Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:57:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081919.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_SRR3081919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081919.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:57:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,894,457
Mapped reads	2,678,788 / 92.55%
Unmapped reads	215,669 / 7.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,697 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	139,997 / 4.84%
Duplication rate	4.18%
Clipped reads	972,472 / 33.6%

2.2. ACGT Content

Number/percentage of A's	52,201,215 / 28.49%
Number/percentage of C's	33,558,363 / 18.32%
Number/percentage of T's	58,506,024 / 31.93%
Number/percentage of G's	38,918,646 / 21.24%
Number/percentage of N's	23,978 / 0.01%
GC Percentage	39.56%

2.3. Coverage

Mean	0.0592

Standard Deviation	0.5041

2.4. Mapping Quality

Mean Mapping Quality	47.22

2.5. Mismatches and indels

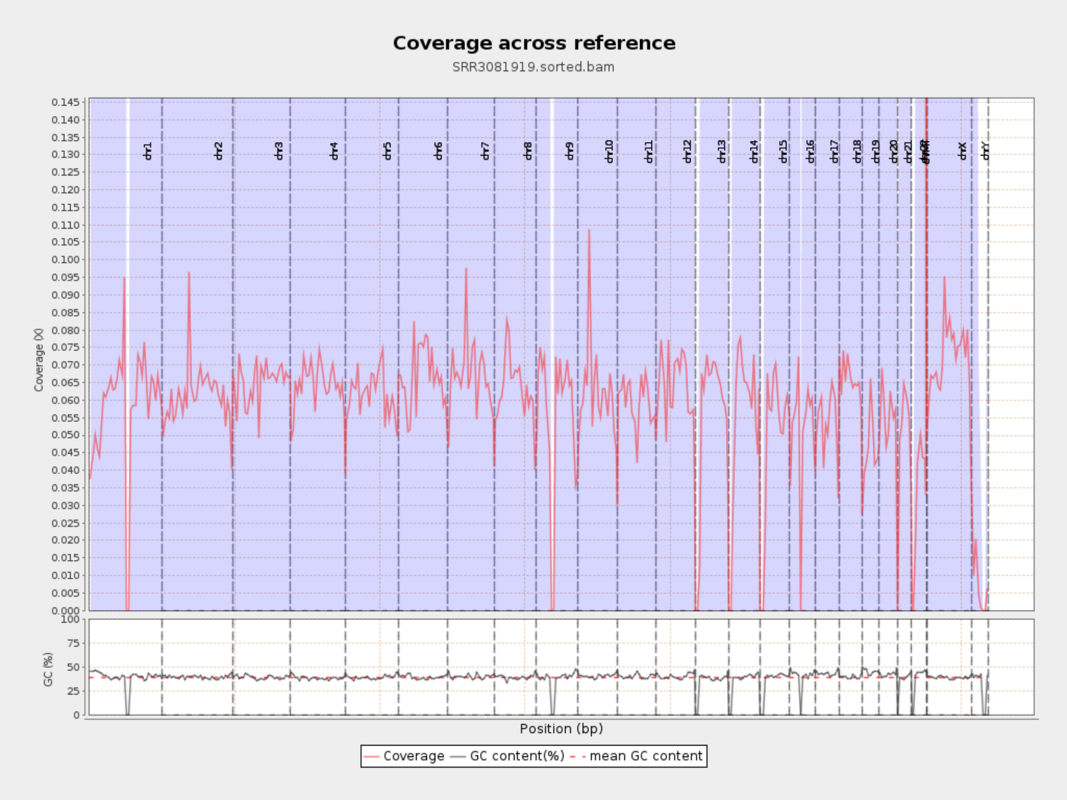
General error rate	0.76%
Mismatches	1,374,399
Insertions	13,048
Mapped reads with at least one insertion	0.48%
Deletions	38,588
Mapped reads with at least one deletion	1.43%
Homopolymer indels	48.26%

2.6. Chromosome stats

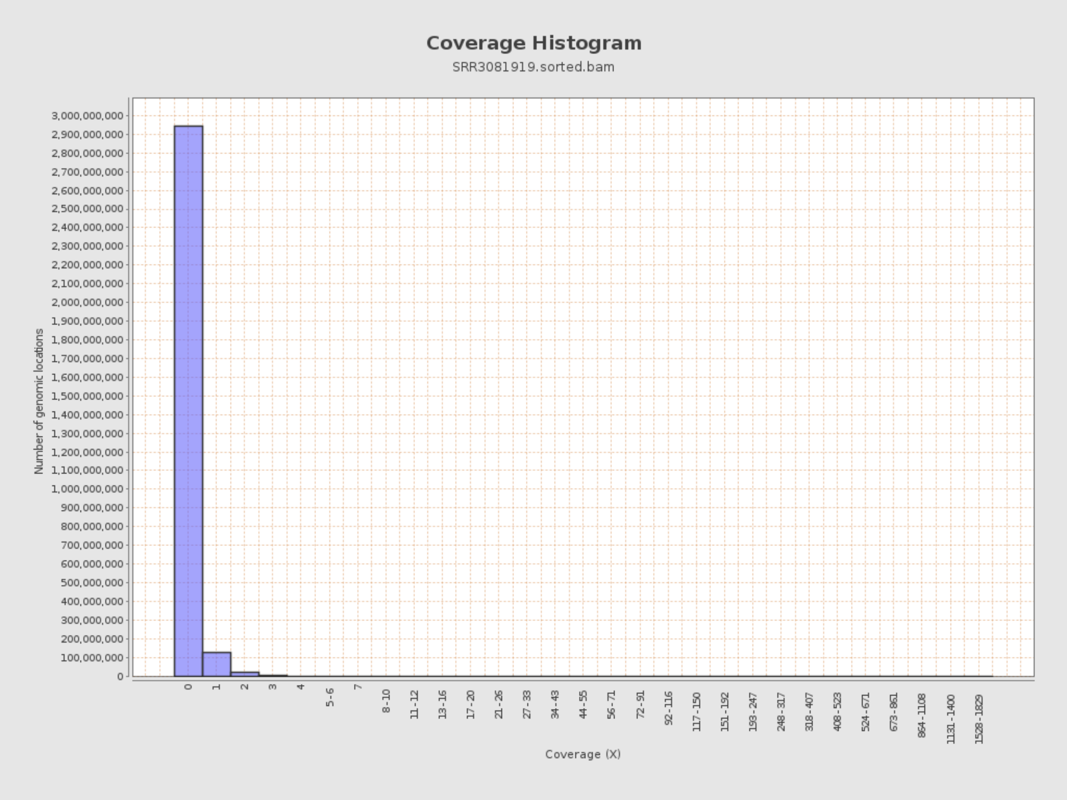
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14483412	0.0581	0.8156
chr2	243199373	14927094	0.0614	0.5
chr3	198022430	12931718	0.0653	0.3039
chr4	191154276	12298699	0.0643	0.3076
chr5	180915260	11208607	0.062	0.29
chr6	171115067	11423368	0.0668	0.3634
chr7	159138663	10787129	0.0678	0.6049

chr8	146364022	9238430	0.0631	1.1294
chr9	141213431	7899051	0.0559	0.435
chr10	135534747	8486829	0.0626	0.5588
chr11	135006516	7972237	0.0591	0.3586
chr12	133851895	8615653	0.0644	0.2984
chr13	115169878	6246857	0.0542	0.2719
chr14	107349540	5774487	0.0538	0.2883
chr15	102531392	4967580	0.0484	0.2567
chr16	90354753	4640008	0.0514	0.3107
chr17	81195210	4310071	0.0531	0.2891
chr18	78077248	5168158	0.0662	0.7761
chr19	59128983	2762890	0.0467	0.6342
chr20	63025520	3483534	0.0553	0.2808
chr21	48129895	2356222	0.049	0.2751
chr22	51304566	1594759	0.0311	0.2017
chrMT	16571	116478	7.029	4.4028
chrX	155270560	11148271	0.0718	0.3471
chrY	59373566	435458	0.0073	0.154

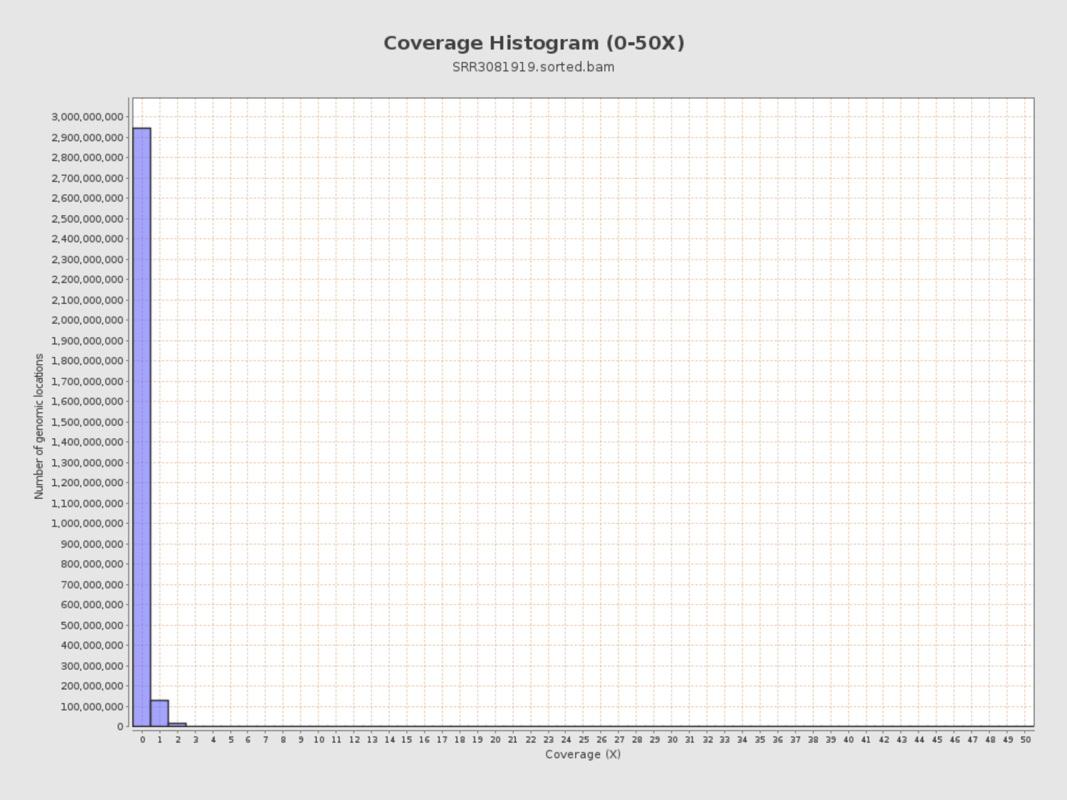
3. Results : Coverage across reference



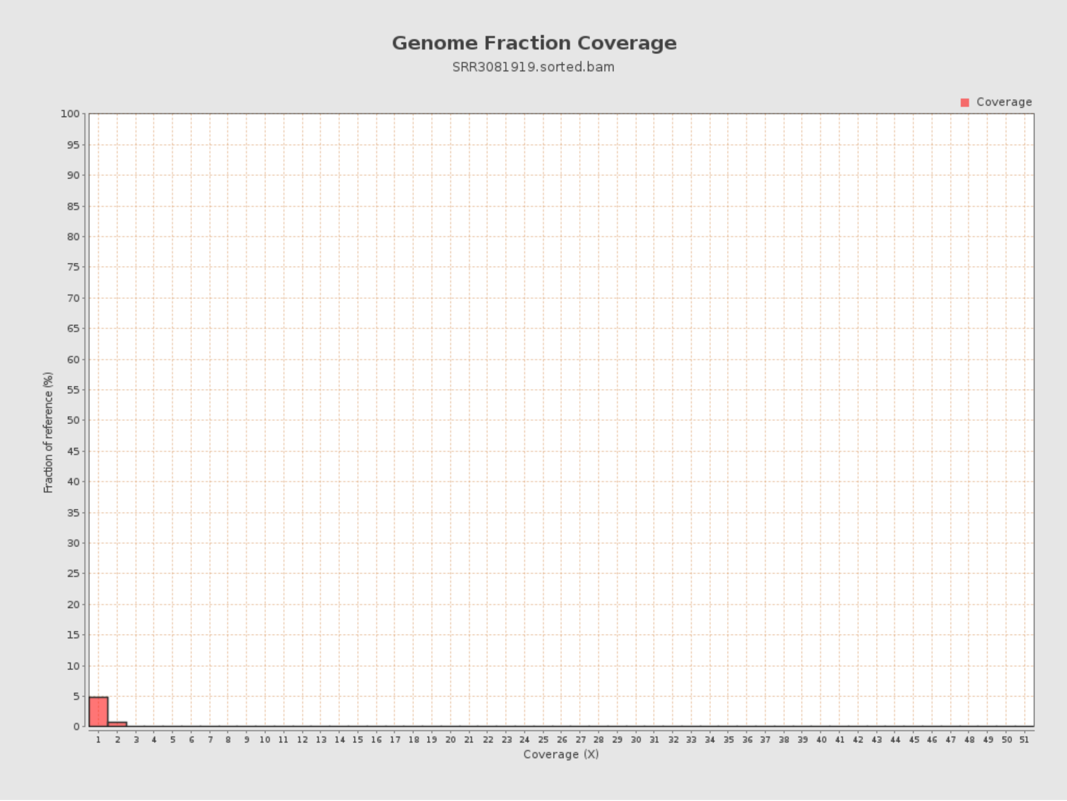
4. Results : Coverage Histogram



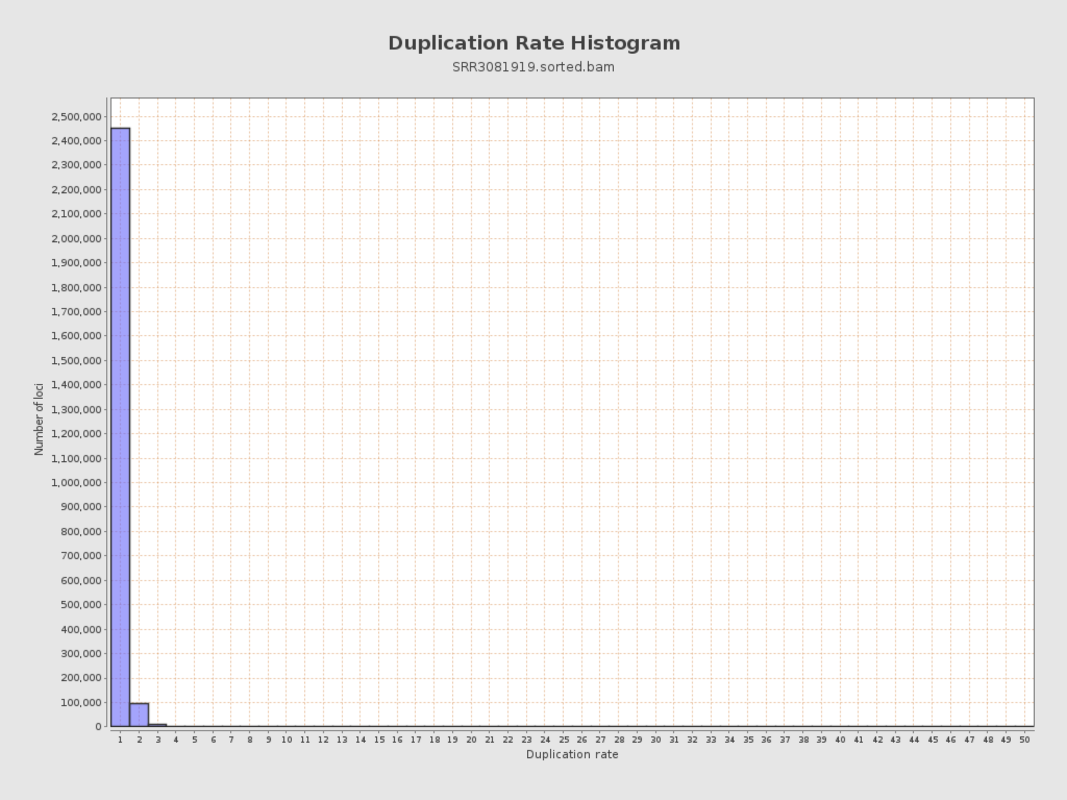
5. Results : Coverage Histogram (0-50X)



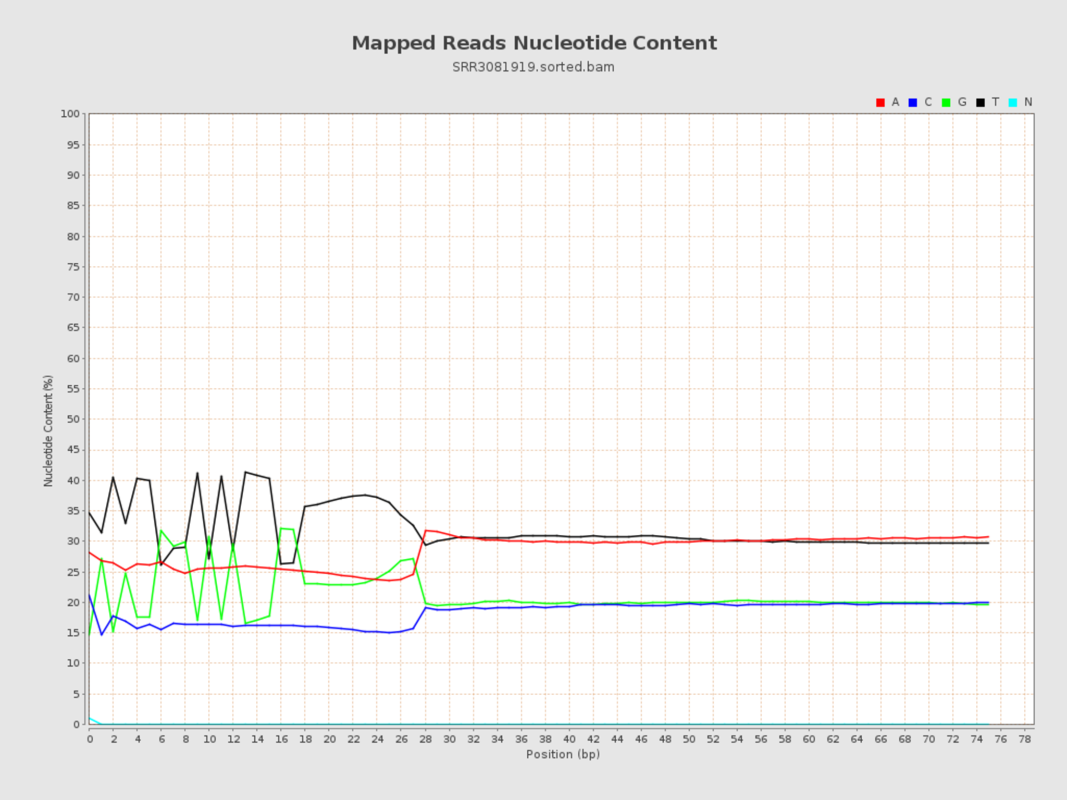
6. Results : Genome Fraction Coverage



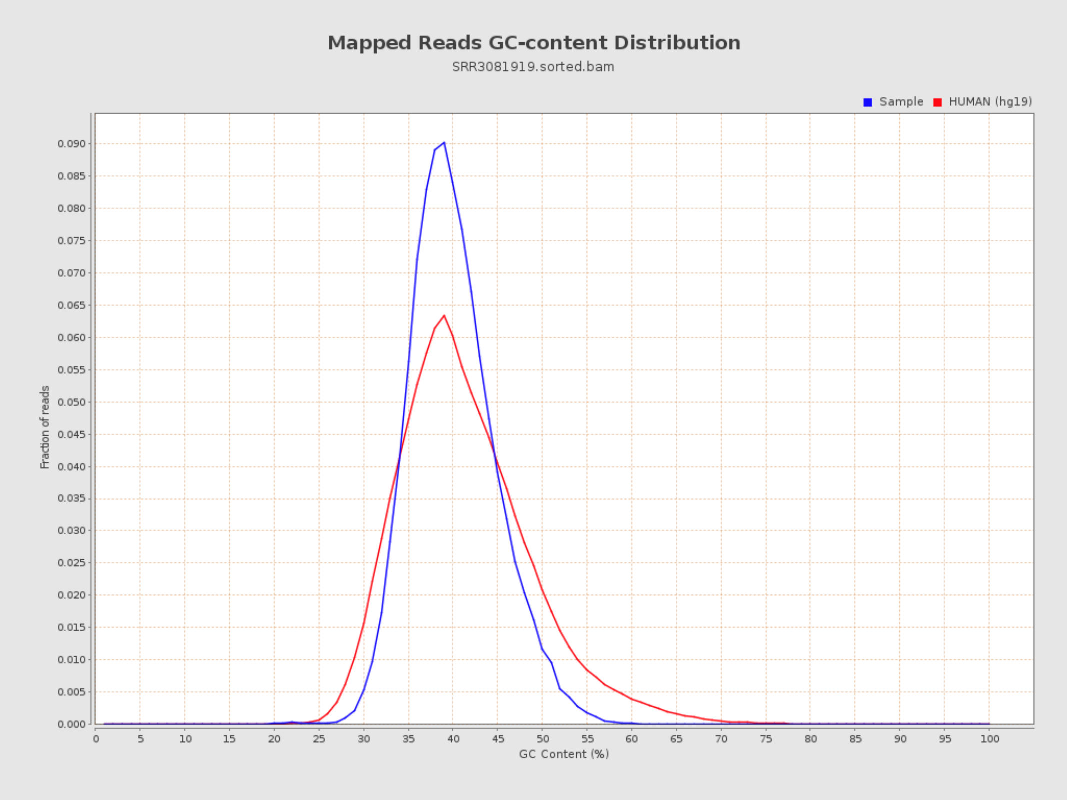
7. Results : Duplication Rate Histogram



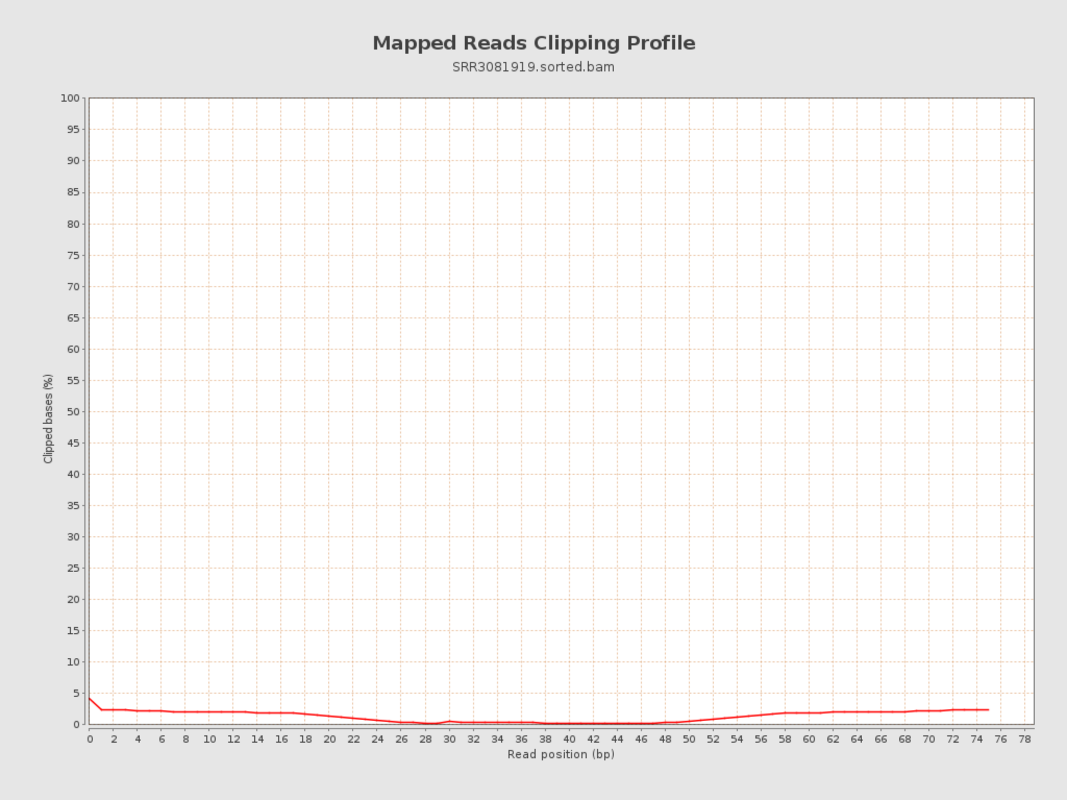
8. Results : Mapped Reads Nucleotide Content



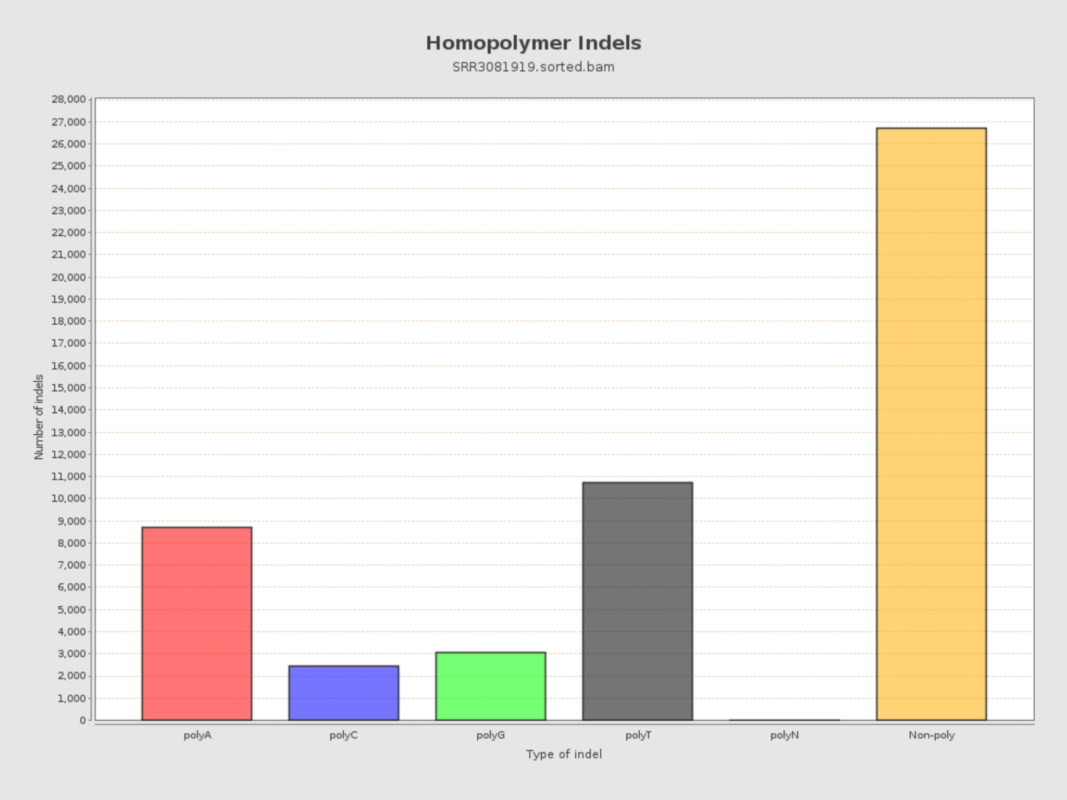
9. Results : Mapped Reads GC-content Distribution



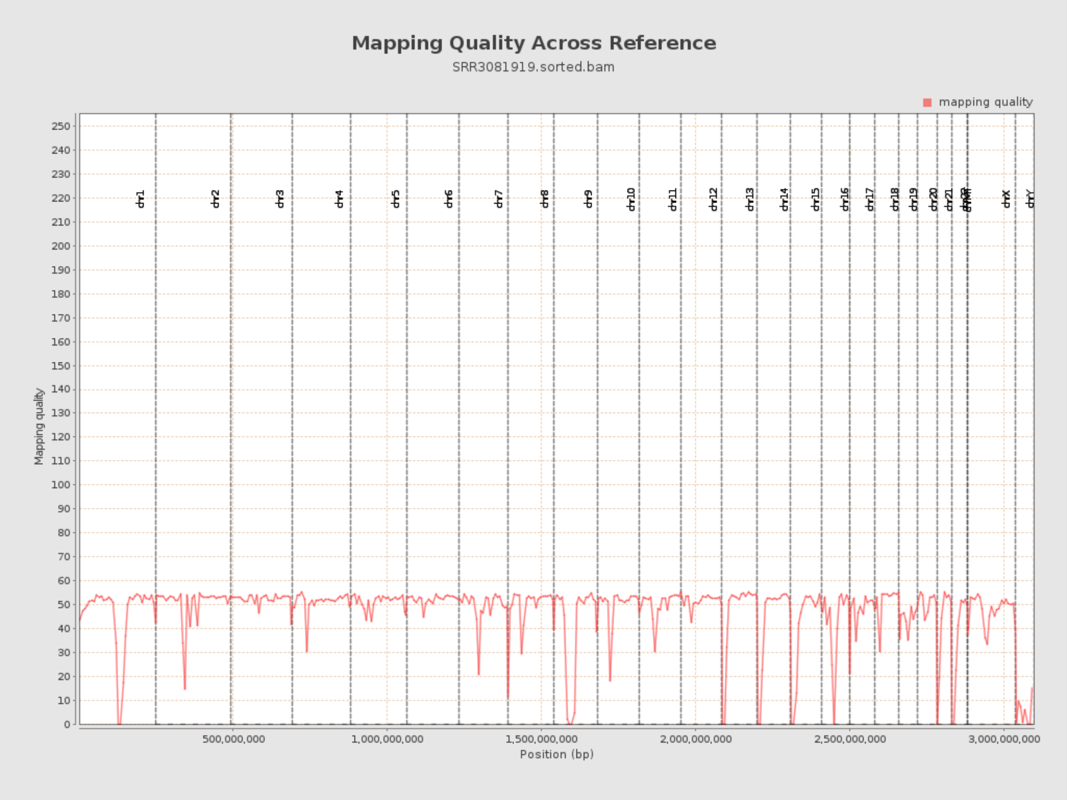
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram