Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:17:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083634.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_SRR3083634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083634.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:17:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,417,483
Mapped reads	1,993,310 / 82.45%
Unmapped reads	424,173 / 17.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,012 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	57,228 / 2.37%
Duplication rate	2.35%
Clipped reads	1,331,758 / 55.09%

2.2. ACGT Content

Number/percentage of A's	36,028,024 / 29.7%
Number/percentage of C's	23,524,811 / 19.4%
Number/percentage of T's	35,779,046 / 29.5%
Number/percentage of G's	25,943,608 / 21.39%
Number/percentage of N's	16,594 / 0.01%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0392

Standard Deviation	0.2994

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

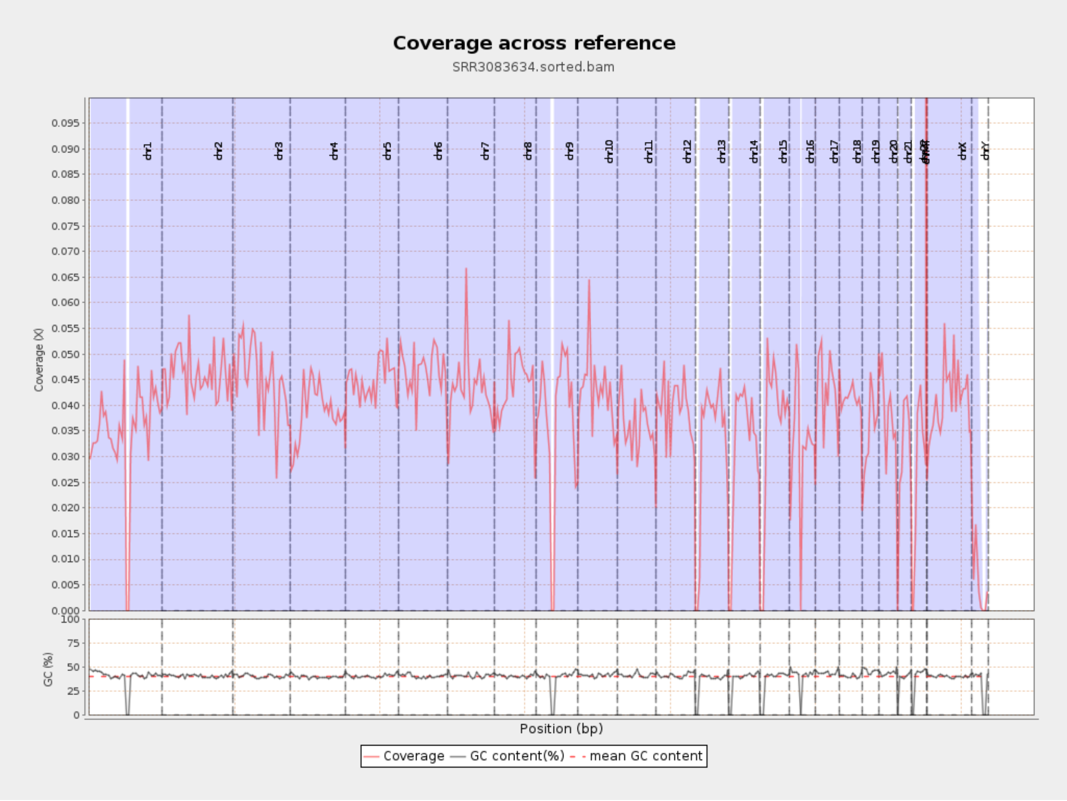
General error rate	0.86%
Mismatches	1,033,429
Insertions	8,675
Mapped reads with at least one insertion	0.43%
Deletions	25,163
Mapped reads with at least one deletion	1.25%
Homopolymer indels	45.53%

2.6. Chromosome stats

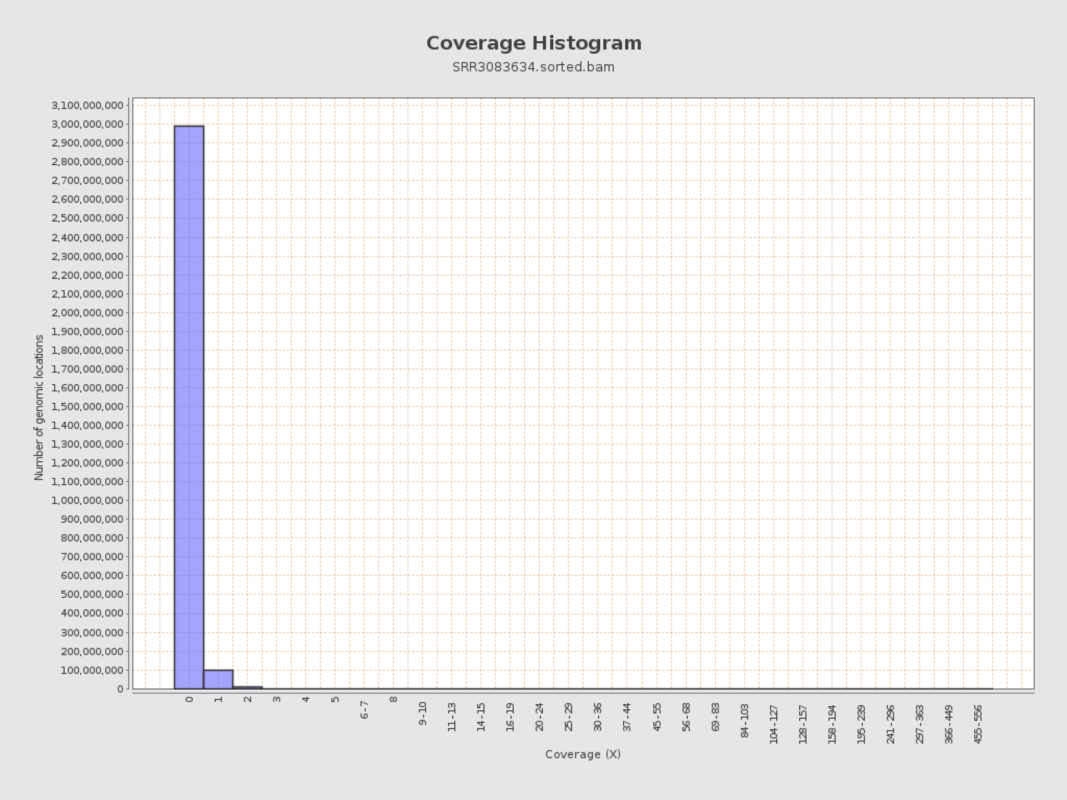
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8650597	0.0347	0.5014
chr2	243199373	11220689	0.0461	0.2923
chr3	198022430	8987335	0.0454	0.2333
chr4	191154276	7394854	0.0387	0.2238
chr5	180915260	8136842	0.045	0.2329
chr6	171115067	7985716	0.0467	0.2655
chr7	159138663	6946736	0.0437	0.4334

chr8	146364022	6403524	0.0438	0.406
chr9	141213431	5243321	0.0371	0.2591
chr10	135534747	5817773	0.0429	0.3201
chr11	135006516	4845915	0.0359	0.2285
chr12	133851895	5292943	0.0395	0.2197
chr13	115169878	3725201	0.0323	0.1966
chr14	107349540	3429029	0.0319	0.1999
chr15	102531392	3646481	0.0356	0.2072
chr16	90354753	2911898	0.0322	0.214
chr17	81195210	3467564	0.0427	0.2558
chr18	78077248	3249877	0.0416	0.4218
chr19	59128983	2097072	0.0355	0.3674
chr20	63025520	2400125	0.0381	0.2152
chr21	48129895	1440115	0.0299	0.1998
chr22	51304566	1315131	0.0256	0.1746
chrMT	16571	75191	4.5375	3.34
chrX	155270560	6338034	0.0408	0.2338
chrY	59373566	310649	0.0052	0.1246

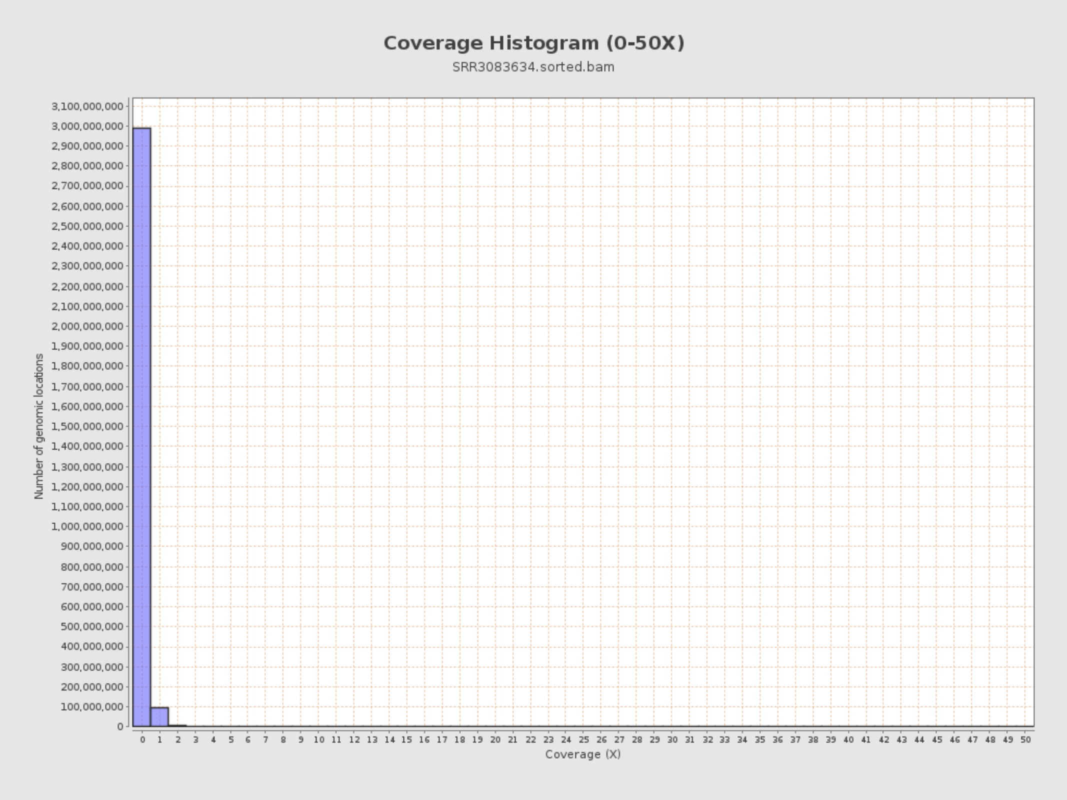
3. Results : Coverage across reference



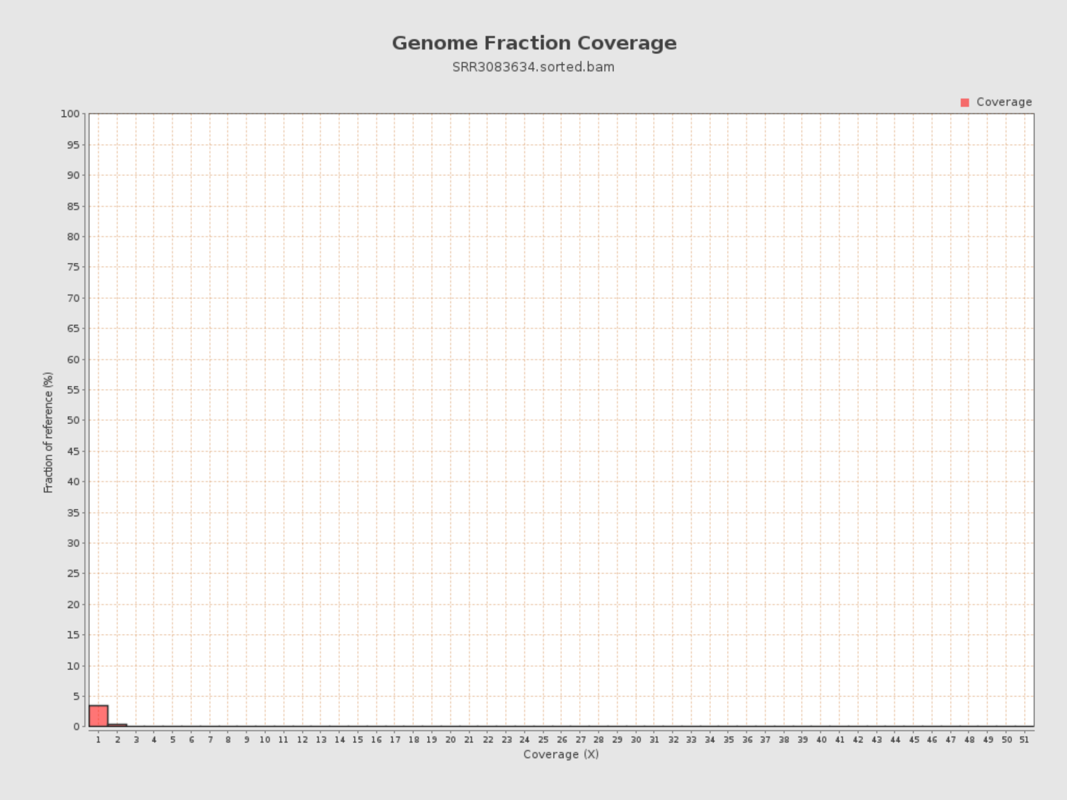
4. Results : Coverage Histogram



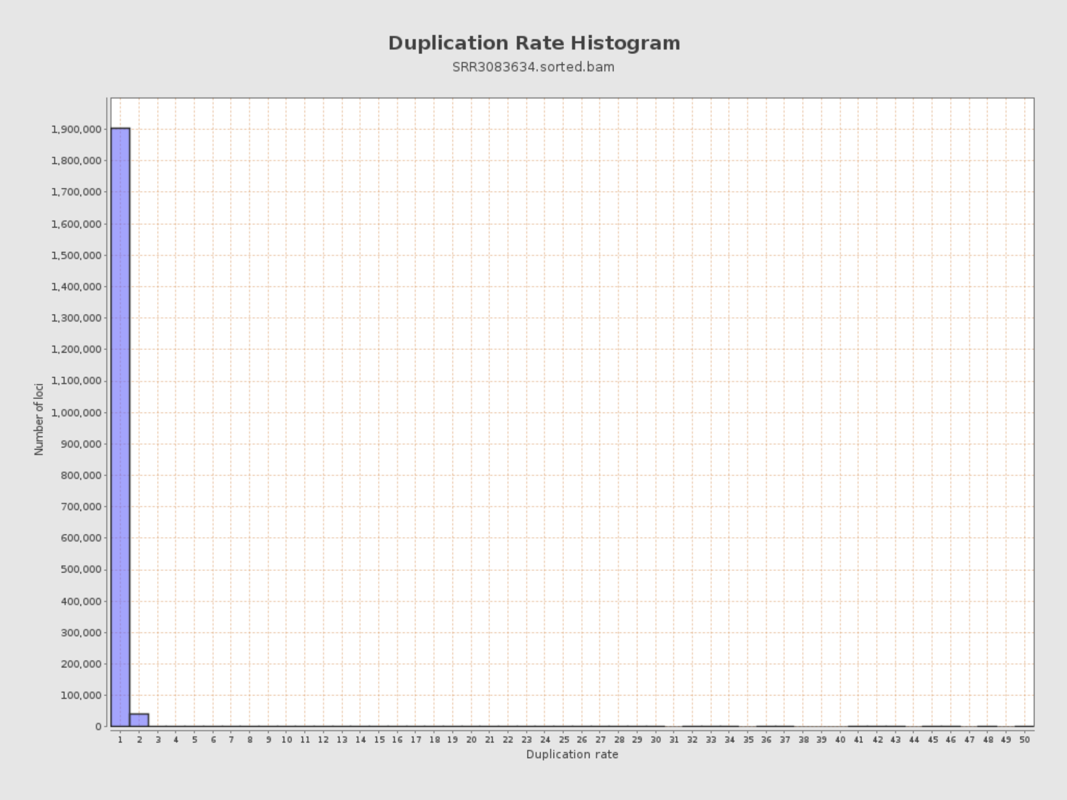
5. Results : Coverage Histogram (0-50X)



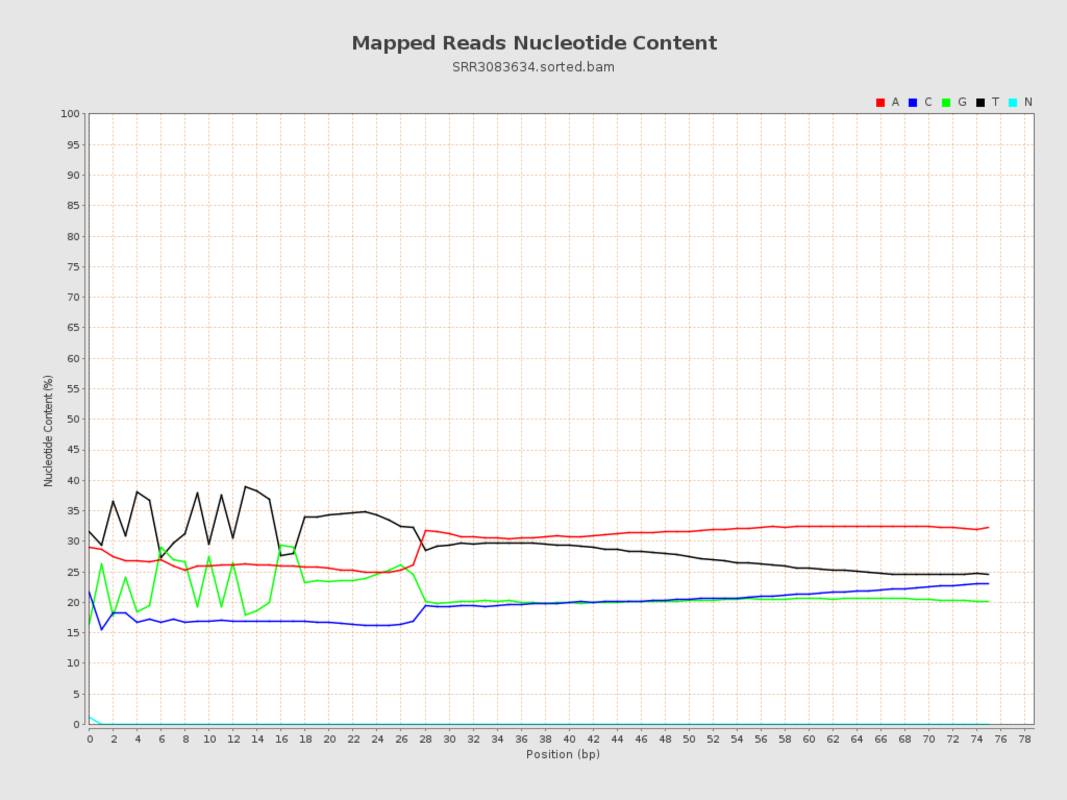
6. Results : Genome Fraction Coverage



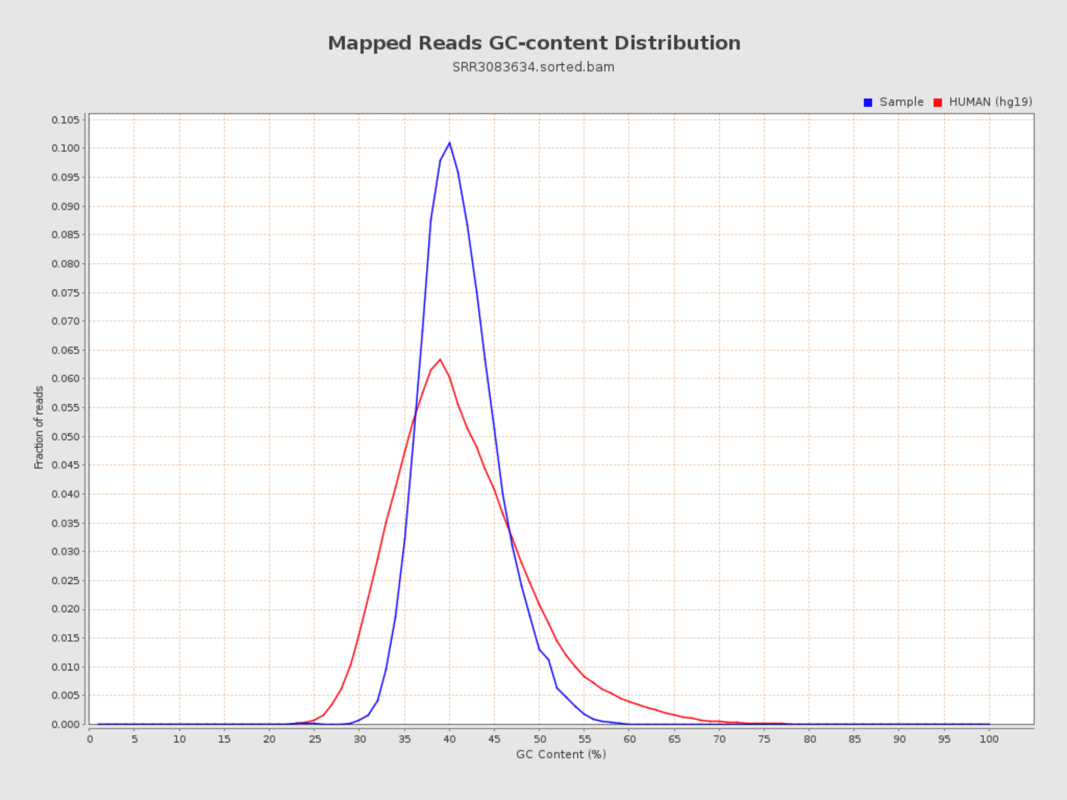
7. Results : Duplication Rate Histogram



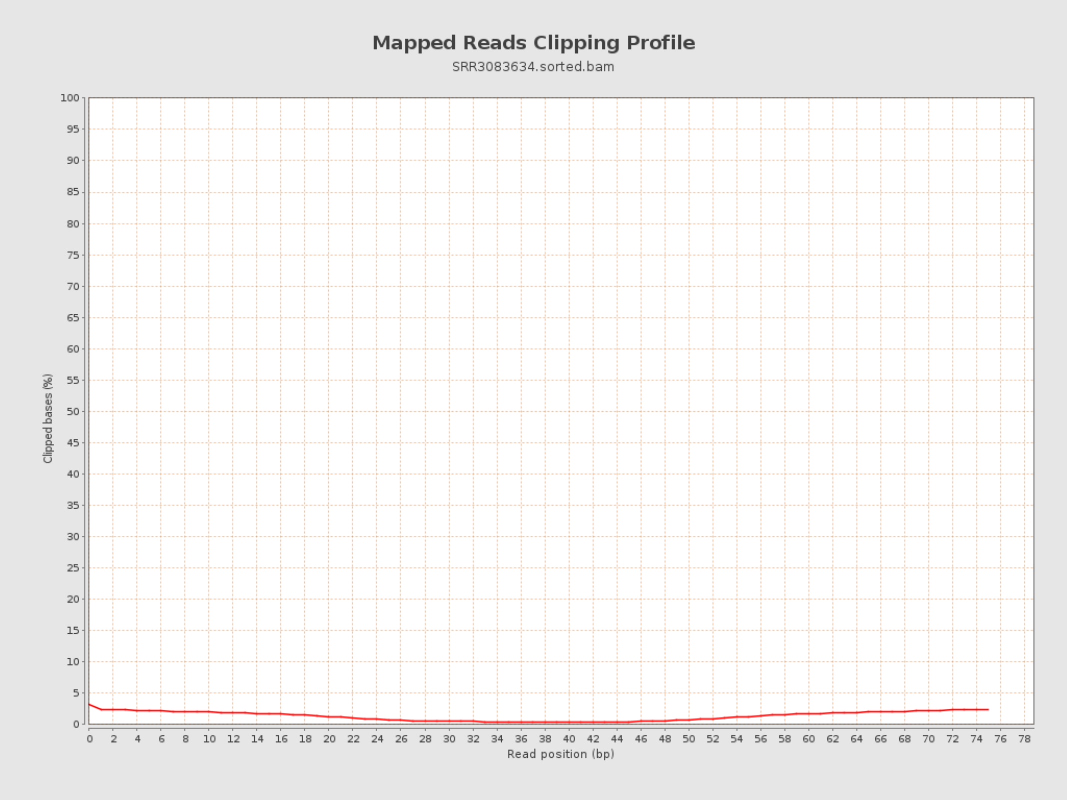
8. Results : Mapped Reads Nucleotide Content



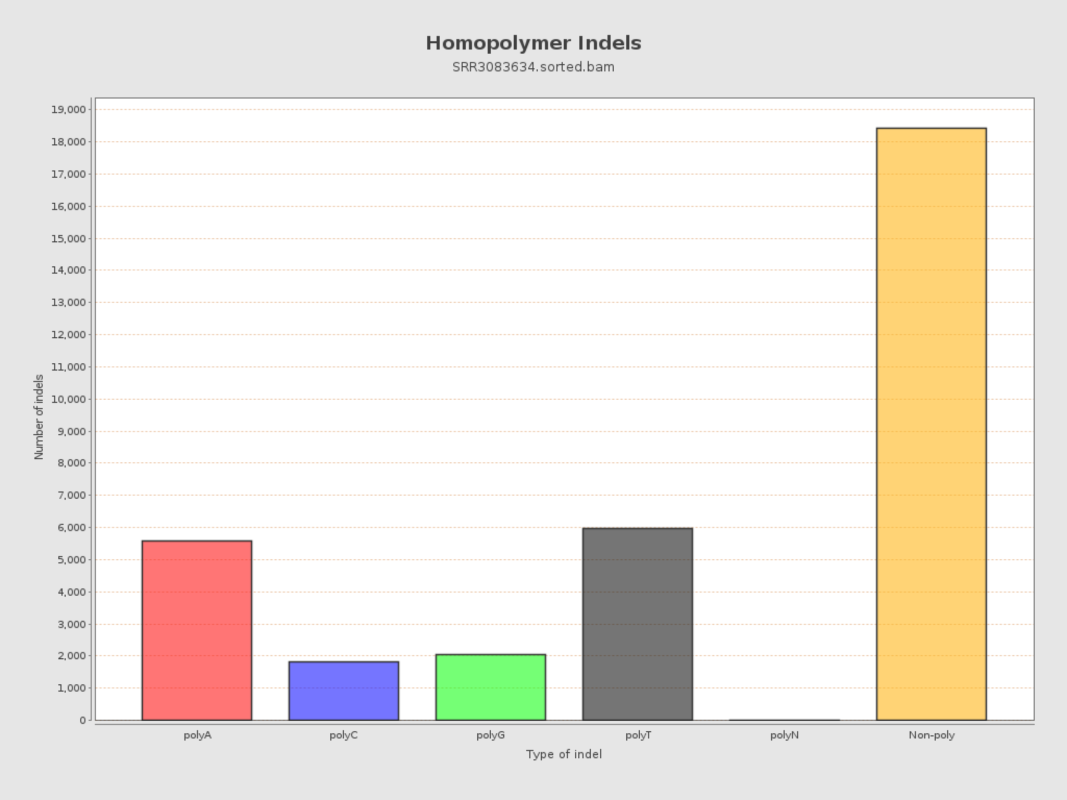
9. Results : Mapped Reads GC-content Distribution



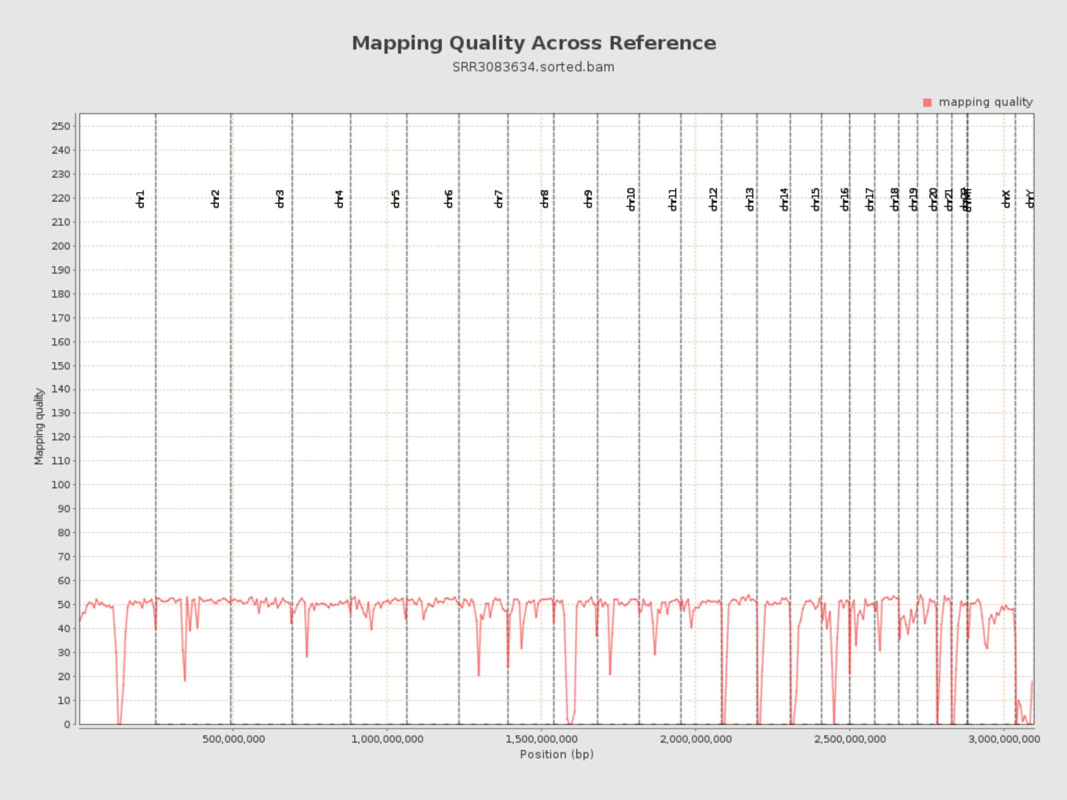
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram