Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:11:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082985.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_SRR3082985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082985.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:11:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,263,673
Mapped reads	3,660,741 / 85.86%
Unmapped reads	602,932 / 14.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,969 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	188,611 / 4.42%
Duplication rate	3.89%
Clipped reads	1,639,519 / 38.45%

2.2. ACGT Content

Number/percentage of A's	67,762,705 / 27.7%
Number/percentage of C's	44,927,763 / 18.37%
Number/percentage of T's	77,925,197 / 31.86%
Number/percentage of G's	53,973,300 / 22.06%
Number/percentage of N's	24,270 / 0.01%
GC Percentage	40.43%

2.3. Coverage

Mean	0.079

Standard Deviation	0.6283

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

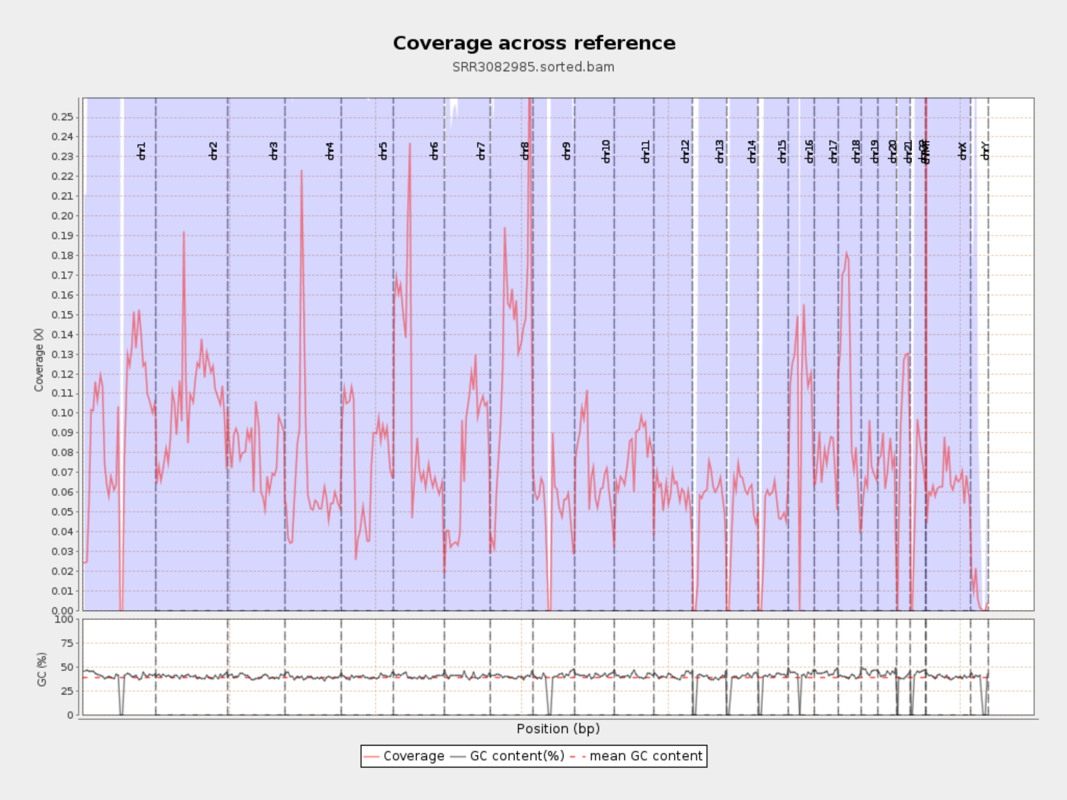
General error rate	0.91%
Mismatches	2,184,098
Insertions	20,432
Mapped reads with at least one insertion	0.55%
Deletions	56,472
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.09%

2.6. Chromosome stats

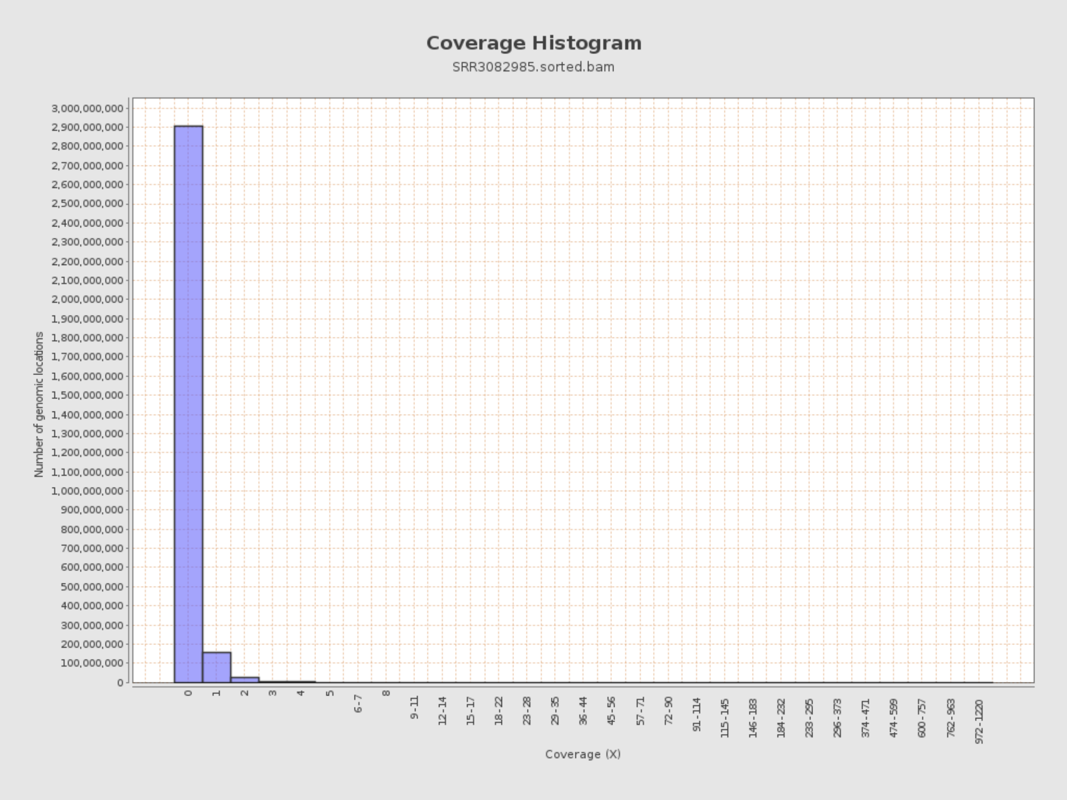
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23110401	0.0927	0.9498
chr2	243199373	25826739	0.1062	1.0021
chr3	198022430	15781000	0.0797	0.3456
chr4	191154276	12926226	0.0676	0.3356
chr5	180915260	13835882	0.0765	0.3442
chr6	171115067	17571324	0.1027	0.6553
chr7	159138663	12314066	0.0774	0.6184

chr8	146364022	19713792	0.1347	0.7626
chr9	141213431	7179871	0.0508	0.6374
chr10	135534747	9730784	0.0718	0.4885
chr11	135006516	10536081	0.078	0.5344
chr12	133851895	7985563	0.0597	0.3151
chr13	115169878	5919939	0.0514	0.2748
chr14	107349540	5620424	0.0524	0.359
chr15	102531392	4571363	0.0446	0.2632
chr16	90354753	9854738	0.1091	0.4709
chr17	81195210	6234244	0.0768	0.4222
chr18	78077248	9368388	0.12	1.4876
chr19	59128983	4079804	0.069	0.8165
chr20	63025520	4713521	0.0748	0.3726
chr21	48129895	4452673	0.0925	0.3886
chr22	51304566	2985689	0.0582	0.2932
chrMT	16571	7974	0.4812	0.9162
chrX	155270560	9970108	0.0642	0.4046
chrY	59373566	420254	0.0071	0.1463

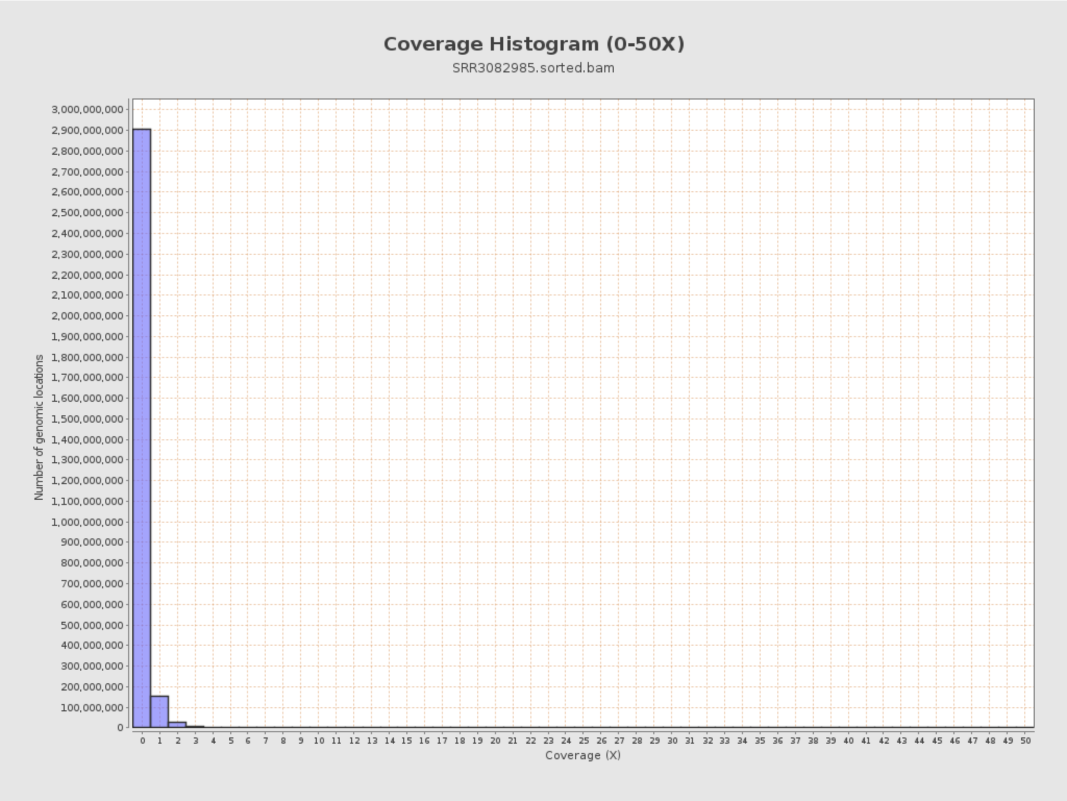
3. Results : Coverage across reference



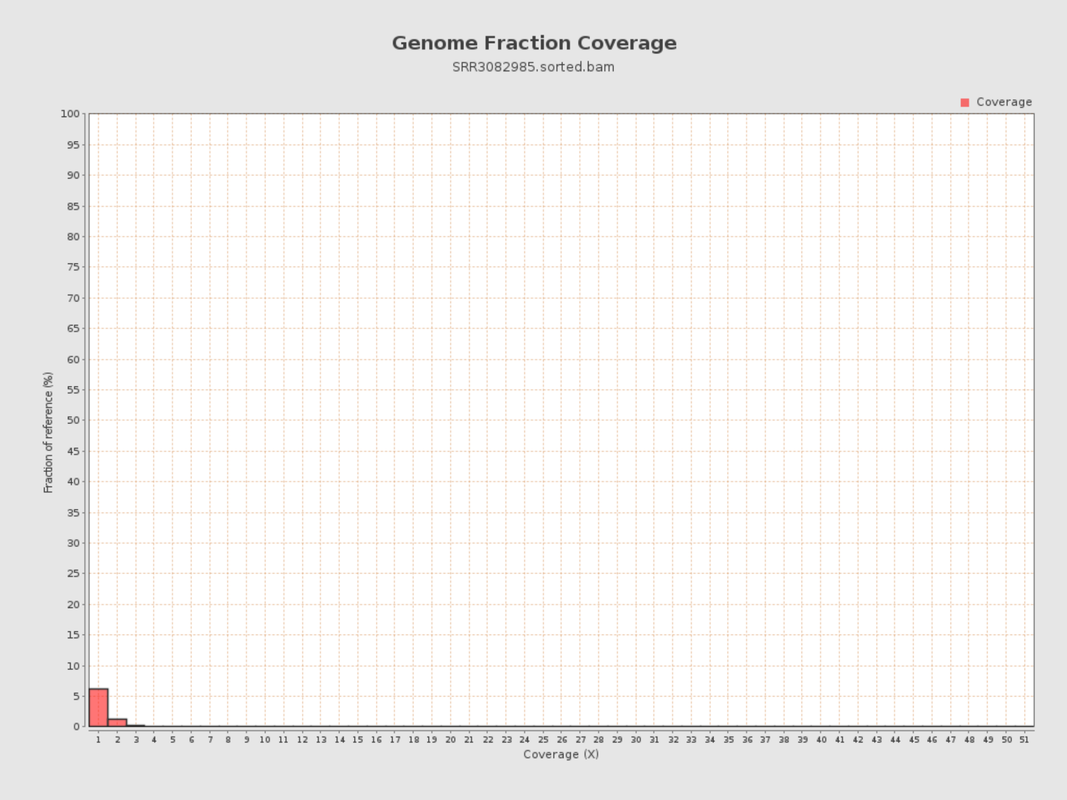
4. Results : Coverage Histogram



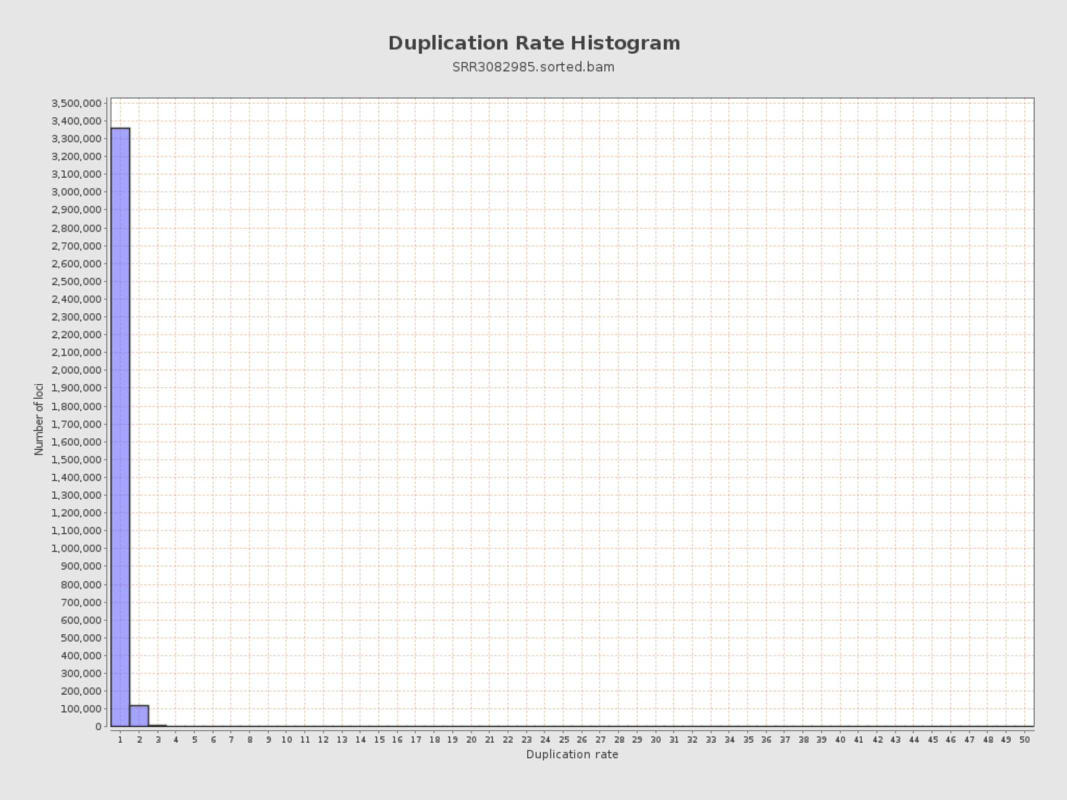
5. Results : Coverage Histogram (0-50X)



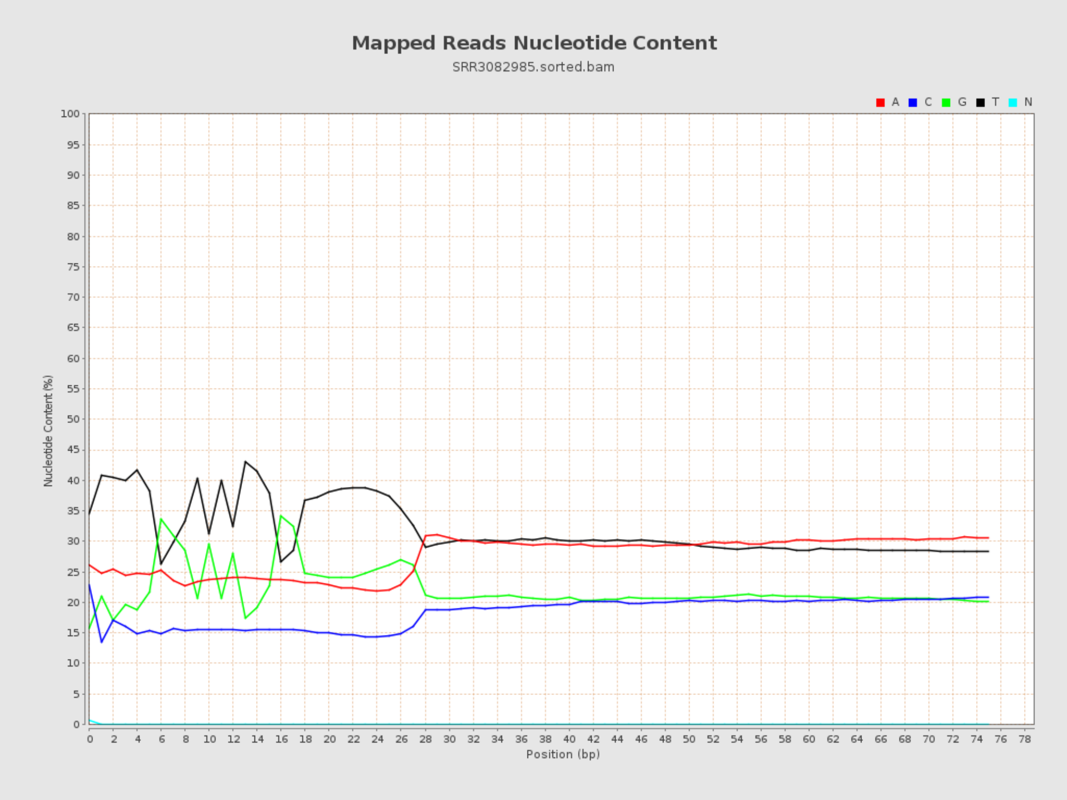
6. Results : Genome Fraction Coverage



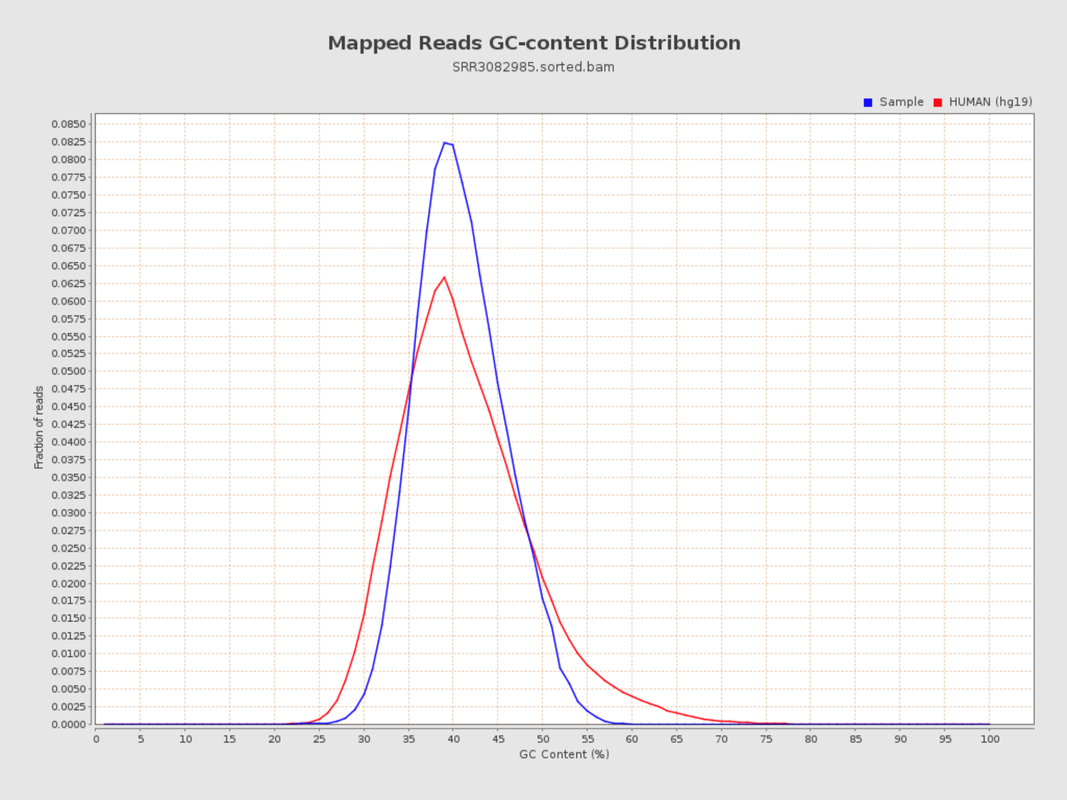
7. Results : Duplication Rate Histogram



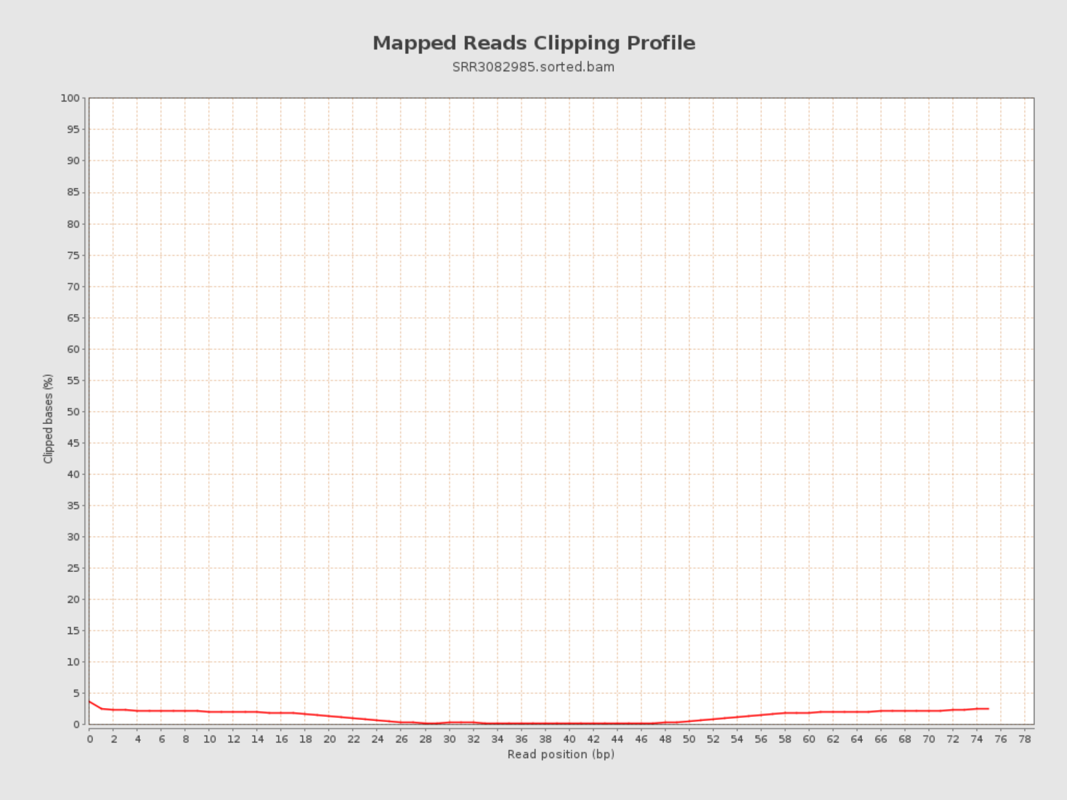
8. Results : Mapped Reads Nucleotide Content



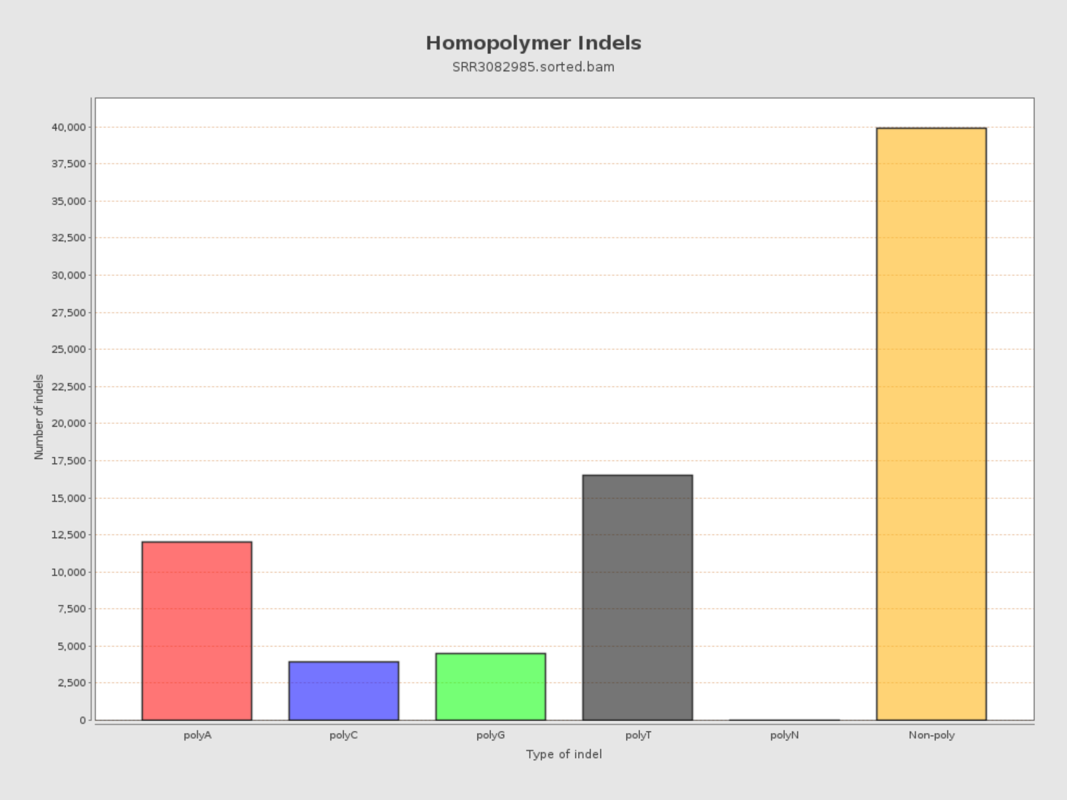
9. Results : Mapped Reads GC-content Distribution



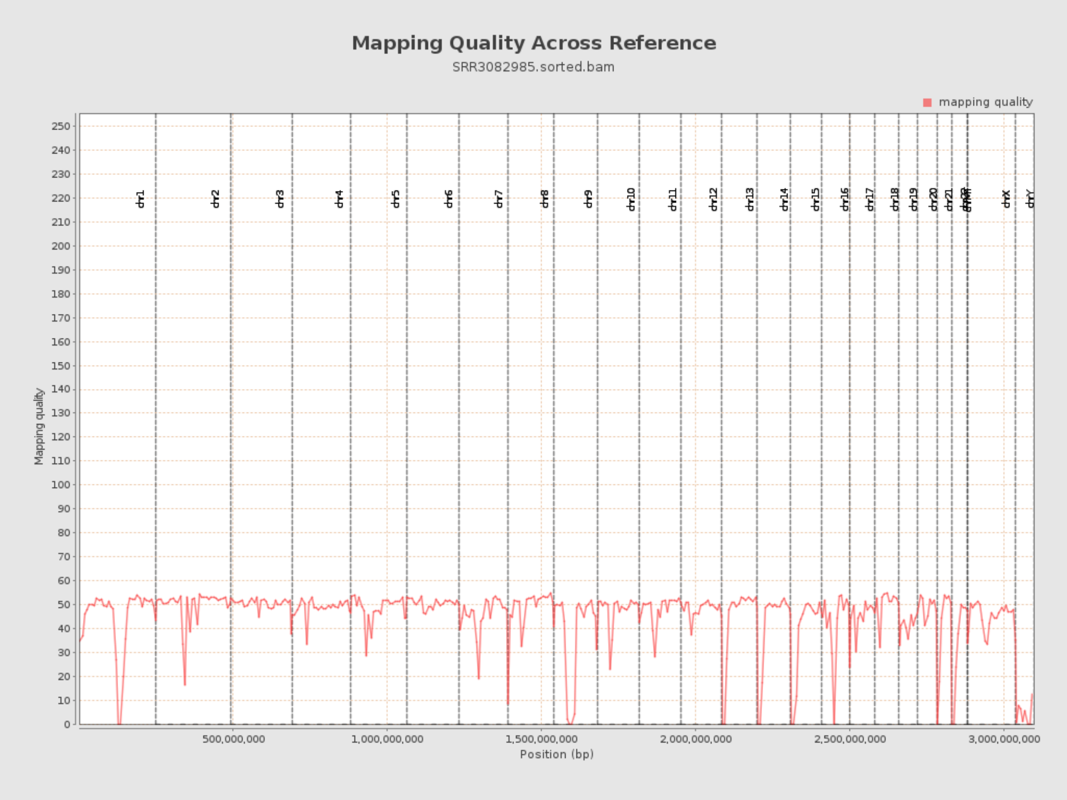
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram