Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 05:30:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083767.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_SRR3083767 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083767.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 05:29:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083767.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,366,431
Mapped reads	1,614,169 / 68.21%
Unmapped reads	752,262 / 31.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,745 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	54,612 / 2.31%
Duplication rate	2.89%
Clipped reads	892,367 / 37.71%

2.2. ACGT Content

Number/percentage of A's	28,448,849 / 27.93%
Number/percentage of C's	19,485,430 / 19.13%
Number/percentage of T's	31,081,149 / 30.51%
Number/percentage of G's	22,848,199 / 22.43%
Number/percentage of N's	1,114 / 0%
GC Percentage	41.56%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.2441

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

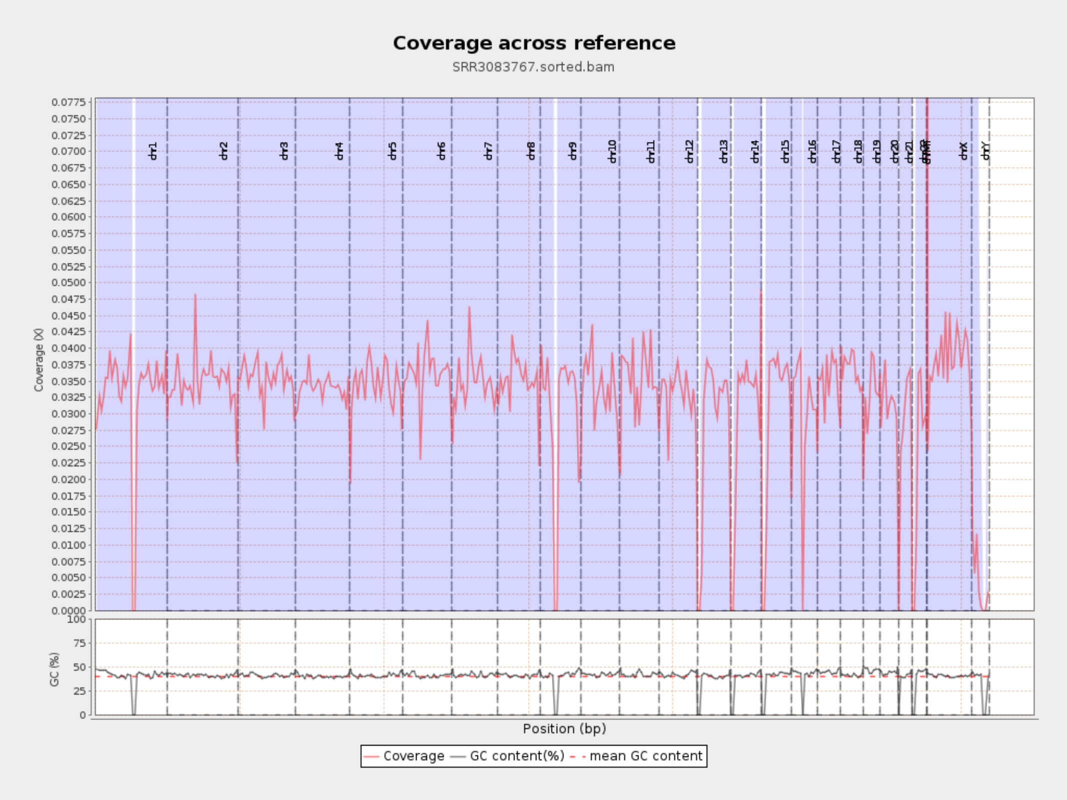
General error rate	0.82%
Mismatches	818,407
Insertions	7,480
Mapped reads with at least one insertion	0.46%
Deletions	20,996
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.63%

2.6. Chromosome stats

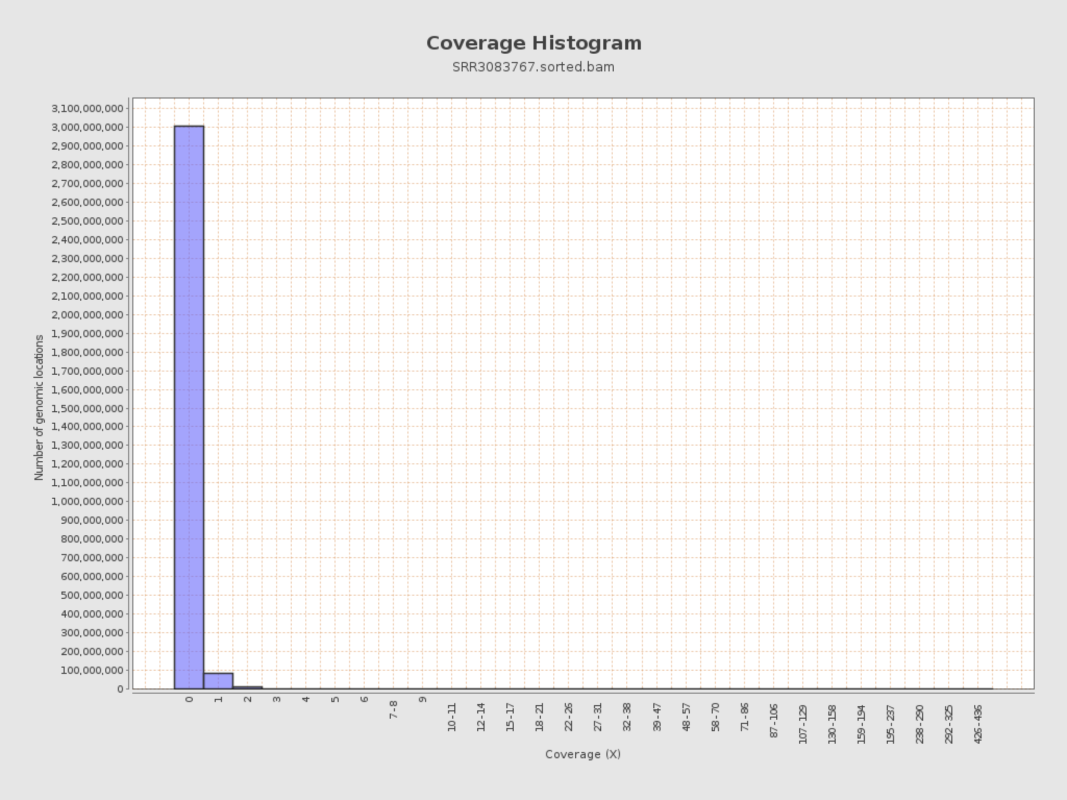
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8182988	0.0328	0.3201
chr2	243199373	8487684	0.0349	0.3127
chr3	198022430	7071267	0.0357	0.2083
chr4	191154276	6502018	0.034	0.2079
chr5	180915260	6305174	0.0349	0.2063
chr6	171115067	6169111	0.0361	0.2322
chr7	159138663	5544456	0.0348	0.2815

chr8	146364022	5120282	0.035	0.2534
chr9	141213431	4276541	0.0303	0.2344
chr10	135534747	4610452	0.034	0.2447
chr11	135006516	4804557	0.0356	0.2331
chr12	133851895	4409002	0.0329	0.2016
chr13	115169878	3244288	0.0282	0.1861
chr14	107349540	3075387	0.0286	0.1966
chr15	102531392	3053874	0.0298	0.1926
chr16	90354753	2670849	0.0296	0.2033
chr17	81195210	2856510	0.0352	0.2285
chr18	78077248	2886181	0.037	0.3972
chr19	59128983	1955834	0.0331	0.2686
chr20	63025520	1969773	0.0313	0.1974
chr21	48129895	1338358	0.0278	0.1896
chr22	51304566	1151319	0.0224	0.1657
chrMT	16571	11242	0.6784	0.9657
chrX	155270560	5956517	0.0384	0.2279
chrY	59373566	244455	0.0041	0.0912

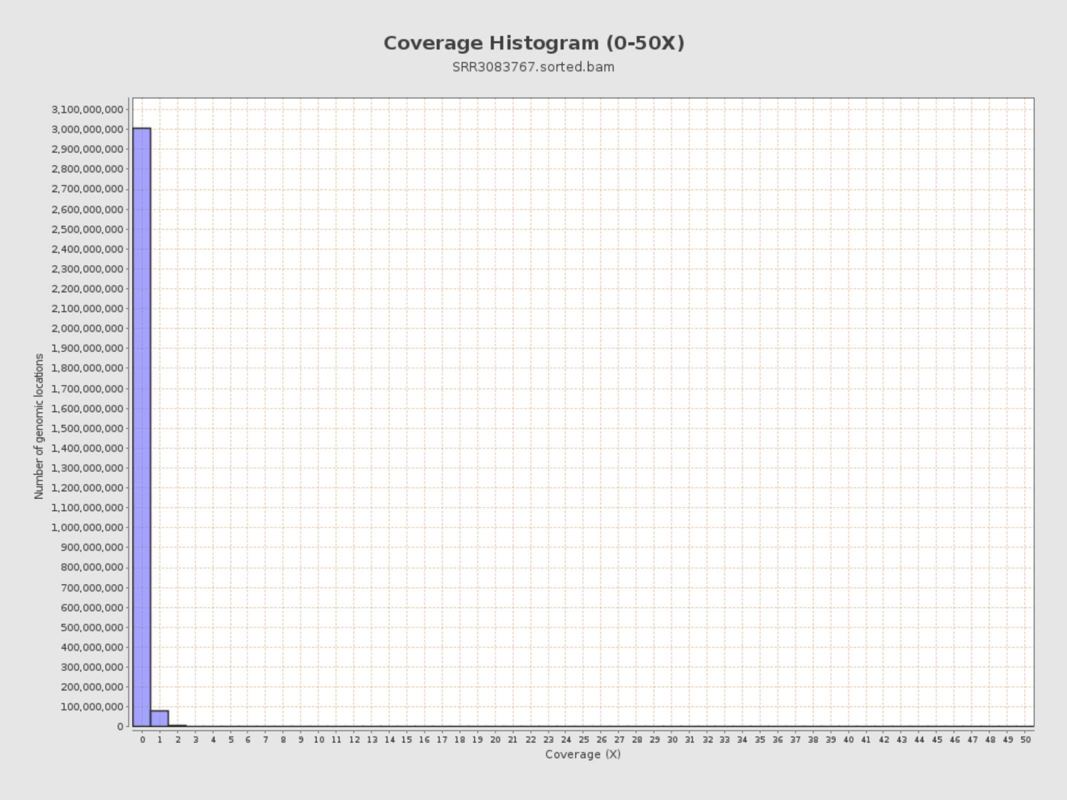
3. Results : Coverage across reference



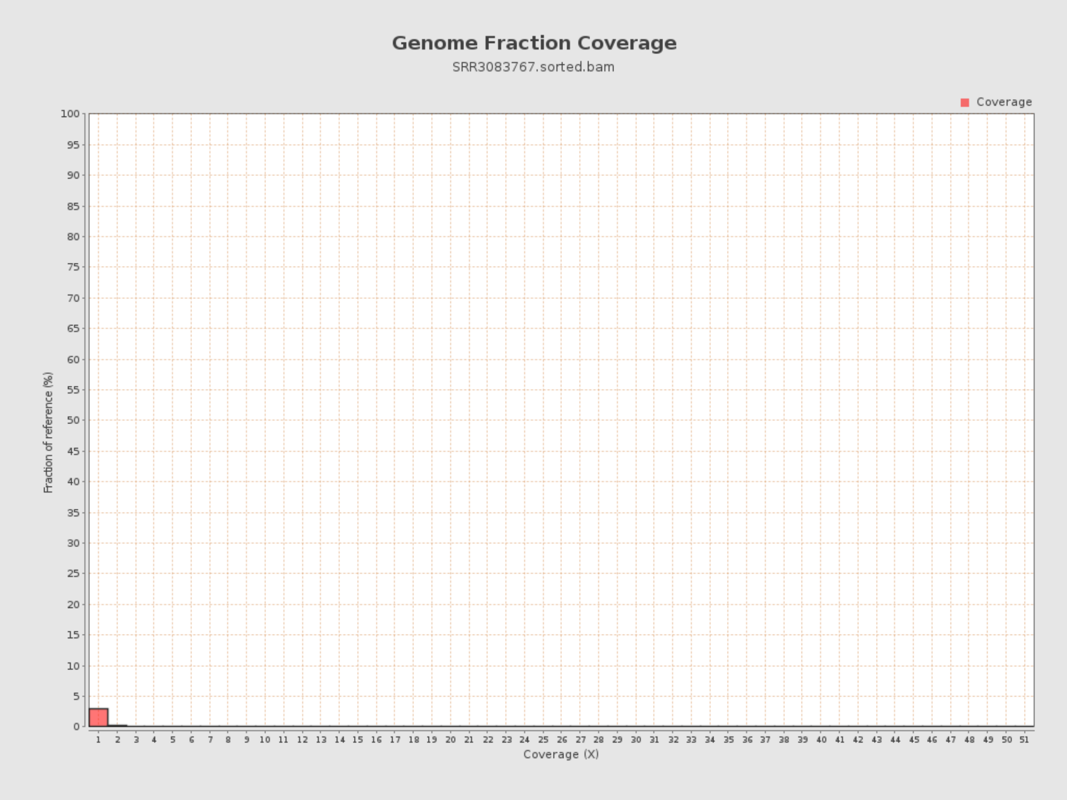
4. Results : Coverage Histogram



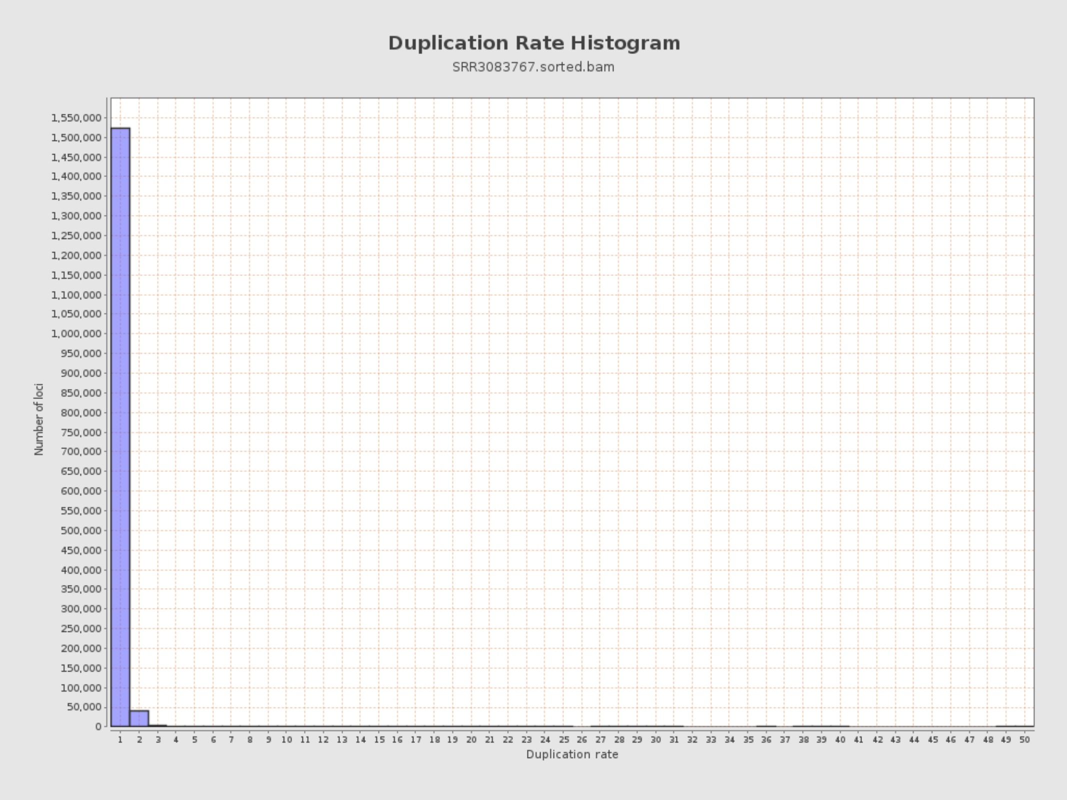
5. Results : Coverage Histogram (0-50X)



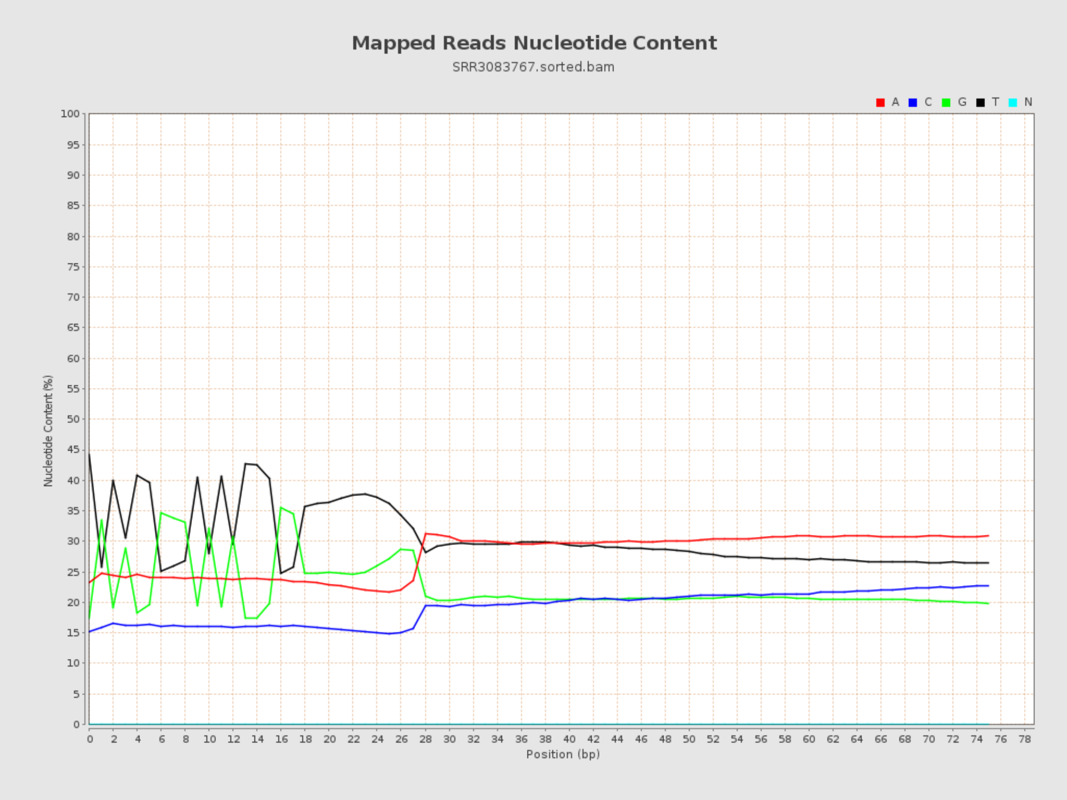
6. Results : Genome Fraction Coverage



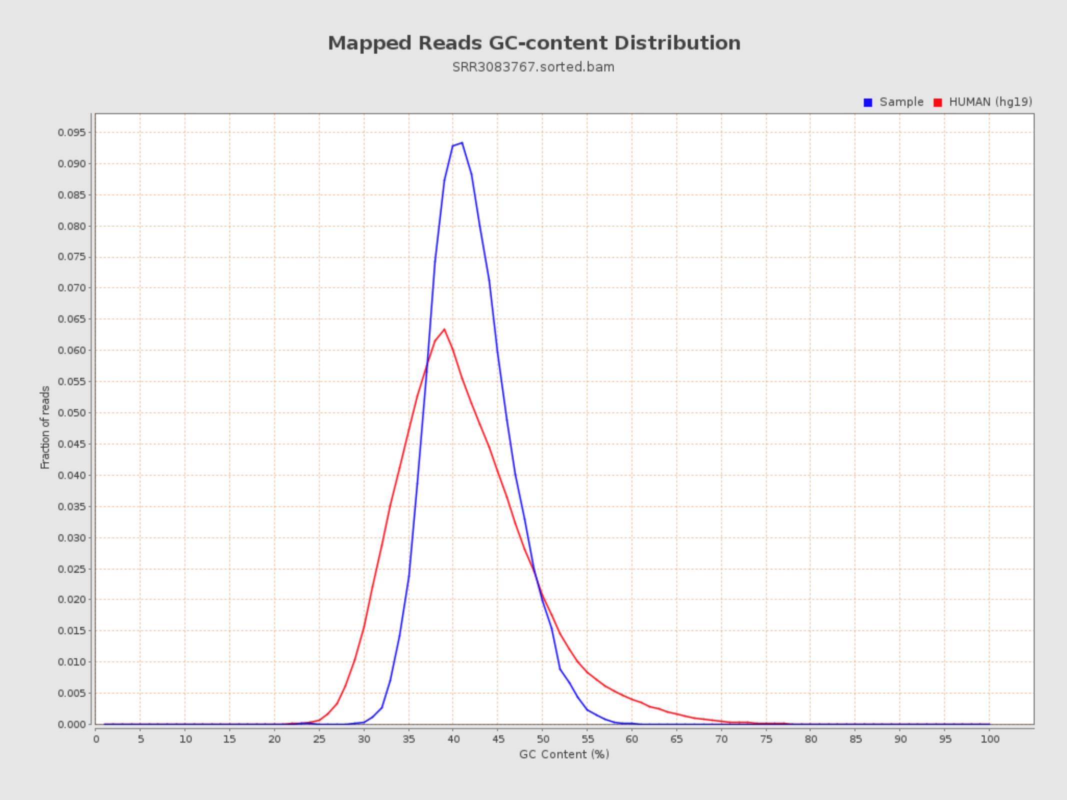
7. Results : Duplication Rate Histogram



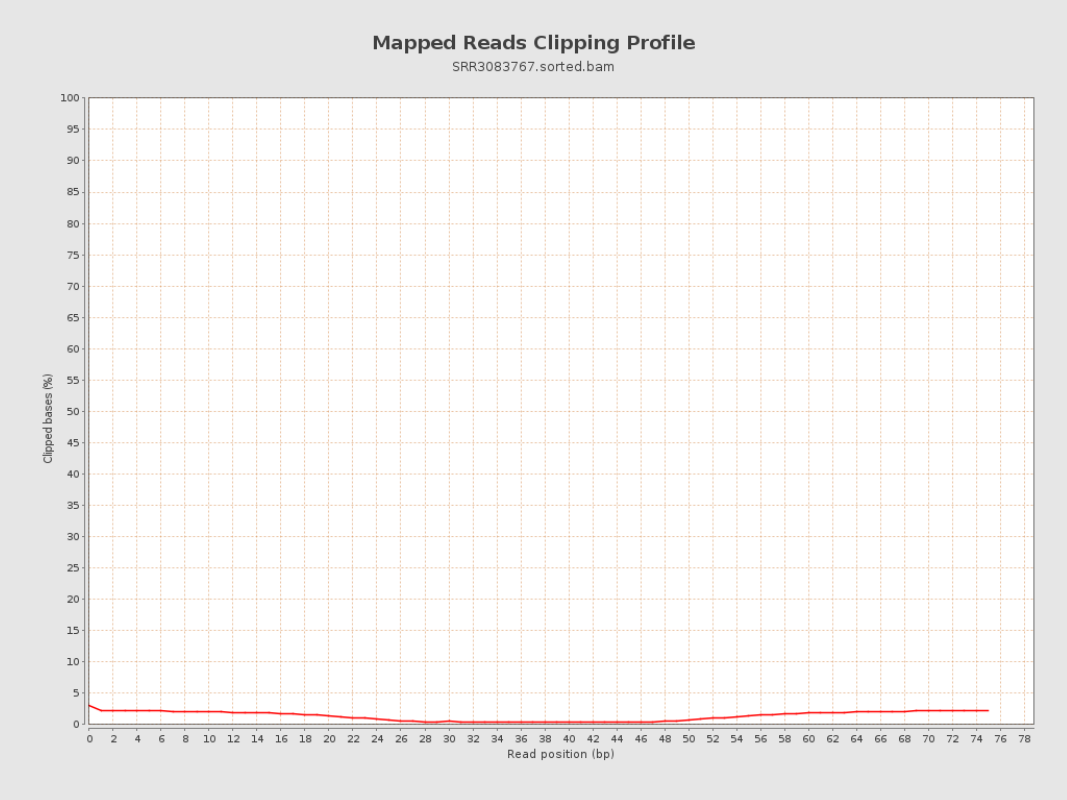
8. Results : Mapped Reads Nucleotide Content



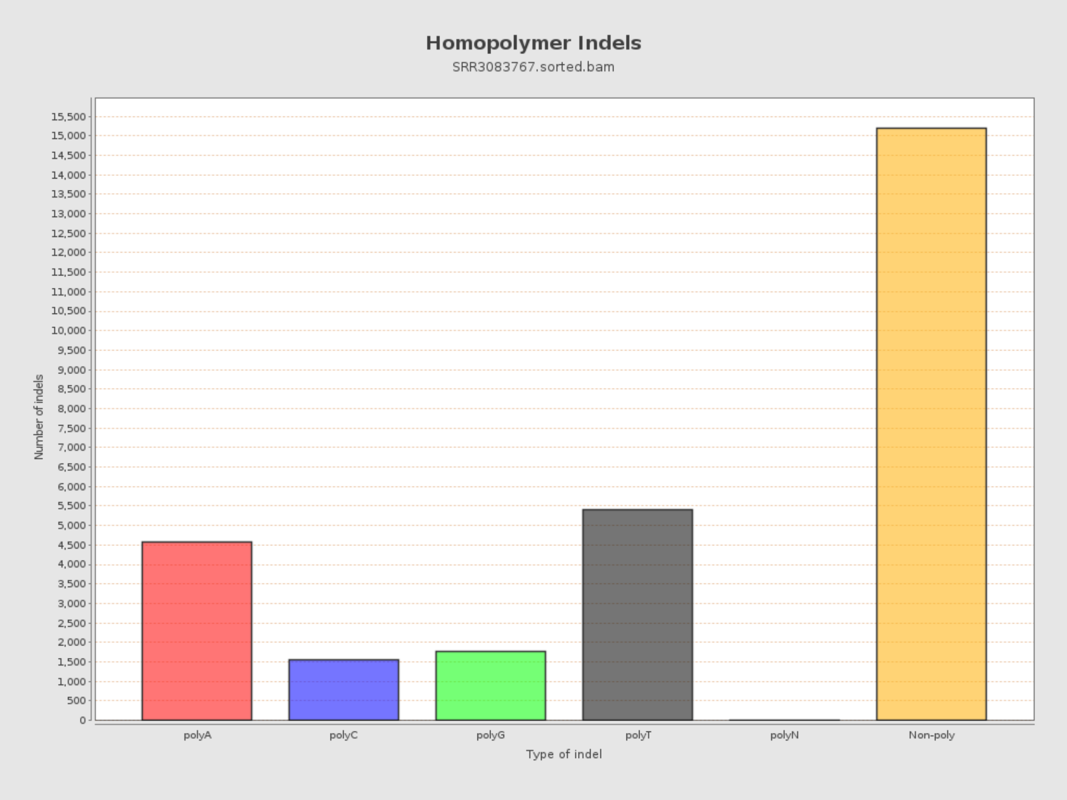
9. Results : Mapped Reads GC-content Distribution



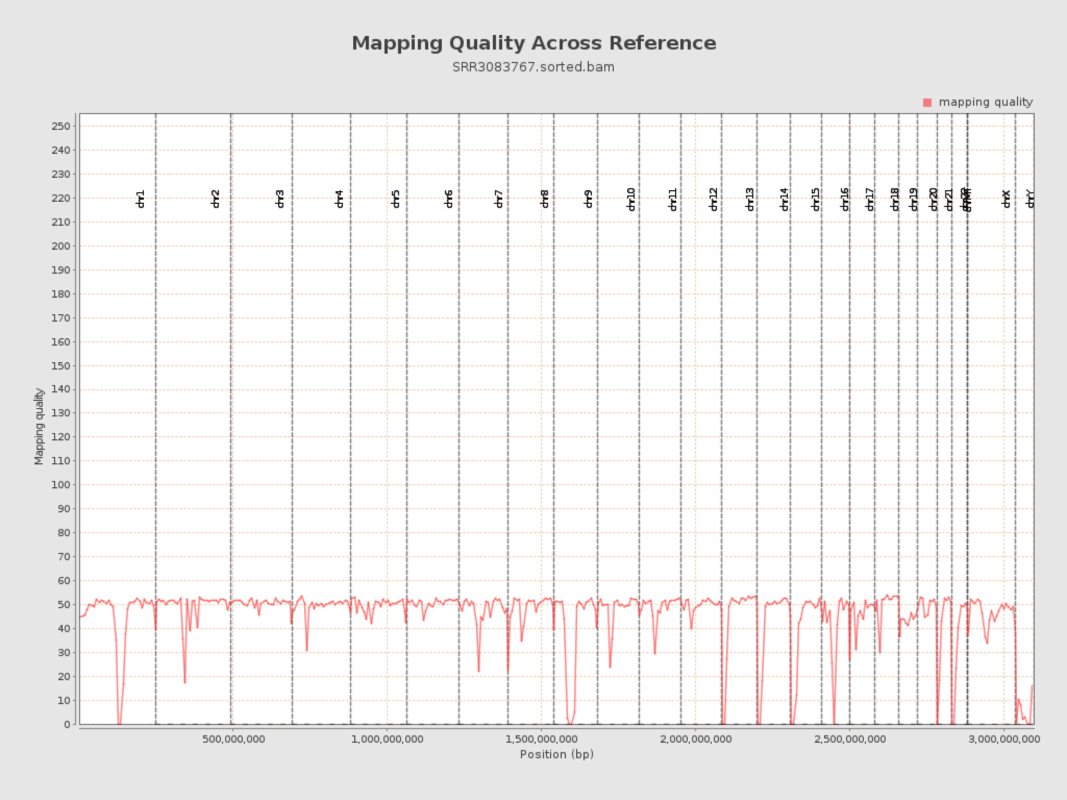
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram