Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:44:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081966.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_SRR3081966 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081966.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:44:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081966.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,040,203
Mapped reads	2,778,072 / 91.38%
Unmapped reads	262,131 / 8.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,998 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	122,126 / 4.02%
Duplication rate	3.12%
Clipped reads	1,001,004 / 32.93%

2.2. ACGT Content

Number/percentage of A's	54,994,568 / 28.81%
Number/percentage of C's	35,417,242 / 18.55%
Number/percentage of T's	59,786,350 / 31.32%
Number/percentage of G's	40,680,193 / 21.31%
Number/percentage of N's	24,339 / 0.01%
GC Percentage	39.86%

2.3. Coverage

Mean	0.0617

Standard Deviation	0.5941

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

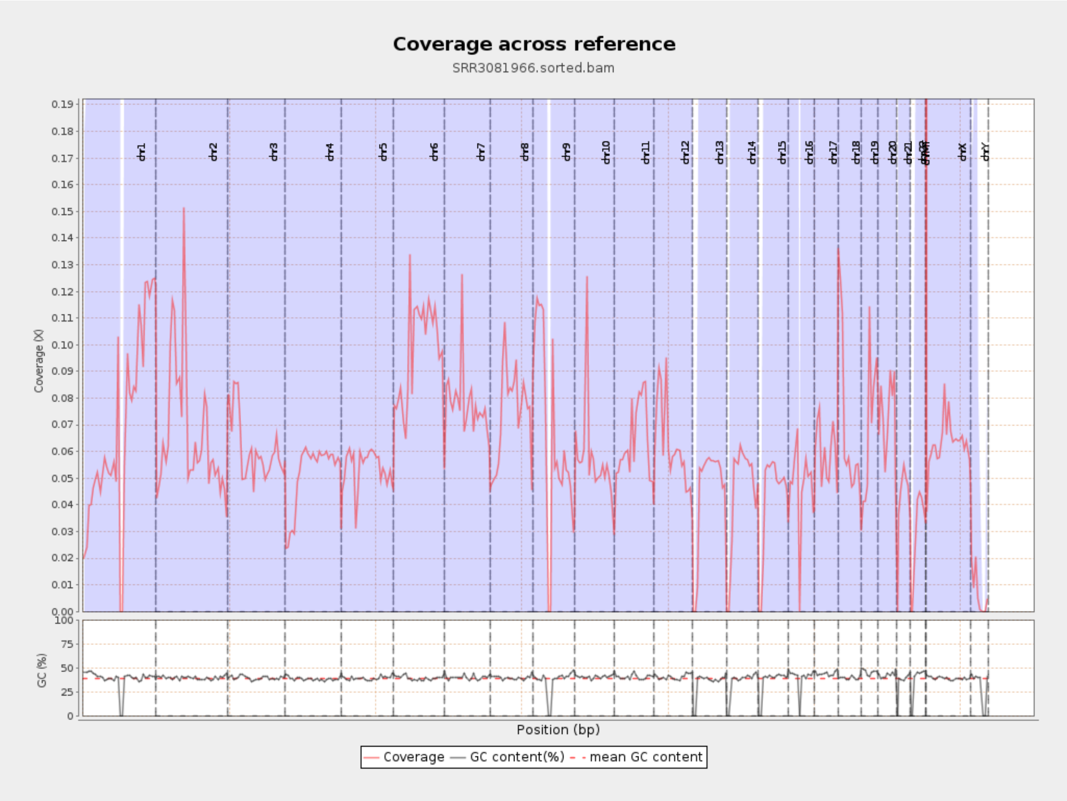
General error rate	0.82%
Mismatches	1,535,785
Insertions	14,334
Mapped reads with at least one insertion	0.51%
Deletions	47,008
Mapped reads with at least one deletion	1.67%
Homopolymer indels	47.25%

2.6. Chromosome stats

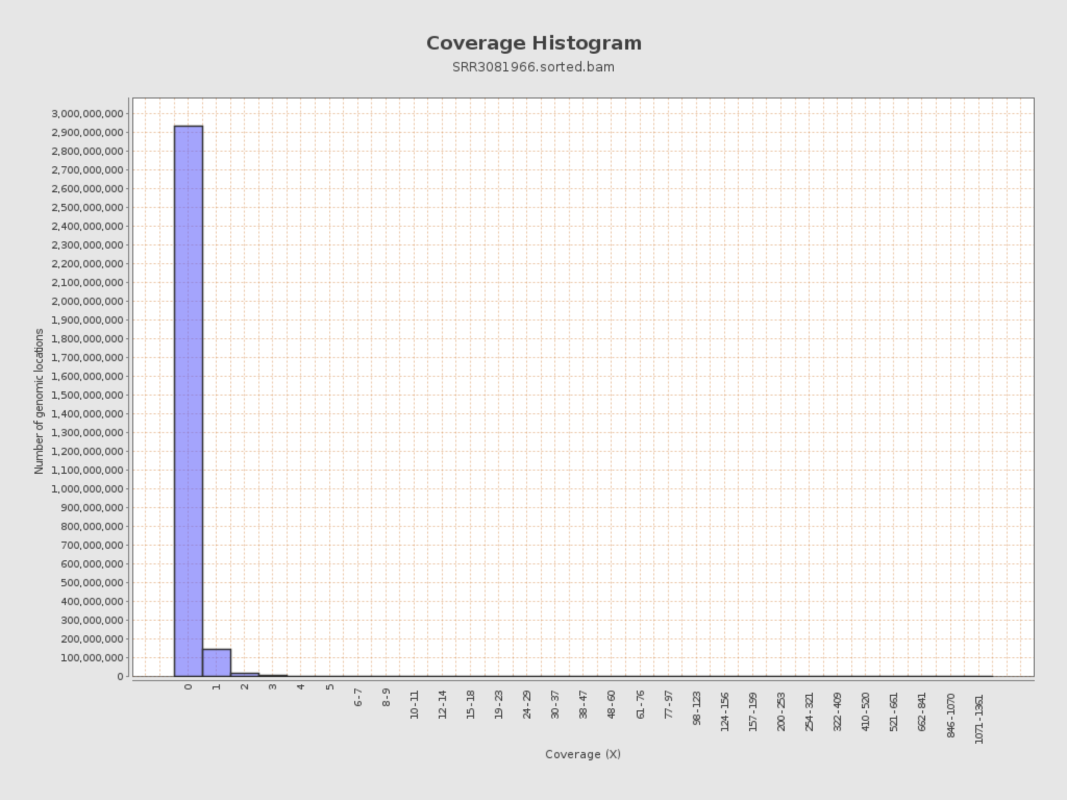
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17229050	0.0691	1.1368
chr2	243199373	16427415	0.0675	0.7535
chr3	198022430	12152205	0.0614	0.2785
chr4	191154276	9891042	0.0517	0.2752
chr5	180915260	9692071	0.0536	0.2632
chr6	171115067	16829200	0.0984	0.4766
chr7	159138663	12330034	0.0775	0.8379

chr8	146364022	10904124	0.0745	0.9224
chr9	141213431	9392662	0.0665	0.5902
chr10	135534747	7822717	0.0577	0.6
chr11	135006516	8599496	0.0637	0.3961
chr12	133851895	8356933	0.0624	0.2973
chr13	115169878	5154533	0.0448	0.2358
chr14	107349540	4894534	0.0456	0.2865
chr15	102531392	4276468	0.0417	0.2292
chr16	90354753	4159074	0.046	0.3055
chr17	81195210	4909291	0.0605	0.3108
chr18	78077248	5430778	0.0696	0.9965
chr19	59128983	4088331	0.0691	0.793
chr20	63025520	4667293	0.0741	0.3137
chr21	48129895	1987776	0.0413	0.2684
chr22	51304566	1502001	0.0293	0.1884
chrMT	16571	72785	4.3923	2.9674
chrX	155270560	9809107	0.0632	0.3421
chrY	59373566	405495	0.0068	0.1594

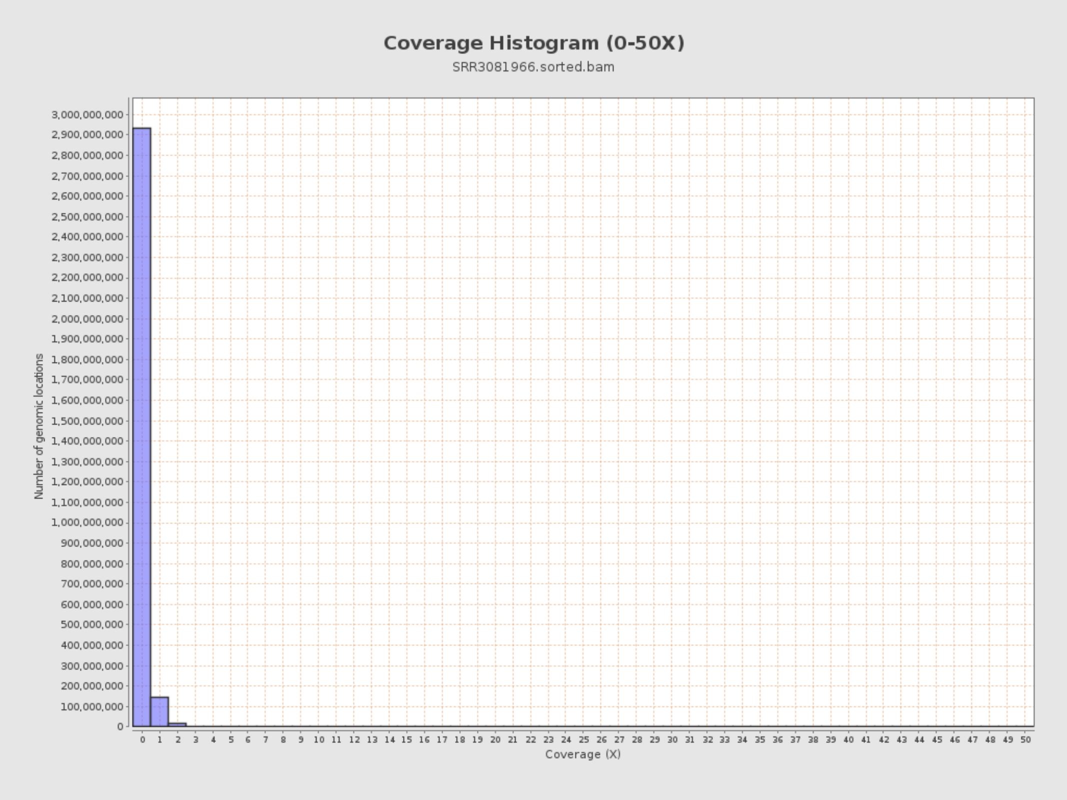
3. Results : Coverage across reference



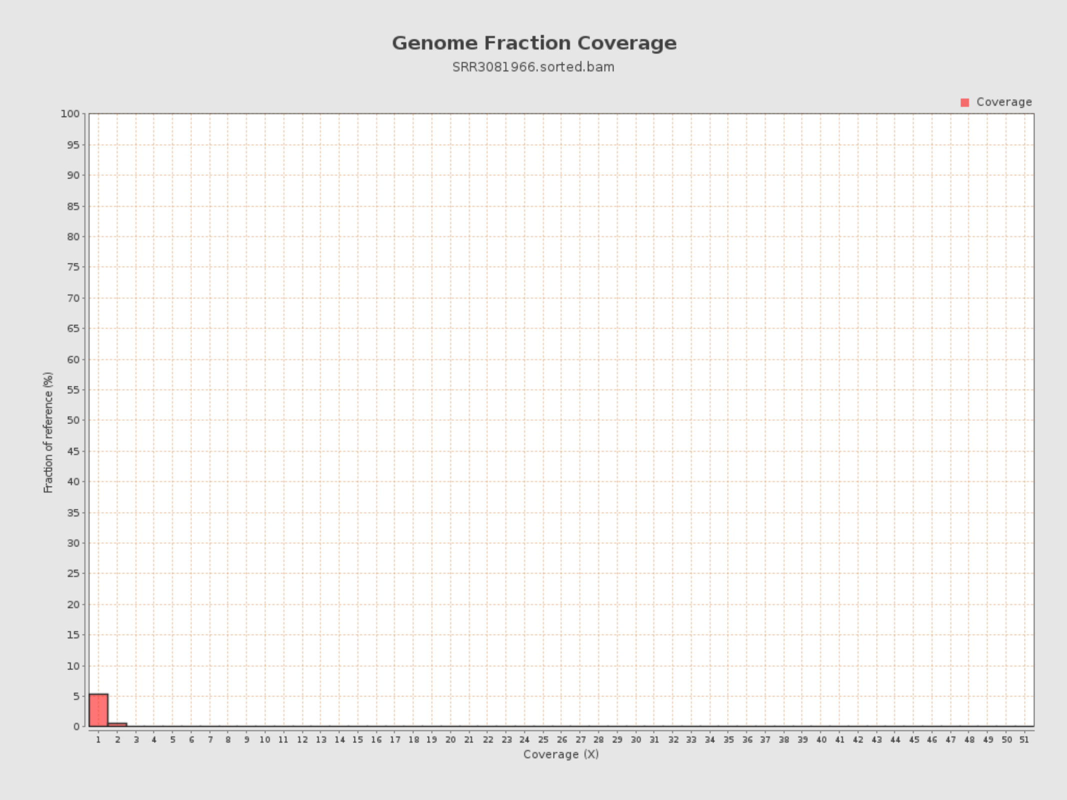
4. Results : Coverage Histogram



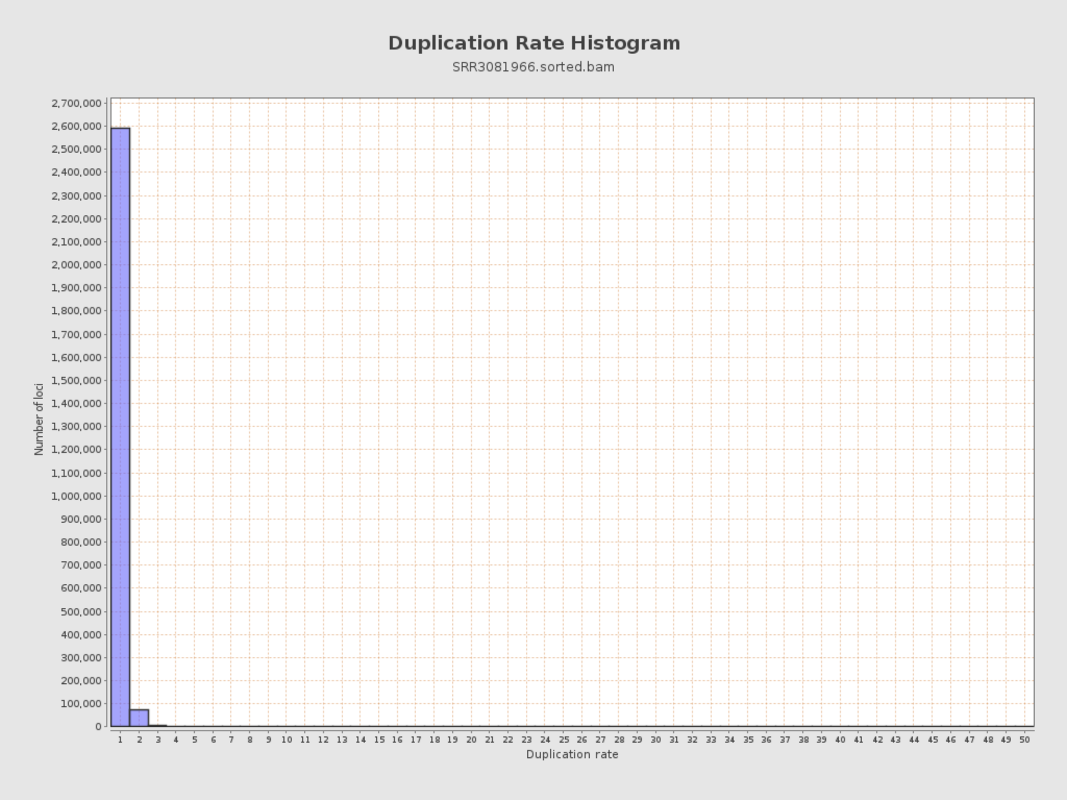
5. Results : Coverage Histogram (0-50X)



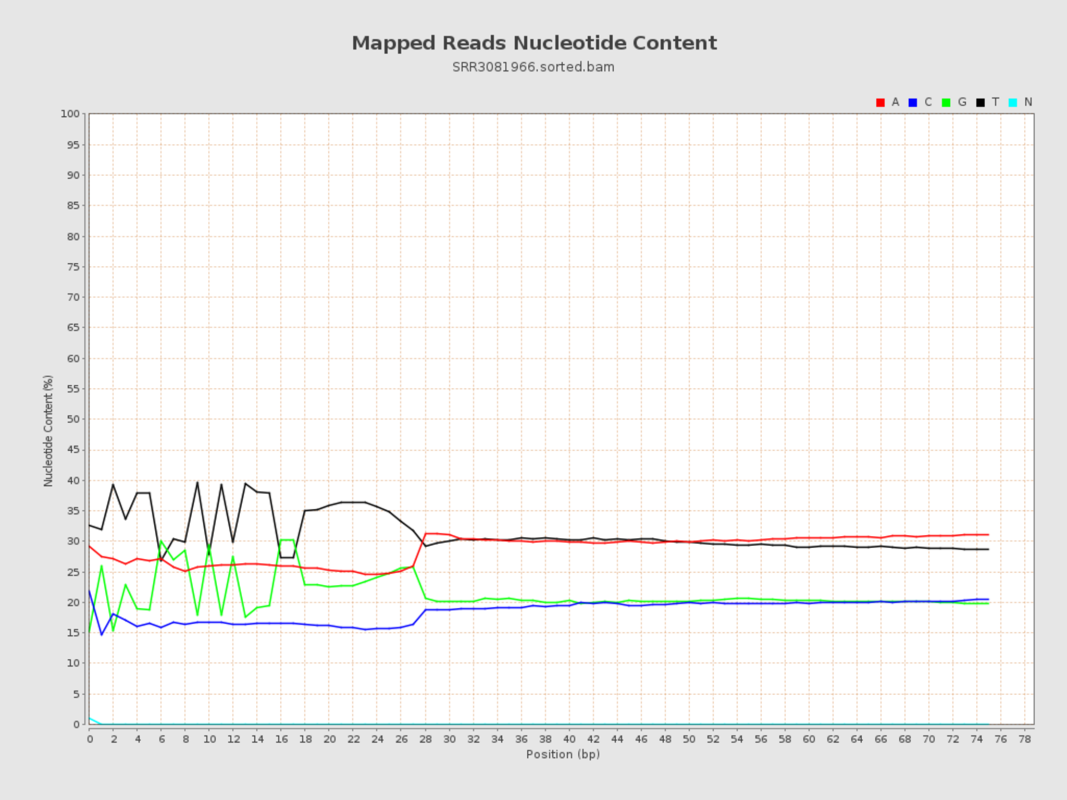
6. Results : Genome Fraction Coverage



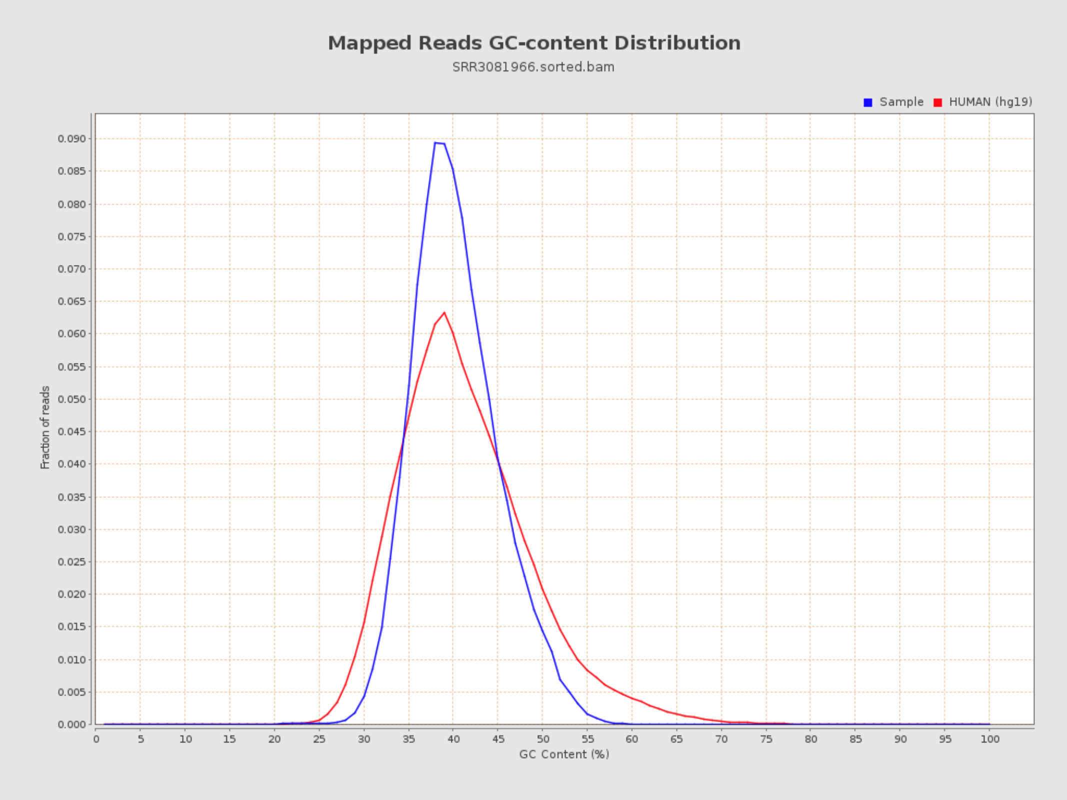
7. Results : Duplication Rate Histogram



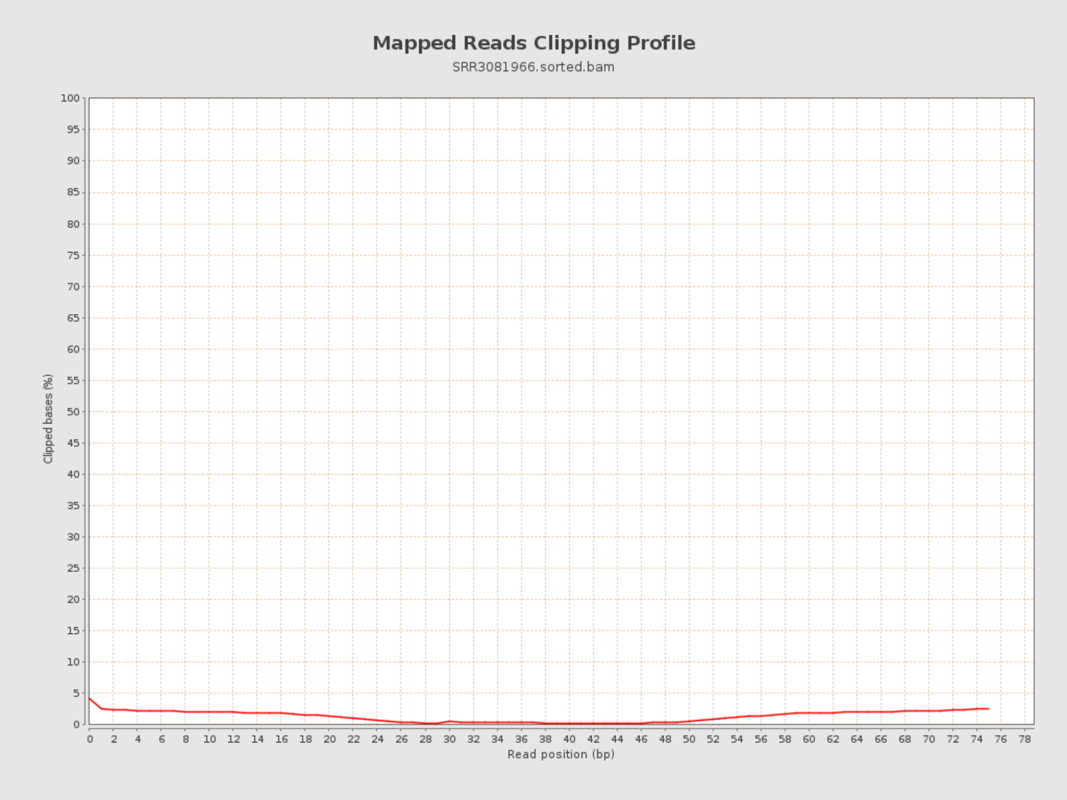
8. Results : Mapped Reads Nucleotide Content



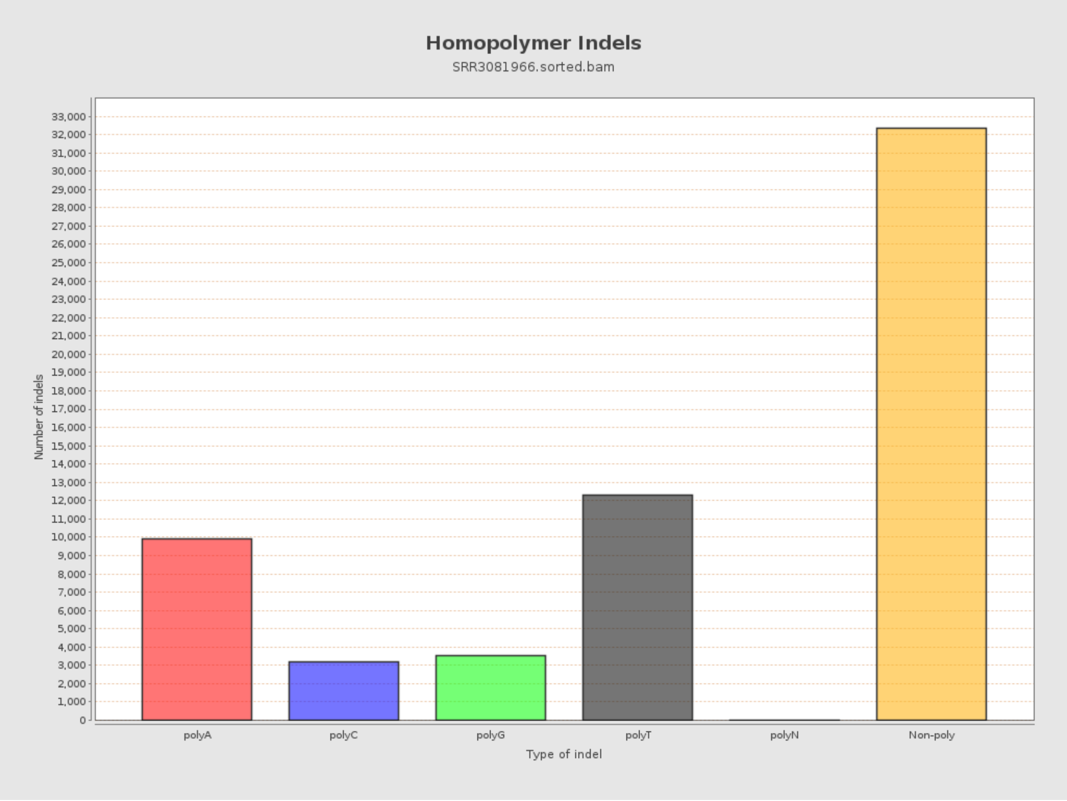
9. Results : Mapped Reads GC-content Distribution



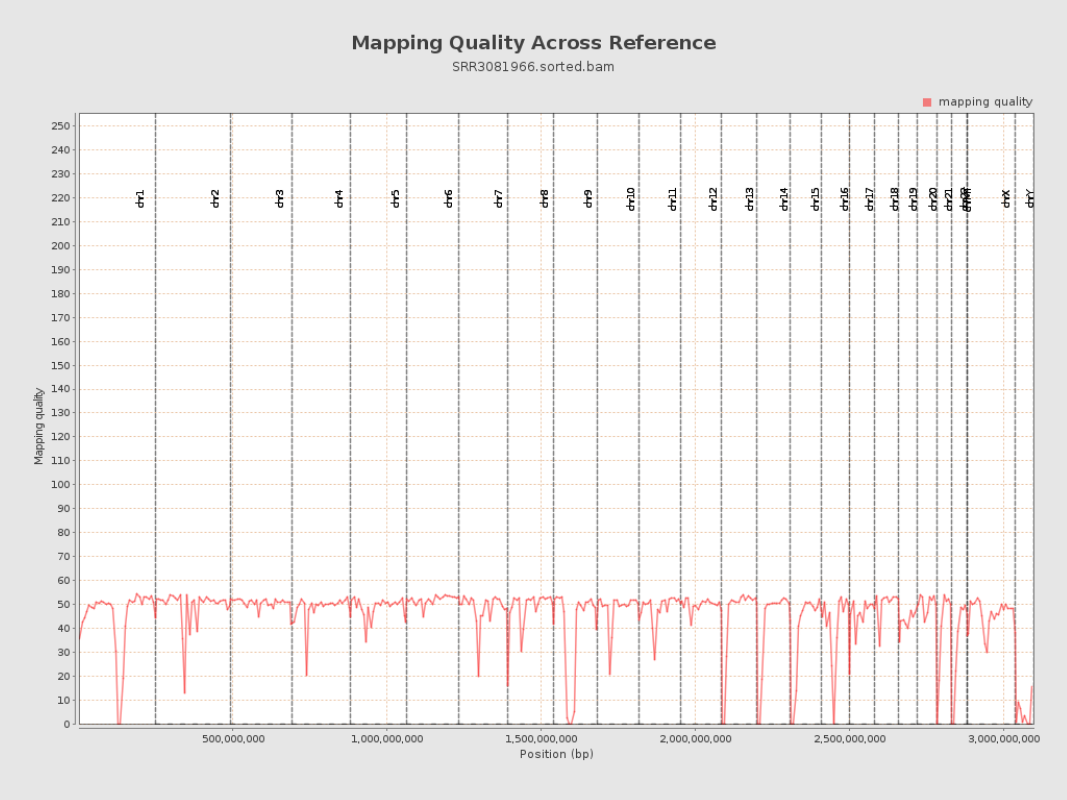
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram