Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:27:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083656.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_SRR3083656 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083656.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:27:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083656.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,905,391
Mapped reads	1,706,124 / 89.54%
Unmapped reads	199,267 / 10.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,384 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	82,944 / 4.35%
Duplication rate	4.14%
Clipped reads	774,941 / 40.67%

2.2. ACGT Content

Number/percentage of A's	30,130,930 / 26.62%
Number/percentage of C's	21,472,089 / 18.97%
Number/percentage of T's	35,199,062 / 31.1%
Number/percentage of G's	26,381,104 / 23.31%
Number/percentage of N's	5,661 / 0.01%
GC Percentage	42.28%

2.3. Coverage

Mean	0.0366

Standard Deviation	0.2968

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

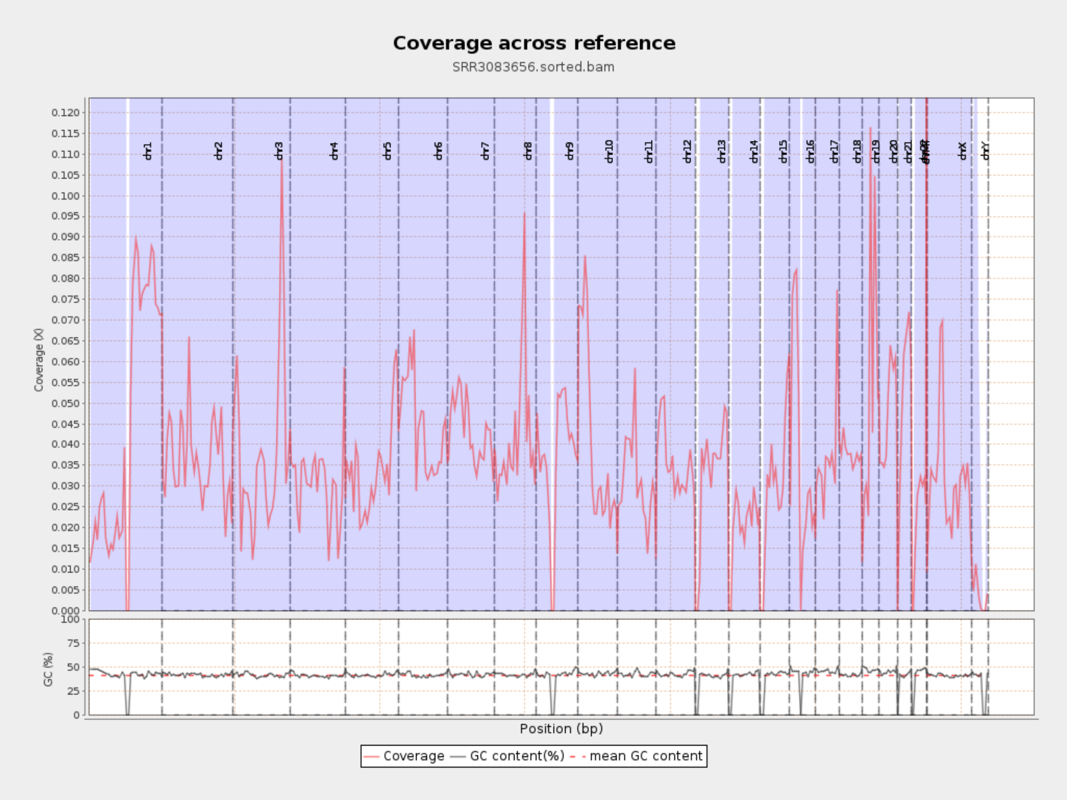
General error rate	0.71%
Mismatches	789,744
Insertions	8,645
Mapped reads with at least one insertion	0.5%
Deletions	25,884
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48%

2.6. Chromosome stats

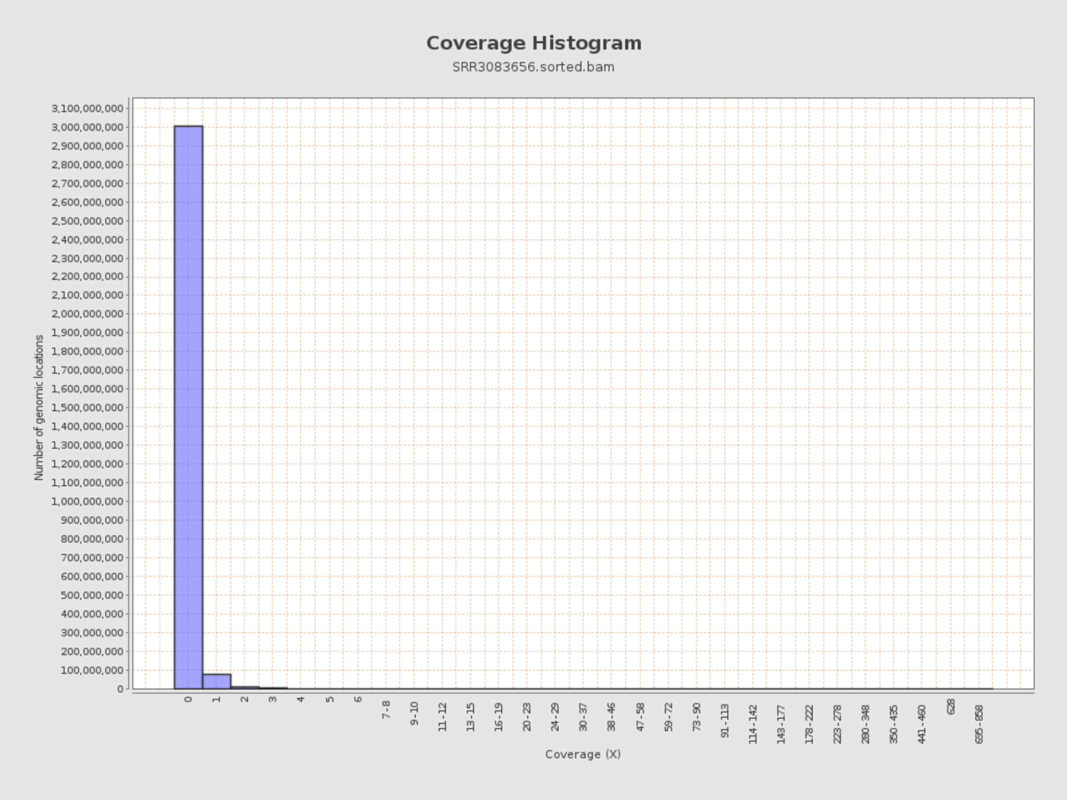
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11013758	0.0442	0.4642
chr2	243199373	8885050	0.0365	0.4468
chr3	198022430	7498365	0.0379	0.2309
chr4	191154276	5788452	0.0303	0.2083
chr5	180915260	6155660	0.034	0.2169
chr6	171115067	7605405	0.0444	0.3021
chr7	159138663	6967791	0.0438	0.3489

chr8	146364022	6152696	0.042	0.2807
chr9	141213431	5166565	0.0366	0.263
chr10	135534747	5644424	0.0416	0.2758
chr11	135006516	4207089	0.0312	0.2439
chr12	133851895	4743242	0.0354	0.2219
chr13	115169878	3748106	0.0325	0.2126
chr14	107349540	2150486	0.02	0.1699
chr15	102531392	3019020	0.0294	0.2101
chr16	90354753	3447758	0.0382	0.2403
chr17	81195210	3114601	0.0384	0.2399
chr18	78077248	2960247	0.0379	0.4185
chr19	59128983	3211743	0.0543	0.366
chr20	63025520	3014542	0.0478	0.2639
chr21	48129895	2434274	0.0506	0.275
chr22	51304566	1121536	0.0219	0.1739
chrMT	16571	3744	0.2259	0.5586
chrX	155270560	4959275	0.0319	0.218
chrY	59373566	217166	0.0037	0.0853

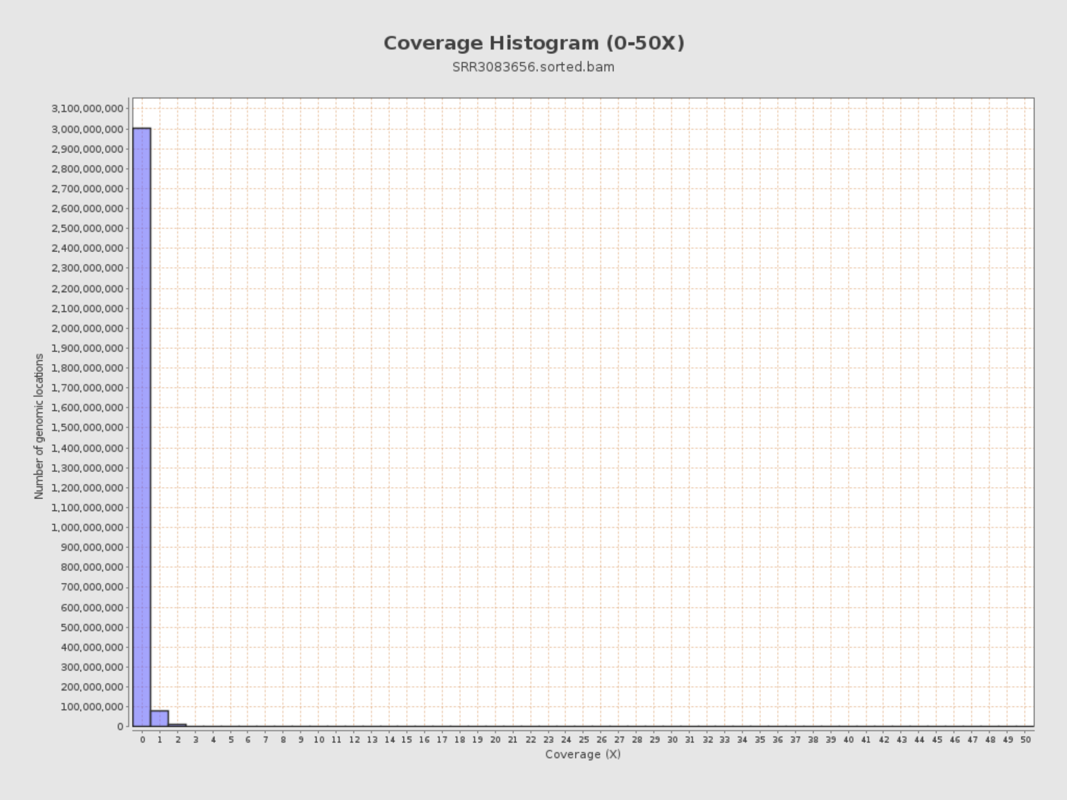
3. Results : Coverage across reference



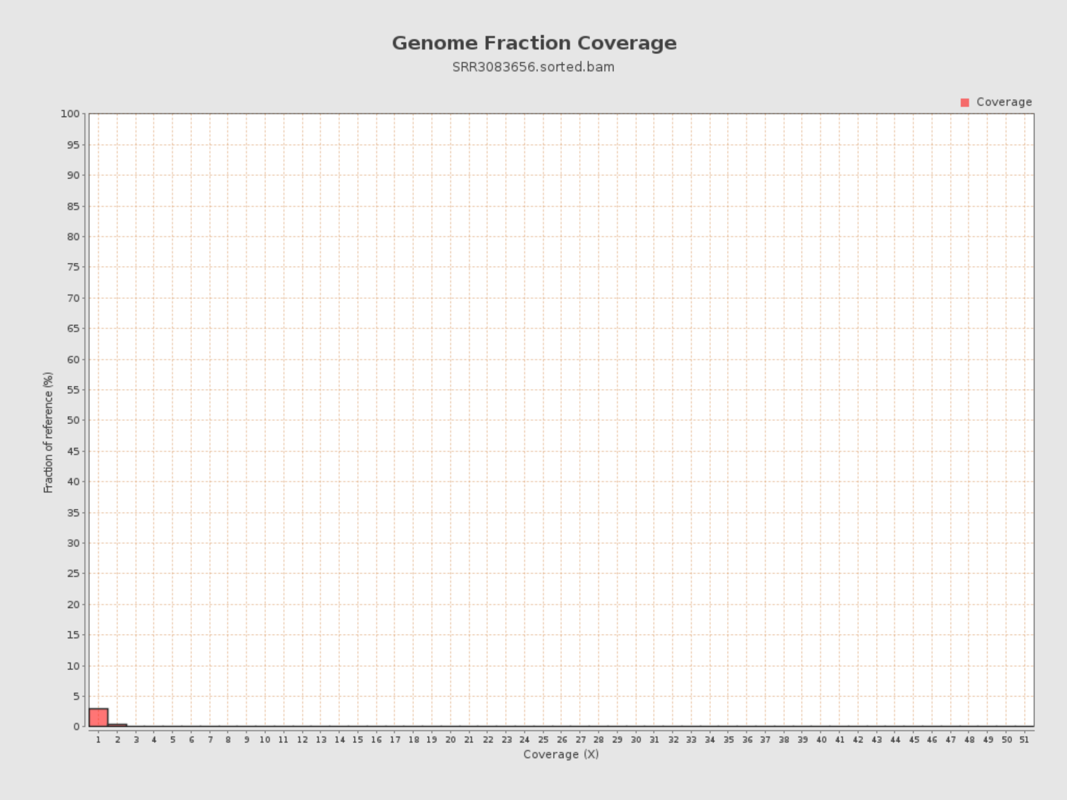
4. Results : Coverage Histogram



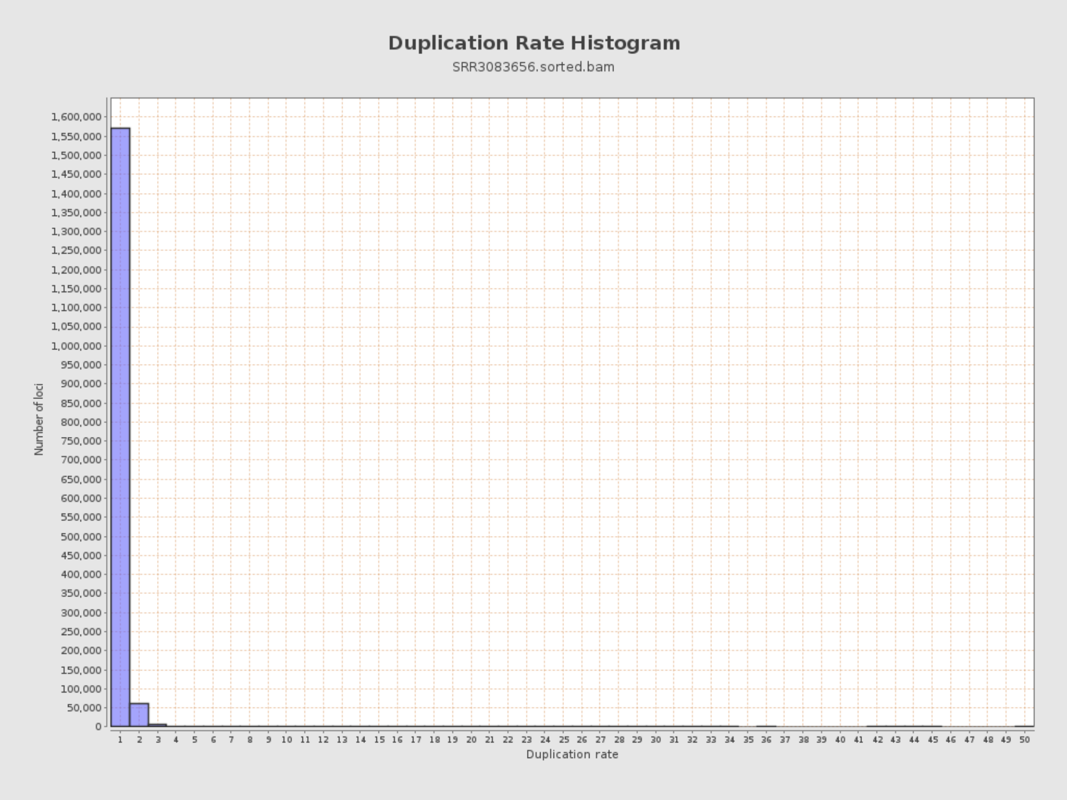
5. Results : Coverage Histogram (0-50X)



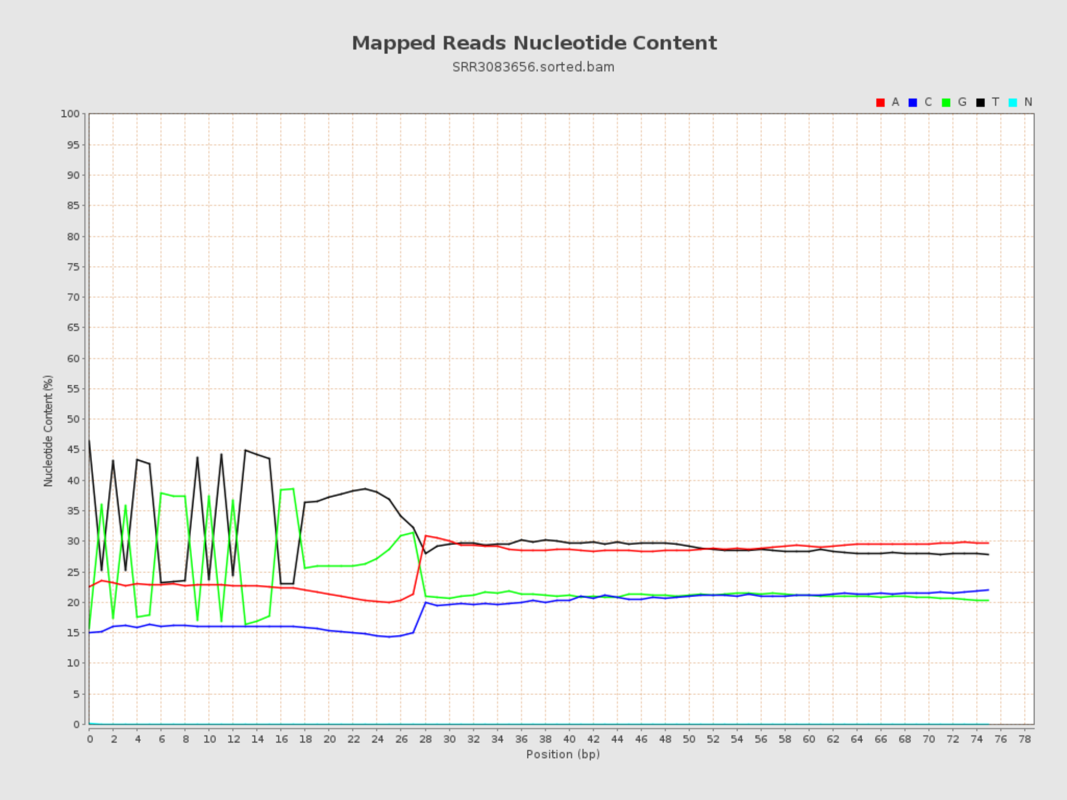
6. Results : Genome Fraction Coverage



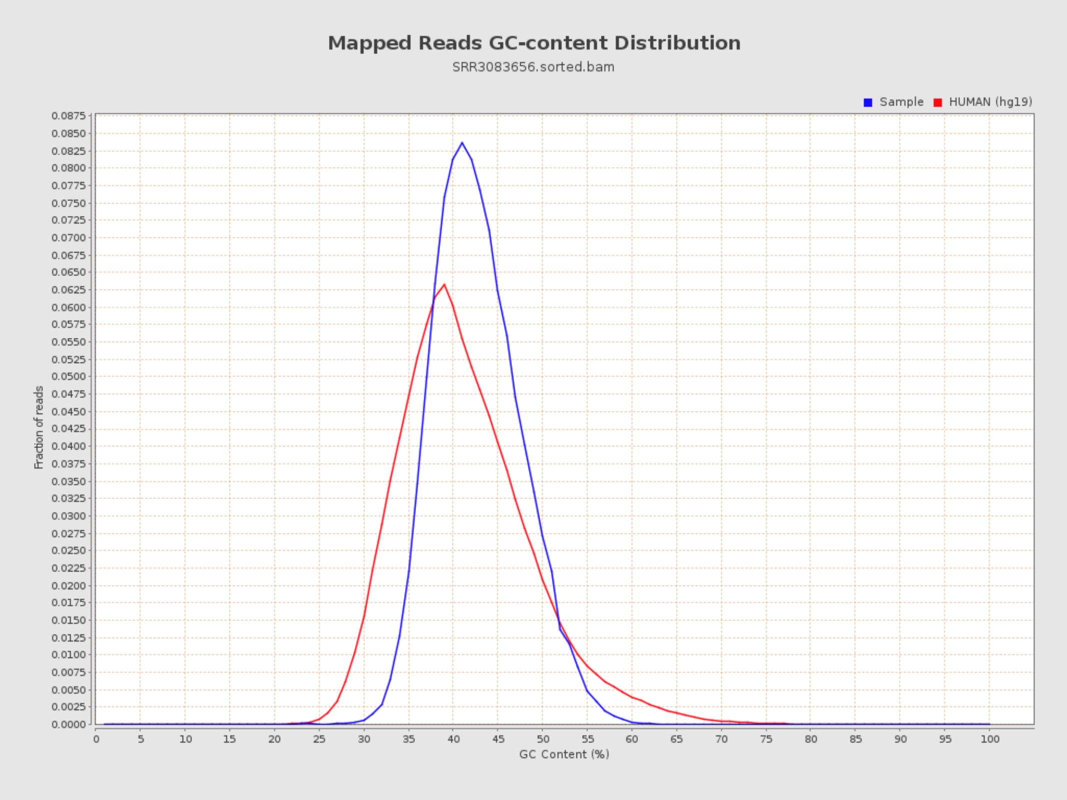
7. Results : Duplication Rate Histogram



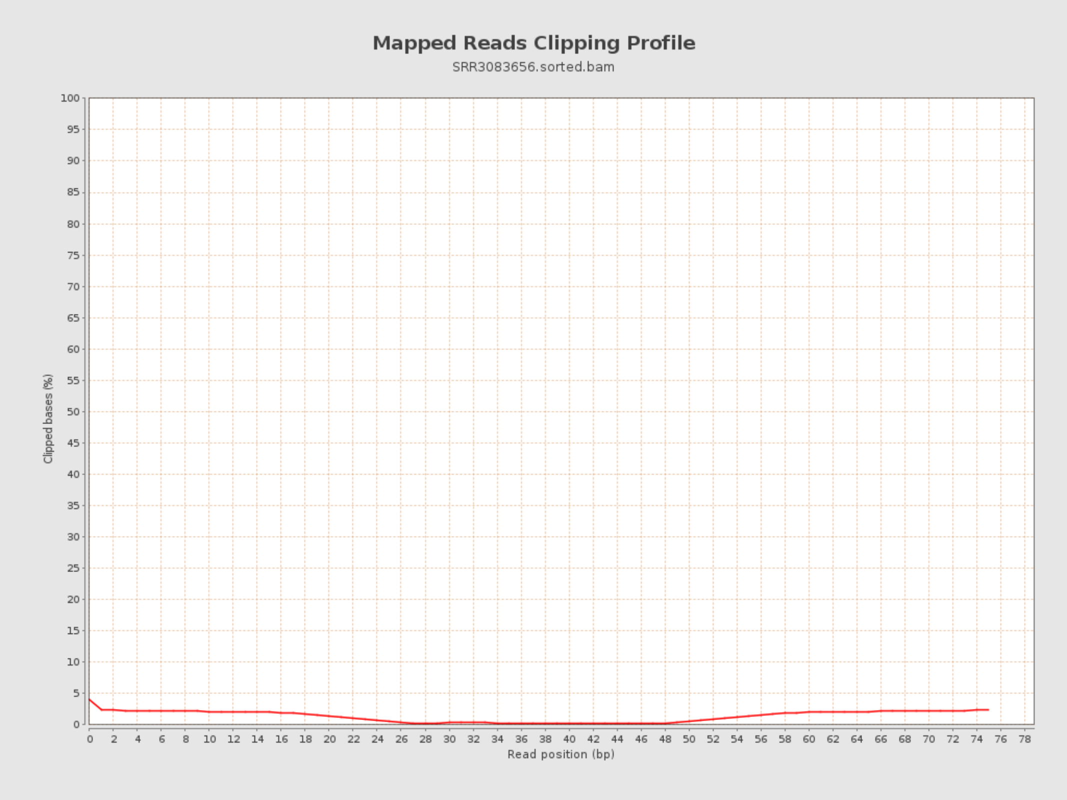
8. Results : Mapped Reads Nucleotide Content



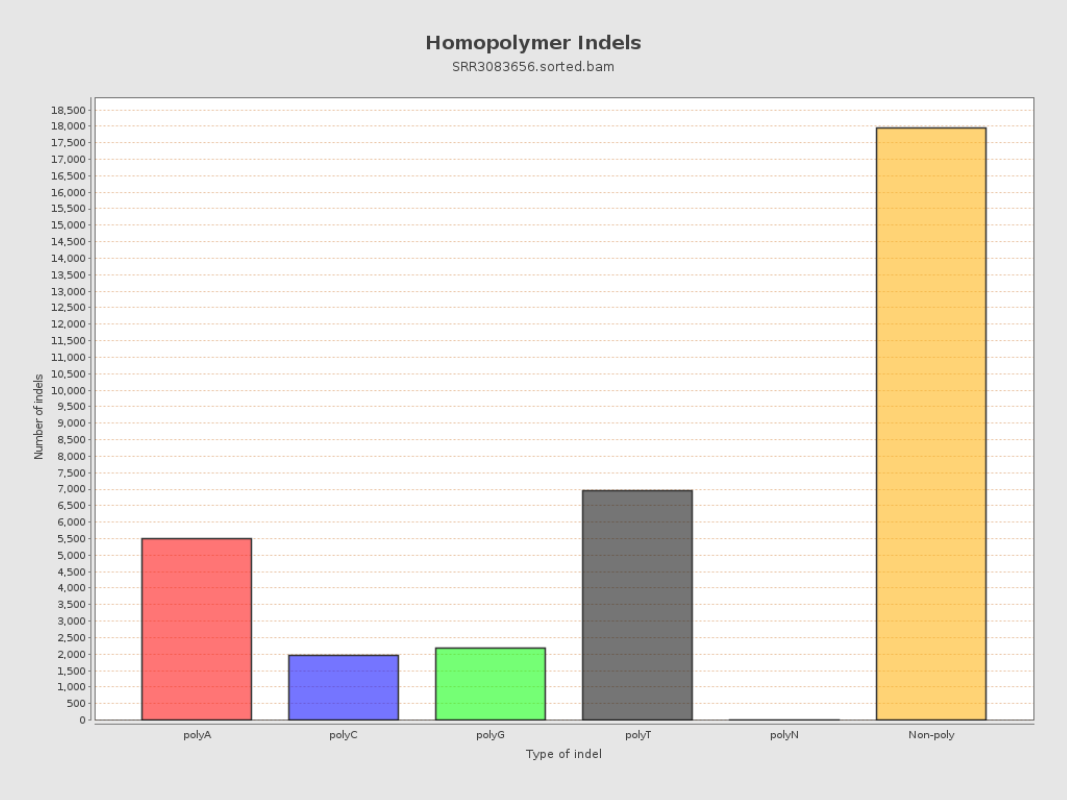
9. Results : Mapped Reads GC-content Distribution



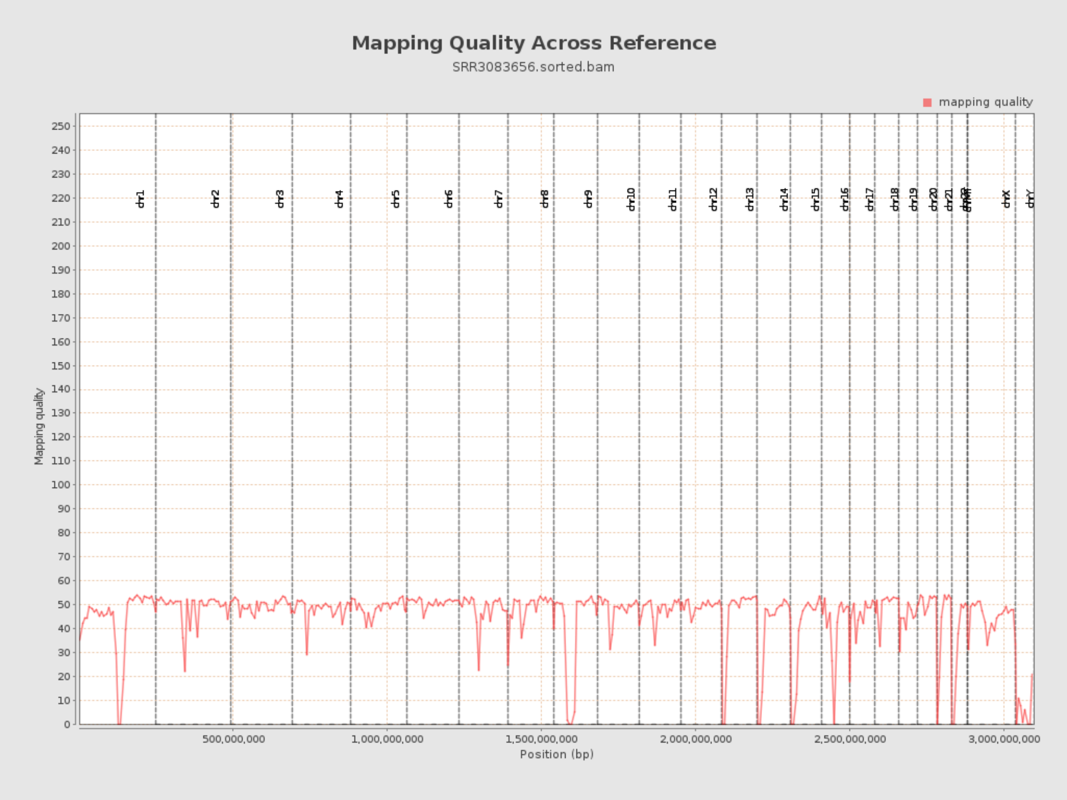
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram