Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:06:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082984.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_SRR3082984 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082984.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:06:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,348,945
Mapped reads	3,714,486 / 85.41%
Unmapped reads	634,459 / 14.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,399 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	187,933 / 4.32%
Duplication rate	3.75%
Clipped reads	1,460,864 / 33.59%

2.2. ACGT Content

Number/percentage of A's	71,894,739 / 28.42%
Number/percentage of C's	46,347,820 / 18.32%
Number/percentage of T's	81,655,227 / 32.27%
Number/percentage of G's	53,075,983 / 20.98%
Number/percentage of N's	25,444 / 0.01%
GC Percentage	39.3%

2.3. Coverage

Mean	0.0818

Standard Deviation	0.6582

2.4. Mapping Quality

Mean Mapping Quality	46.59

2.5. Mismatches and indels

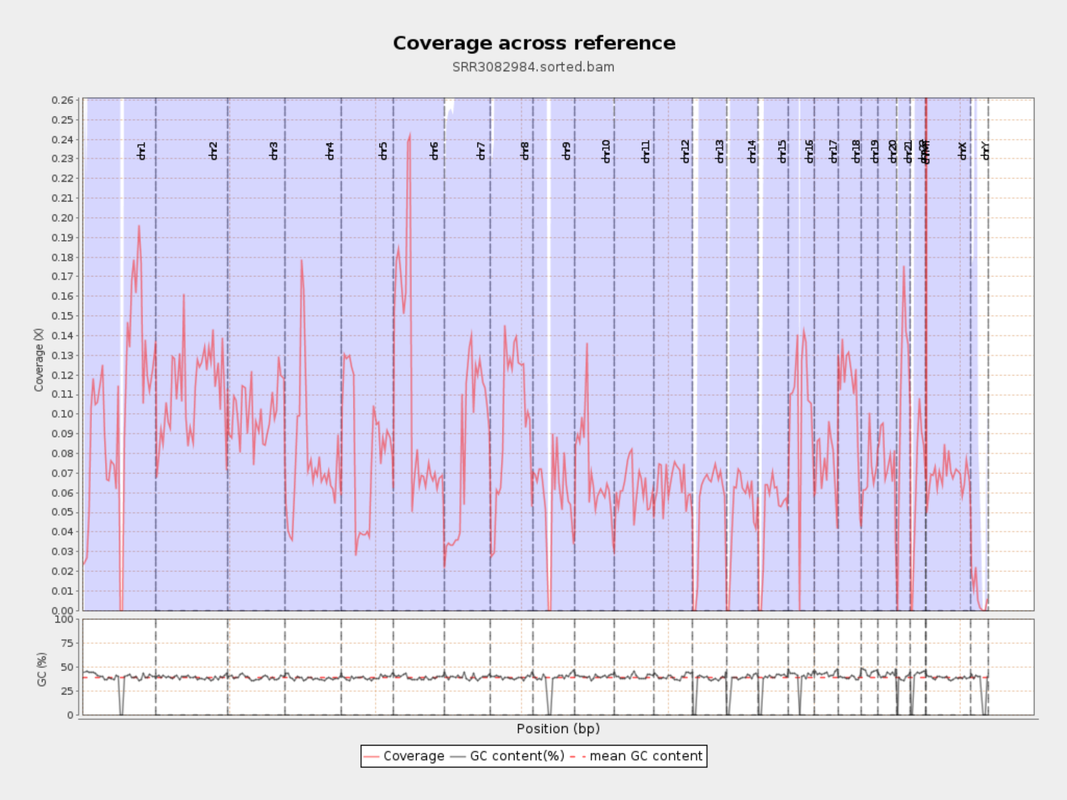
General error rate	0.9%
Mismatches	2,233,406
Insertions	21,039
Mapped reads with at least one insertion	0.56%
Deletions	57,372
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.96%

2.6. Chromosome stats

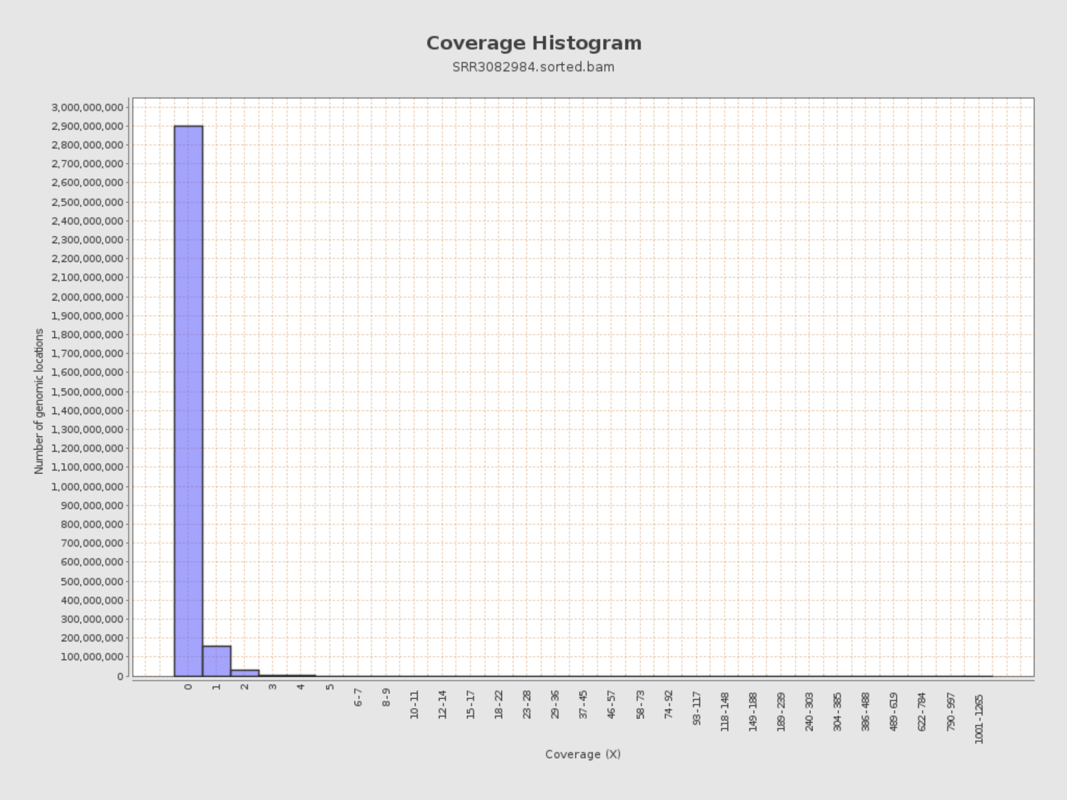
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25774635	0.1034	1.1932
chr2	243199373	27238228	0.112	0.7984
chr3	198022430	19901941	0.1005	0.4414
chr4	191154276	14754831	0.0772	0.4173
chr5	180915260	14639314	0.0809	0.3672
chr6	171115067	18569288	0.1085	0.6501
chr7	159138663	13231208	0.0831	0.7744

chr8	146364022	14201279	0.097	0.8165
chr9	141213431	8127730	0.0576	0.6619
chr10	135534747	9650308	0.0712	0.672
chr11	135006516	8370531	0.062	0.4397
chr12	133851895	8647473	0.0646	0.3234
chr13	115169878	6310478	0.0548	0.3069
chr14	107349540	5523526	0.0515	0.3384
chr15	102531392	4991183	0.0487	0.2686
chr16	90354753	9376285	0.1038	0.4913
chr17	81195210	6106382	0.0752	0.4043
chr18	78077248	8901295	0.114	1.3908
chr19	59128983	4156967	0.0703	0.7989
chr20	63025520	4867449	0.0772	0.3678
chr21	48129895	5274822	0.1096	0.4262
chr22	51304566	3258137	0.0635	0.3063
chrMT	16571	139266	8.4042	5.8444
chrX	155270560	10633634	0.0685	0.4033
chrY	59373566	452066	0.0076	0.1589

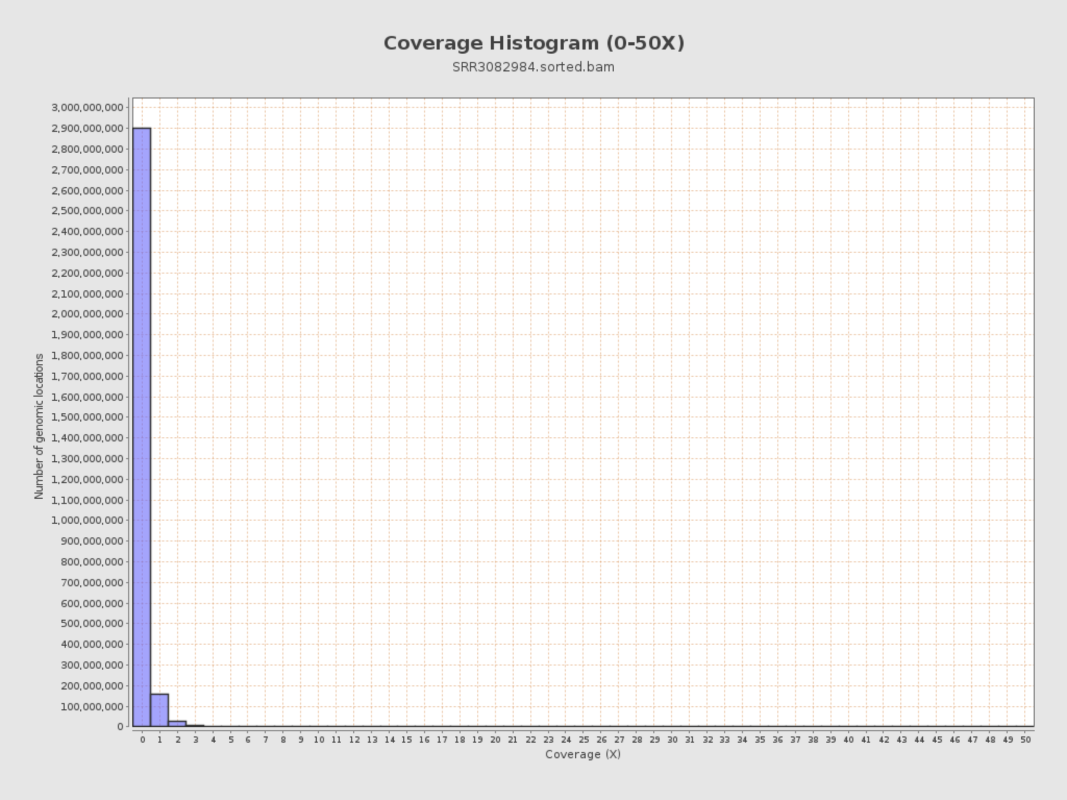
3. Results : Coverage across reference



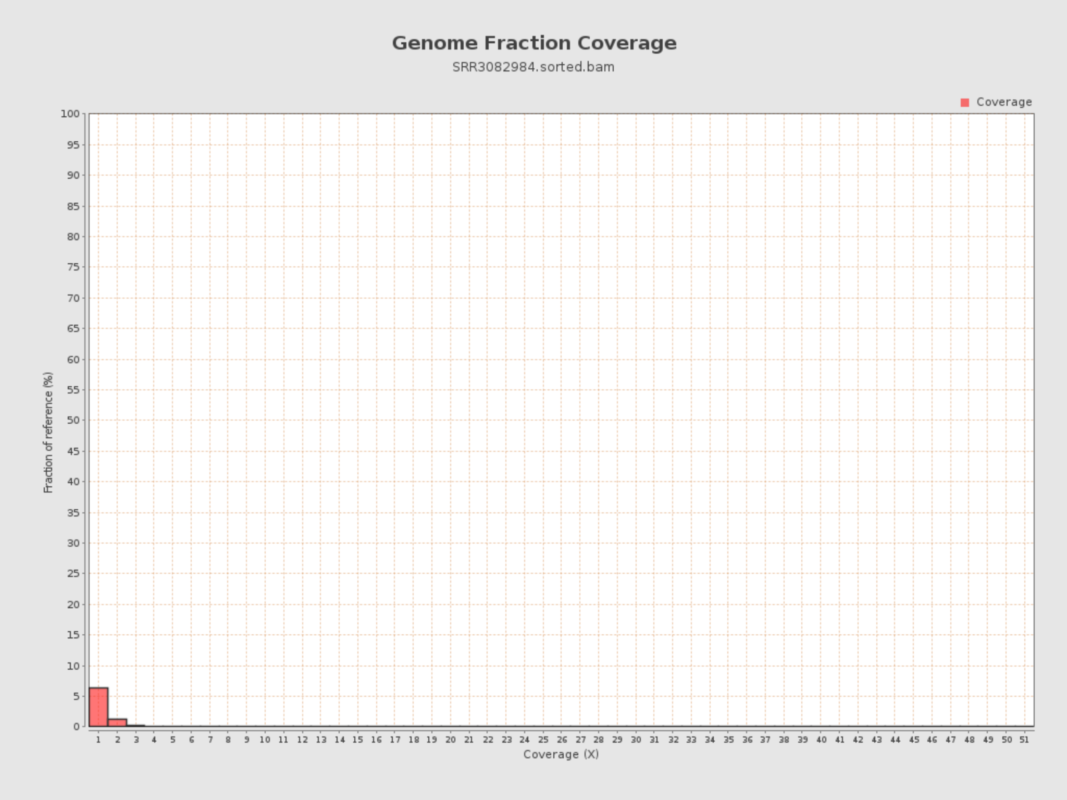
4. Results : Coverage Histogram



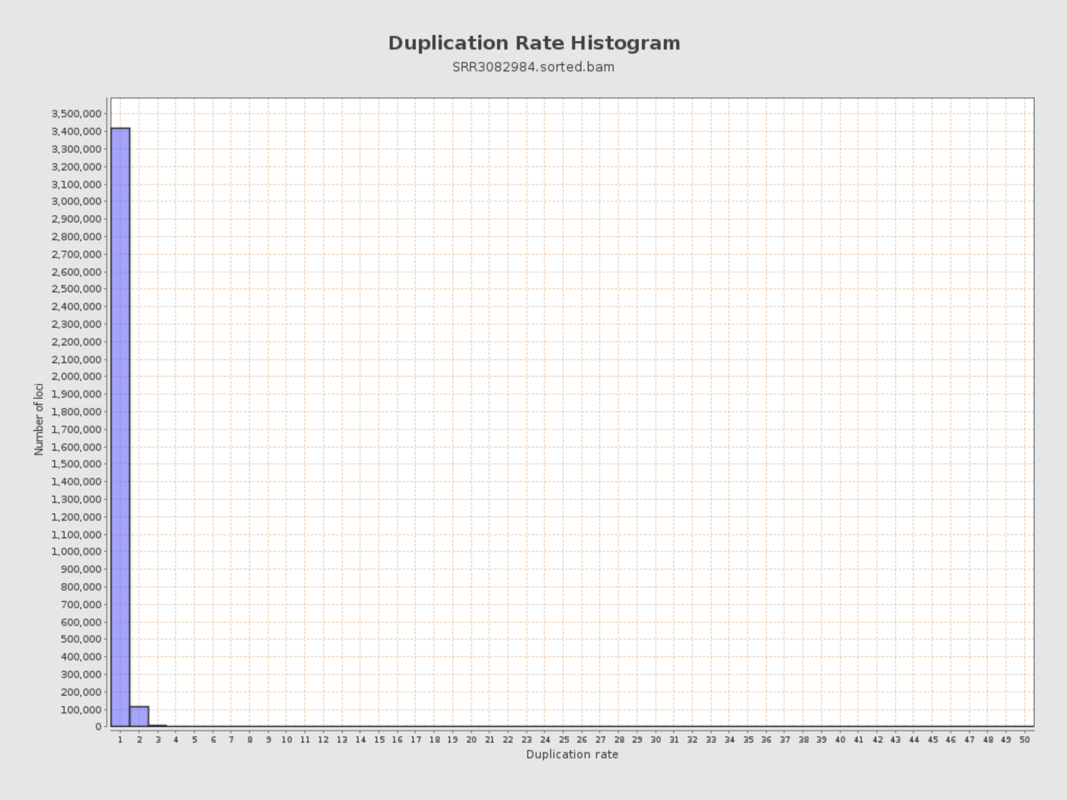
5. Results : Coverage Histogram (0-50X)



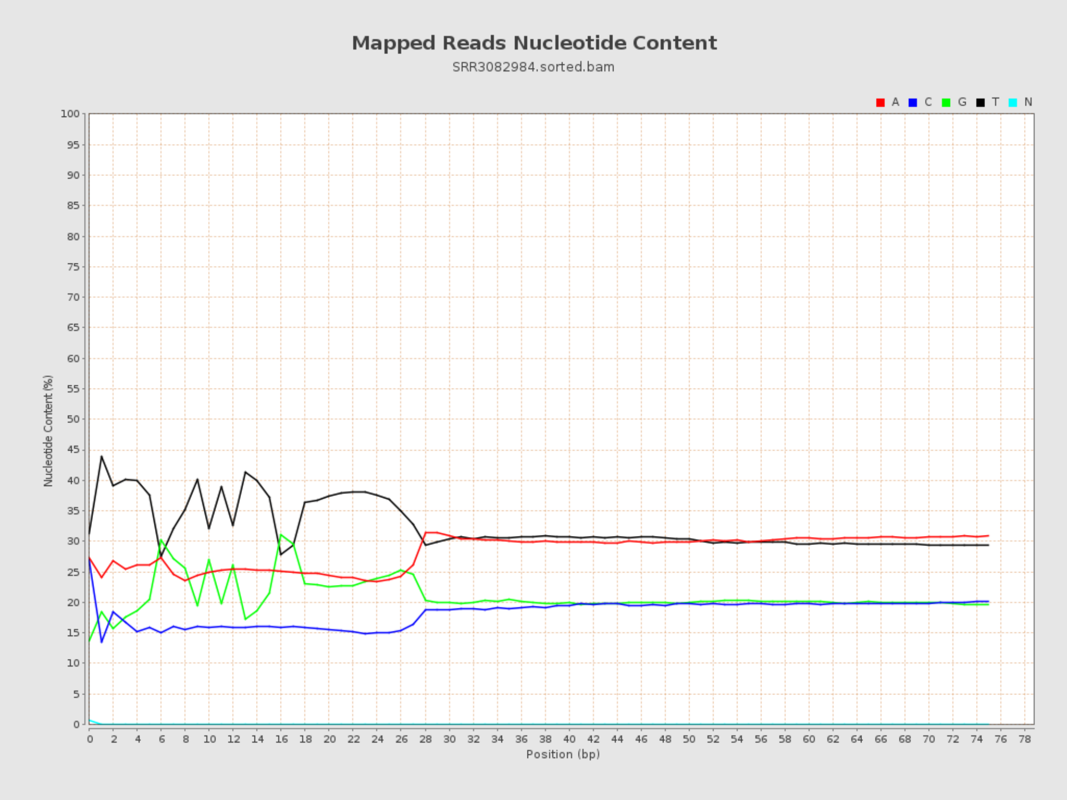
6. Results : Genome Fraction Coverage



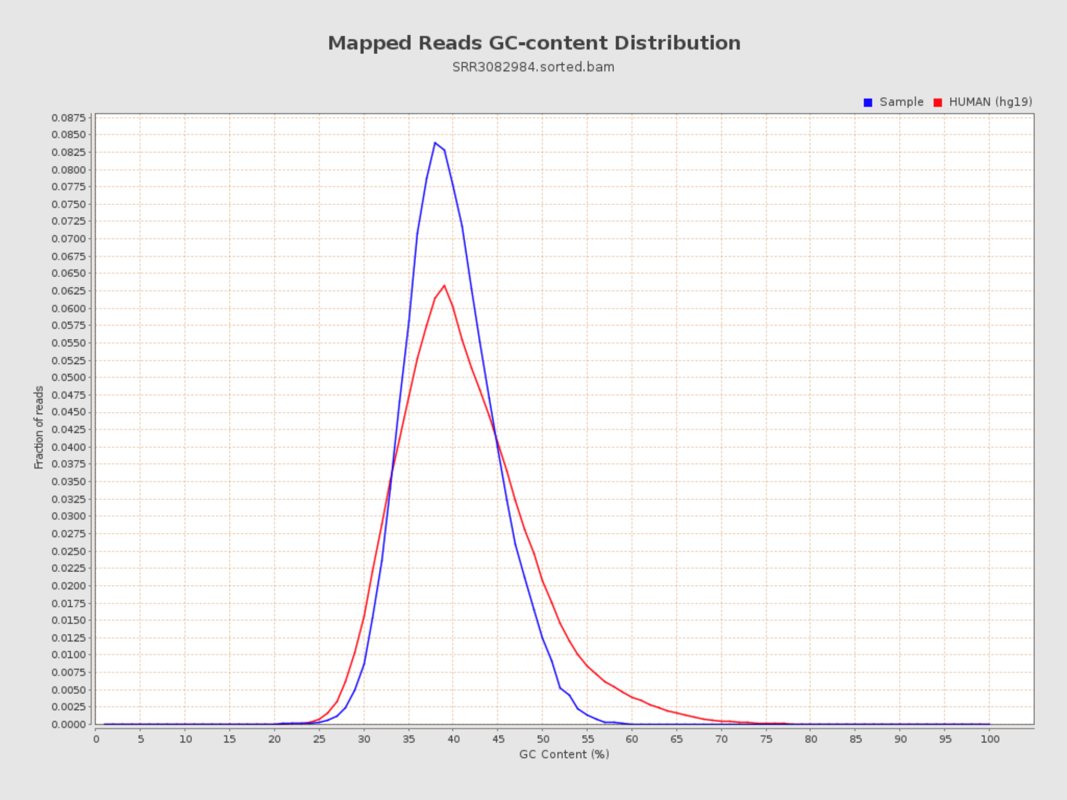
7. Results : Duplication Rate Histogram



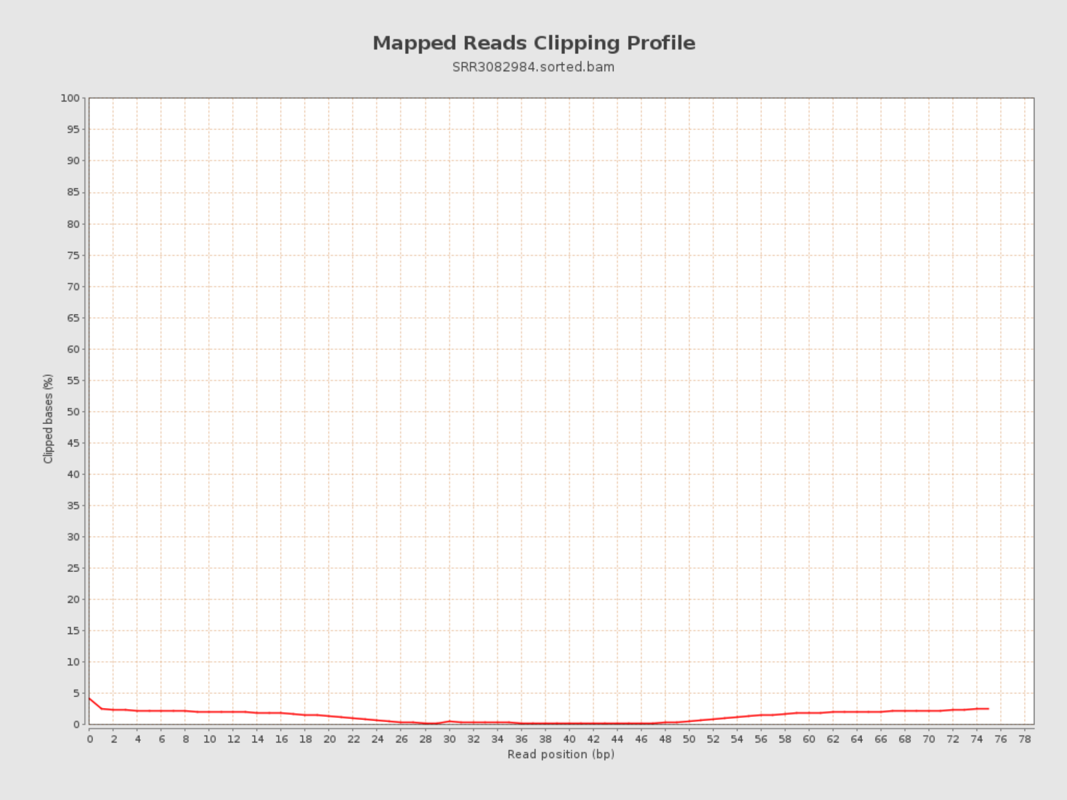
8. Results : Mapped Reads Nucleotide Content



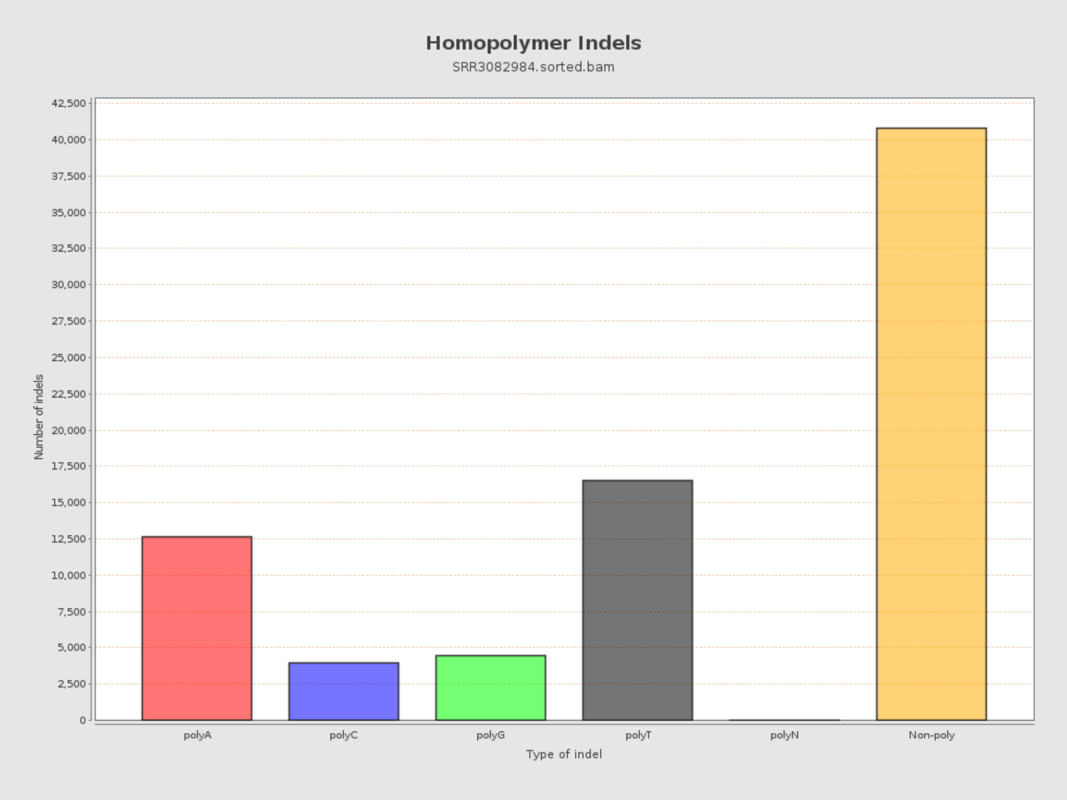
9. Results : Mapped Reads GC-content Distribution



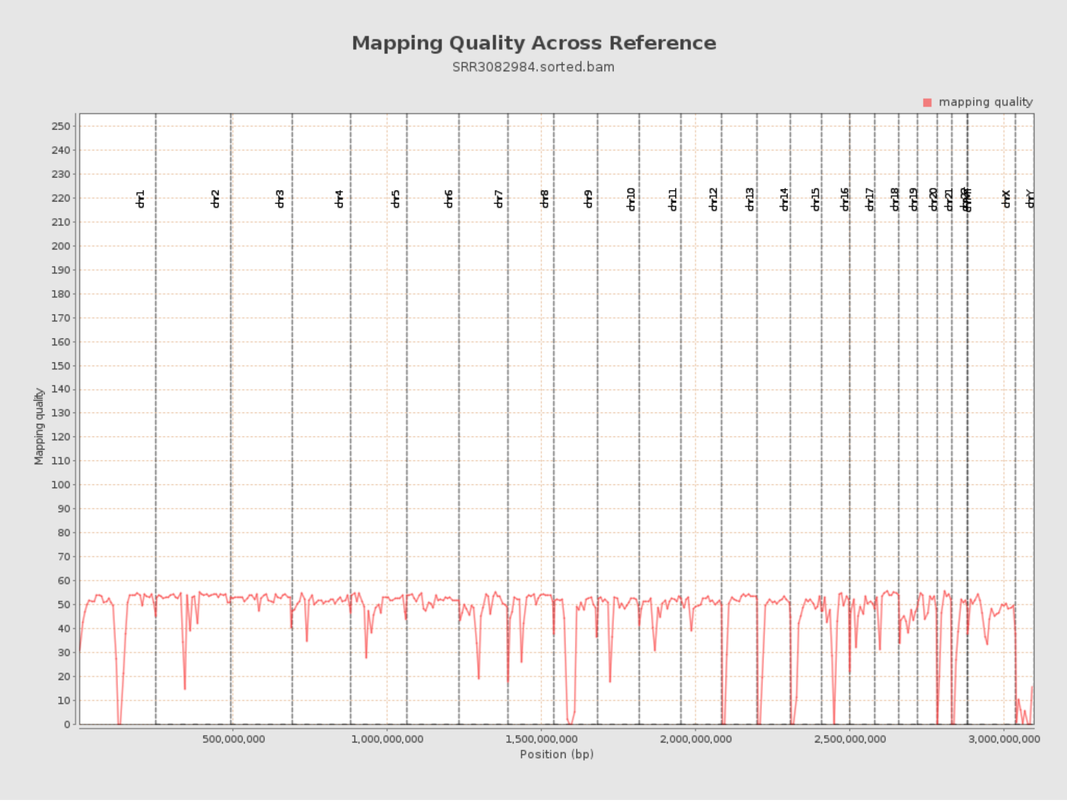
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram