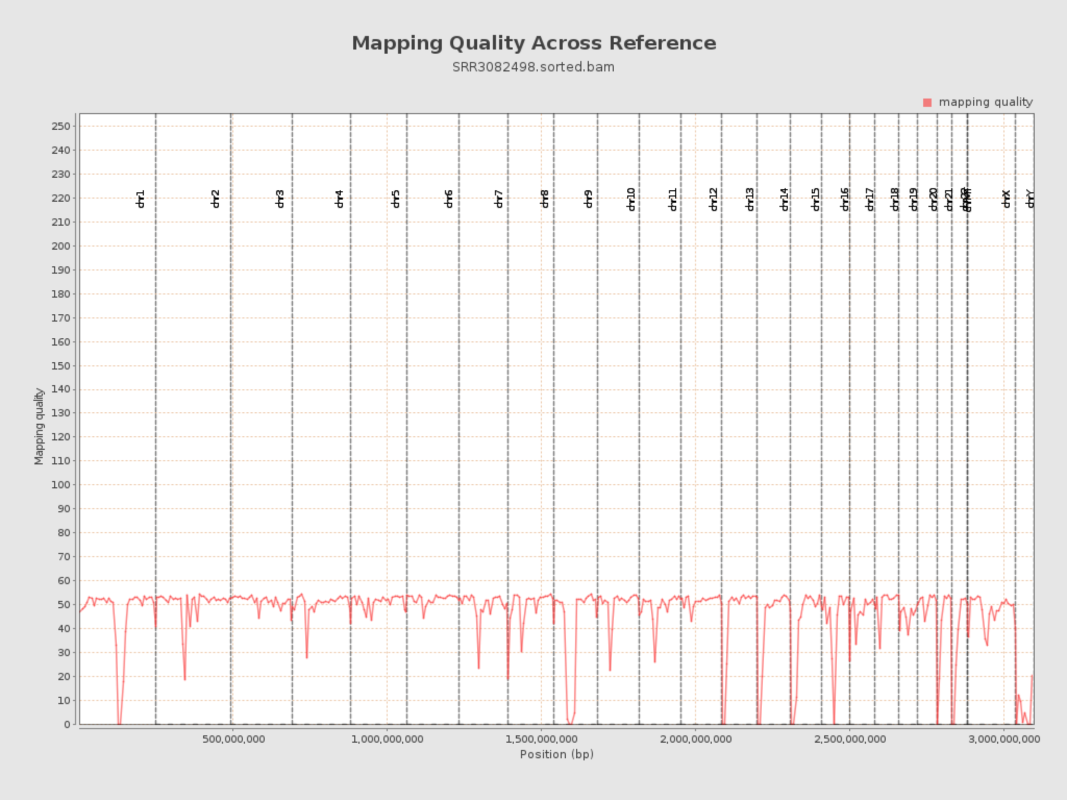
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram