Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:44:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083640.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_SRR3083640 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083640.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:44:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083640.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,245,435
Mapped reads	1,811,480 / 80.67%
Unmapped reads	433,955 / 19.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,918 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	60,205 / 2.68%
Duplication rate	2.68%
Clipped reads	1,289,197 / 57.41%

2.2. ACGT Content

Number/percentage of A's	32,007,173 / 29.66%
Number/percentage of C's	21,056,290 / 19.51%
Number/percentage of T's	31,519,142 / 29.2%
Number/percentage of G's	23,327,748 / 21.61%
Number/percentage of N's	14,961 / 0.01%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0349

Standard Deviation	0.2881

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

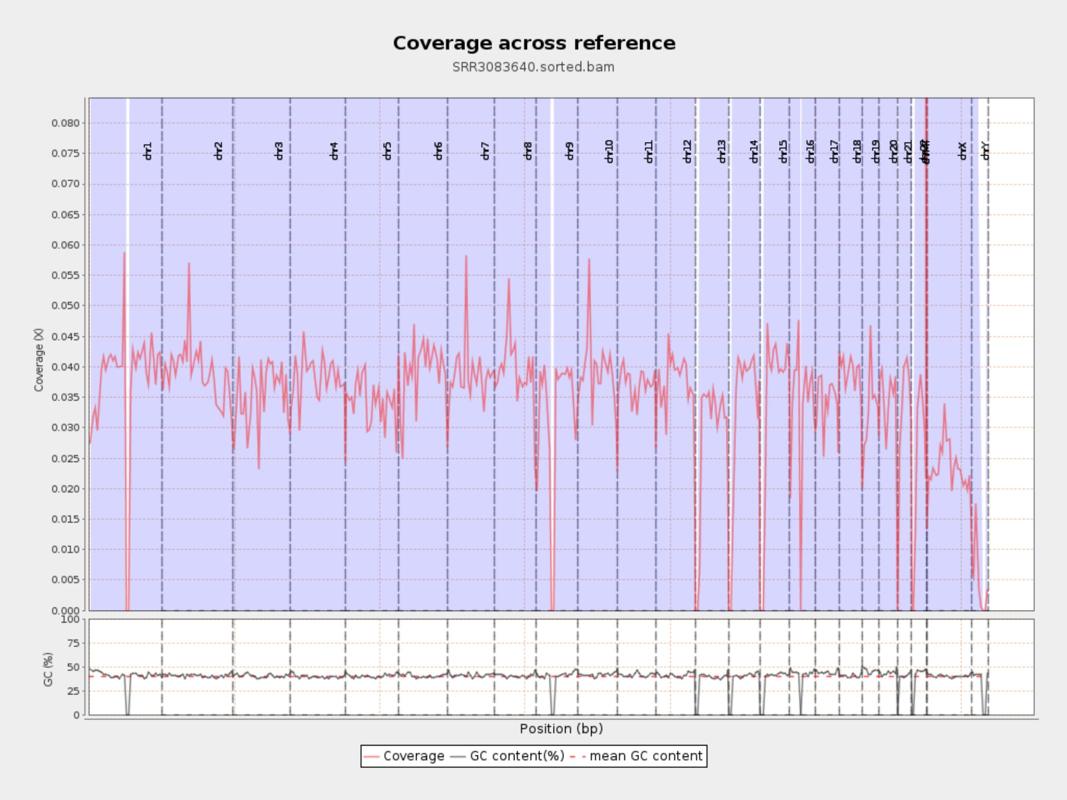
General error rate	0.86%
Mismatches	913,044
Insertions	7,994
Mapped reads with at least one insertion	0.44%
Deletions	22,392
Mapped reads with at least one deletion	1.22%
Homopolymer indels	45.29%

2.6. Chromosome stats

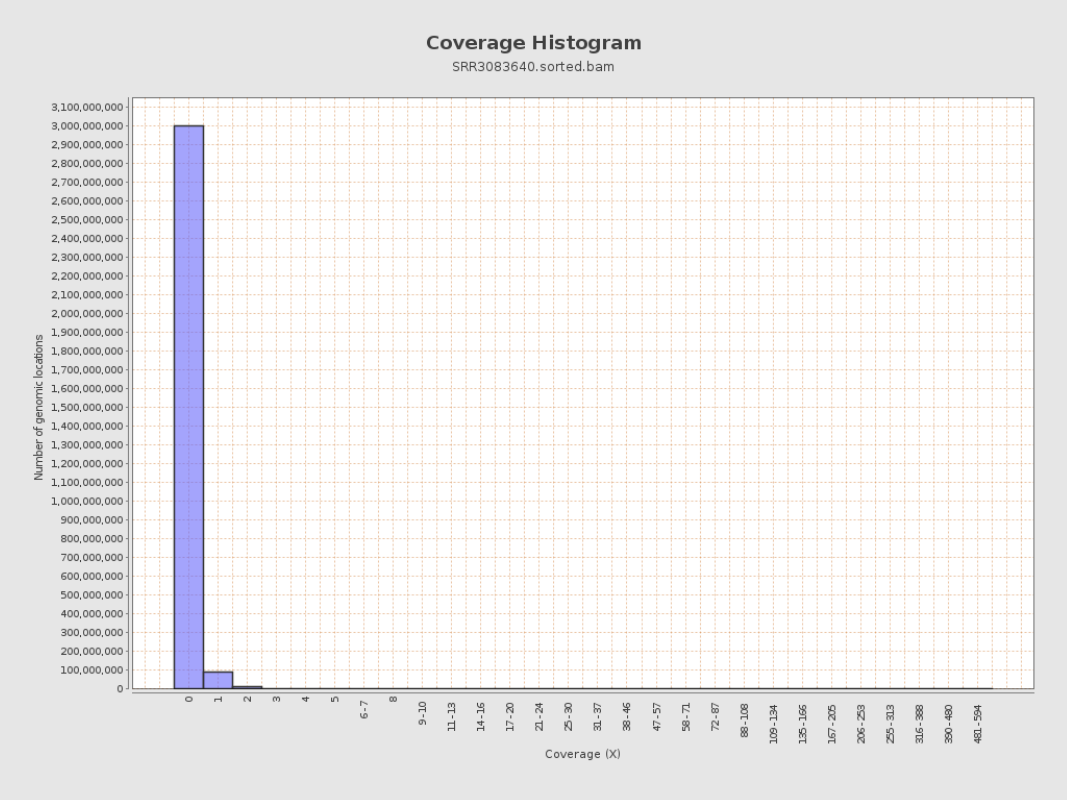
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9322900	0.0374	0.5245
chr2	243199373	9573918	0.0394	0.2823
chr3	198022430	7025600	0.0355	0.2046
chr4	191154276	7340675	0.0384	0.2213
chr5	180915260	6180926	0.0342	0.201
chr6	171115067	6740806	0.0394	0.2388
chr7	159138663	6213045	0.039	0.3743

chr8	146364022	5794895	0.0396	0.3796
chr9	141213431	4525369	0.032	0.249
chr10	135534747	5367179	0.0396	0.2943
chr11	135006516	4996904	0.037	0.2332
chr12	133851895	5060765	0.0378	0.2139
chr13	115169878	3234690	0.0281	0.1811
chr14	107349540	3461367	0.0322	0.2043
chr15	102531392	3488302	0.034	0.2007
chr16	90354753	3016321	0.0334	0.2151
chr17	81195210	2767003	0.0341	0.2146
chr18	78077248	3062762	0.0392	0.4345
chr19	59128983	1960085	0.0331	0.3981
chr20	63025520	2178459	0.0346	0.2073
chr21	48129895	1537132	0.0319	0.2046
chr22	51304566	1191875	0.0232	0.1644
chrMT	16571	25001	1.5087	1.5102
chrX	155270560	3625617	0.0234	0.1818
chrY	59373566	269454	0.0045	0.1354

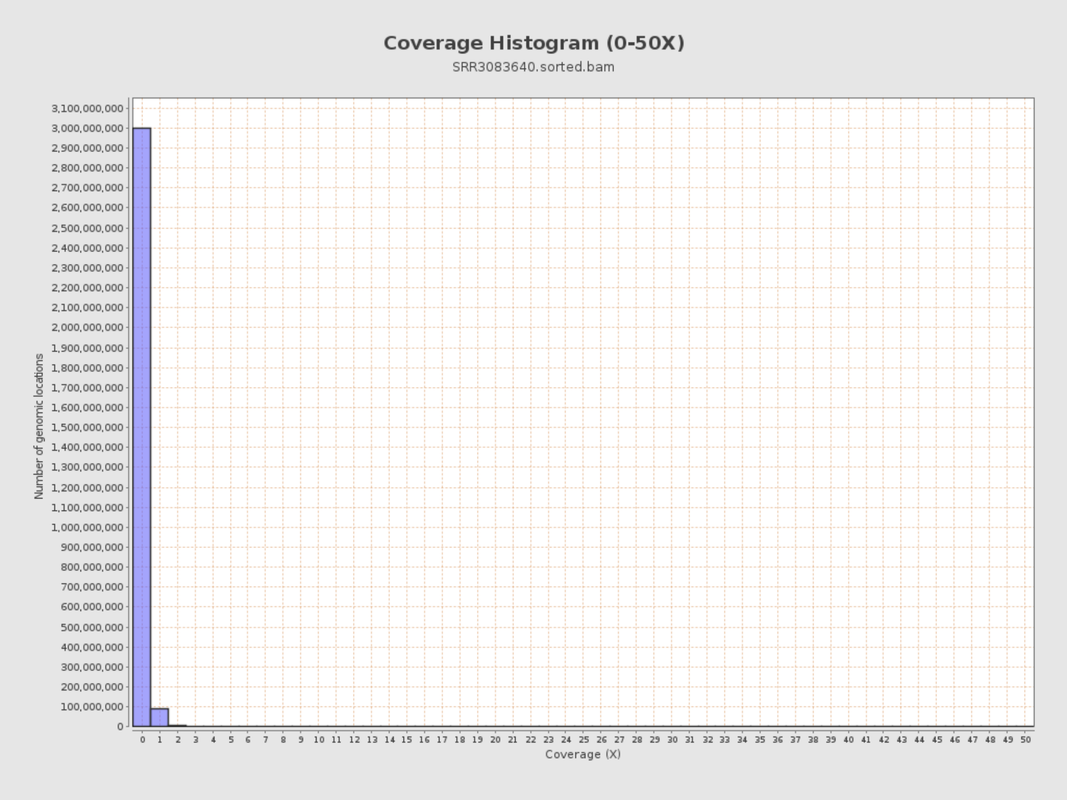
3. Results : Coverage across reference



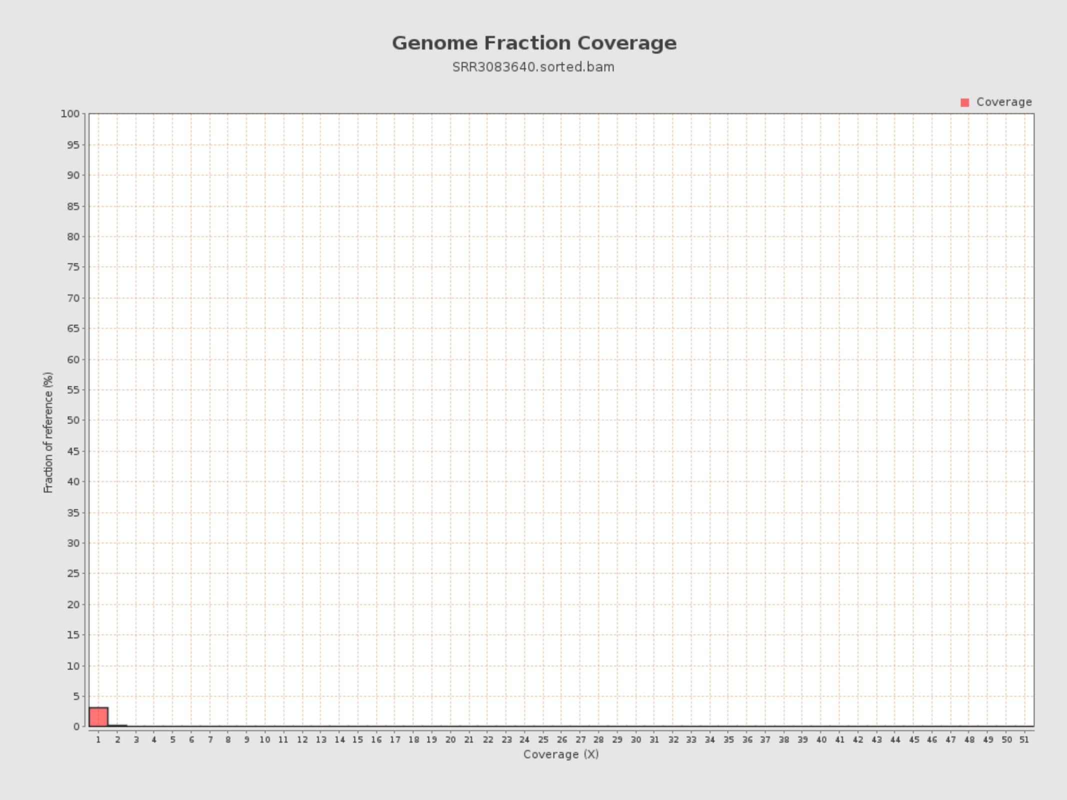
4. Results : Coverage Histogram



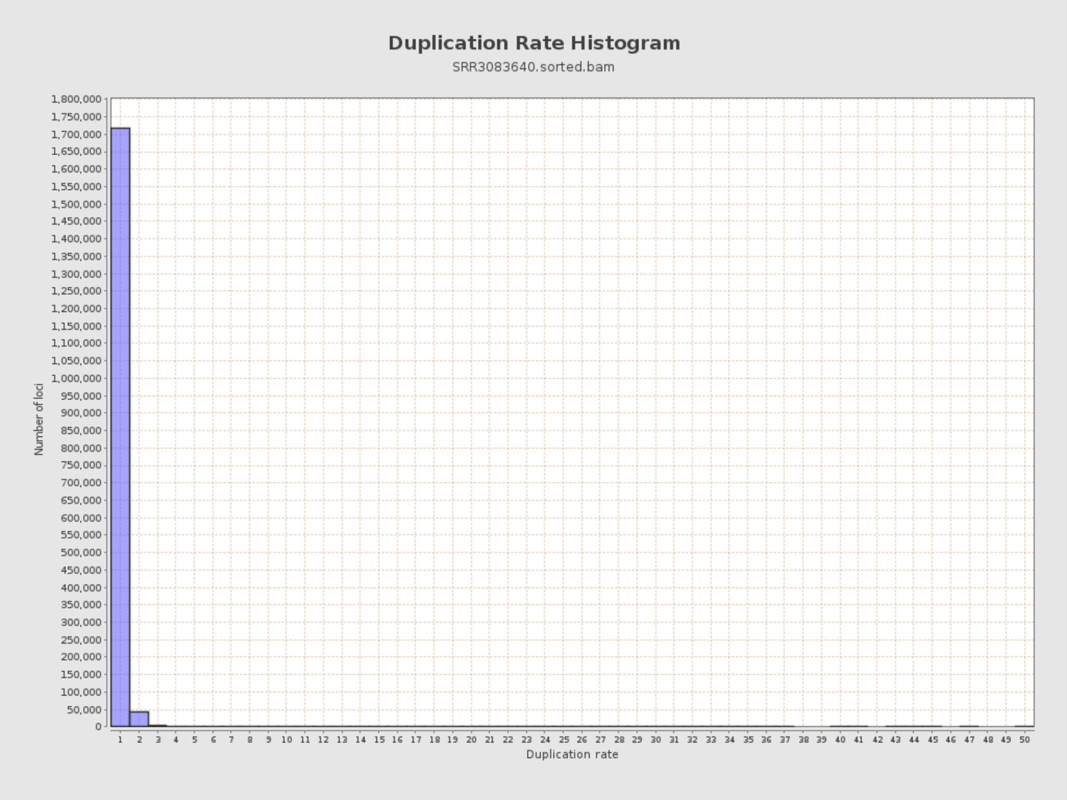
5. Results : Coverage Histogram (0-50X)



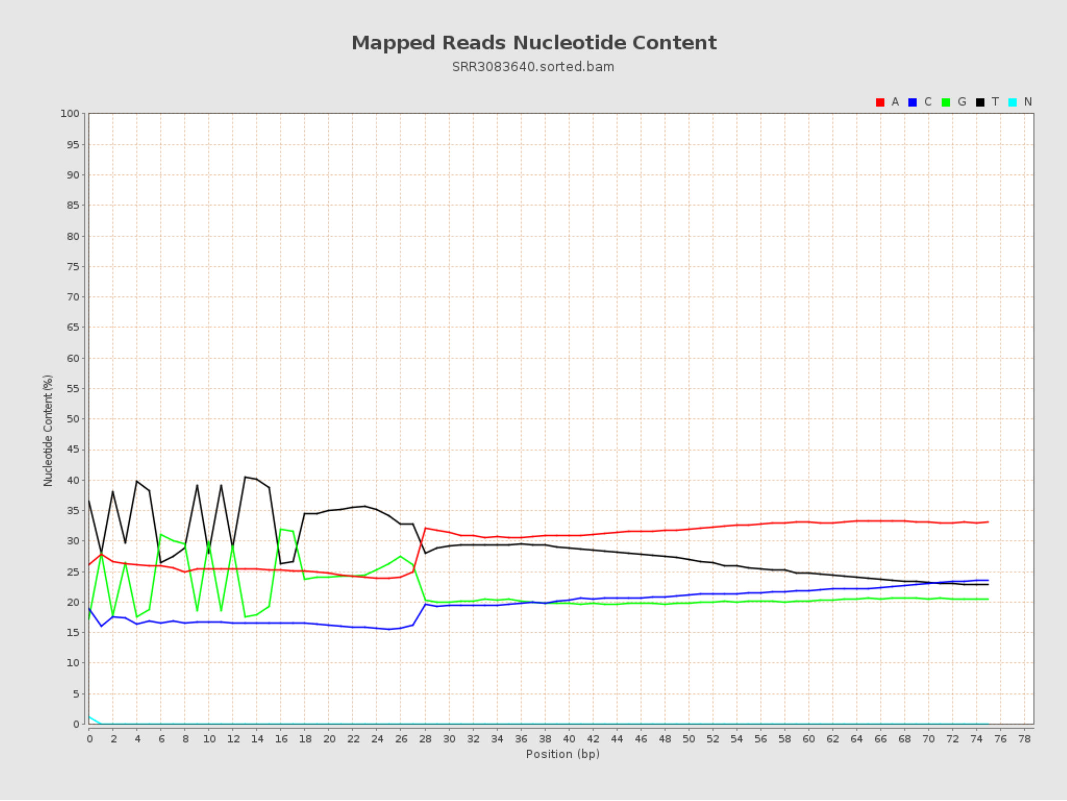
6. Results : Genome Fraction Coverage



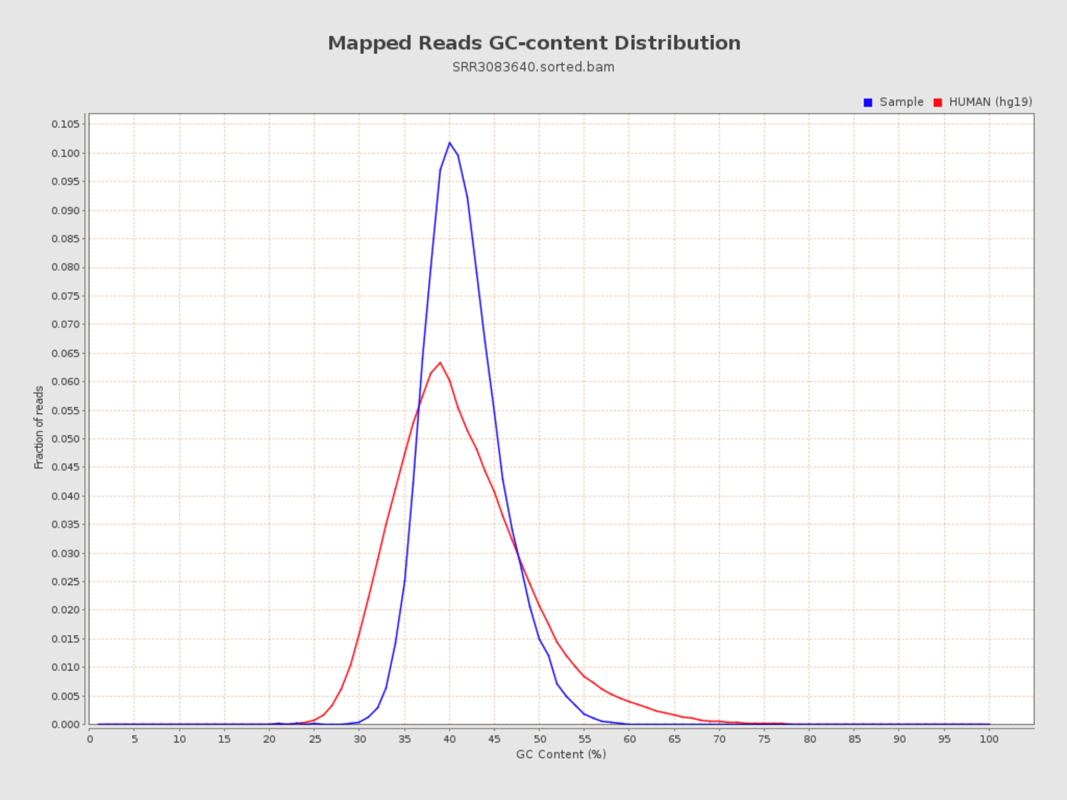
7. Results : Duplication Rate Histogram



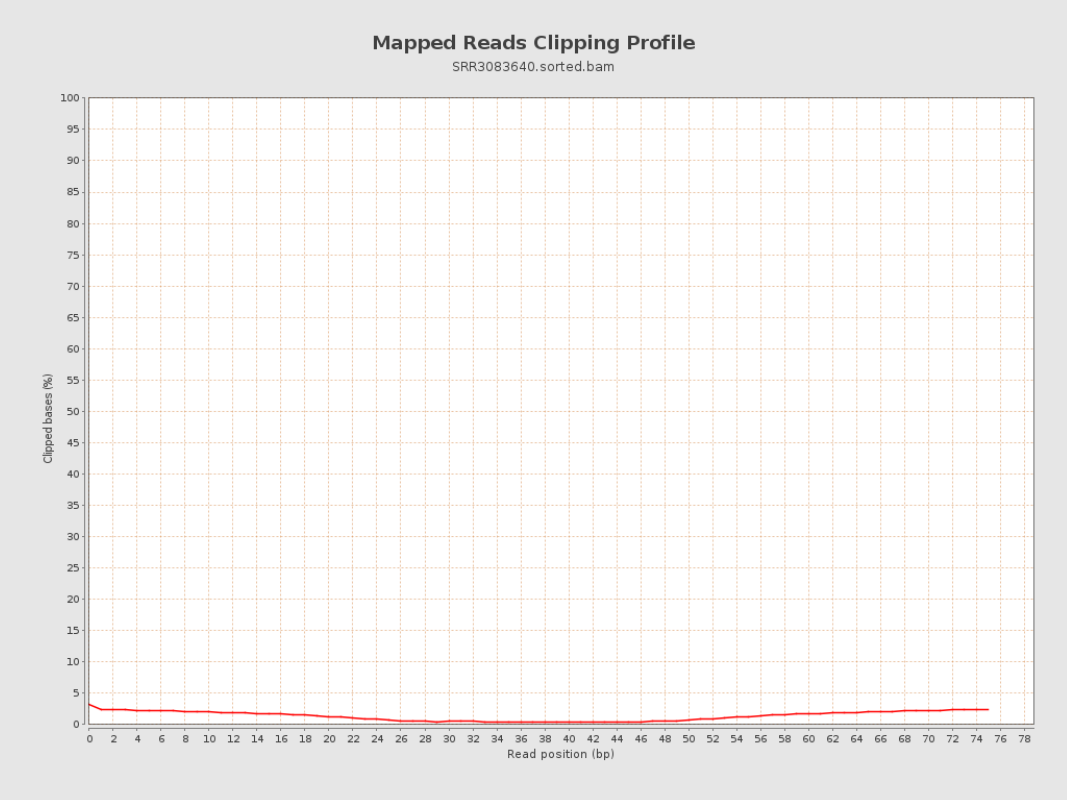
8. Results : Mapped Reads Nucleotide Content



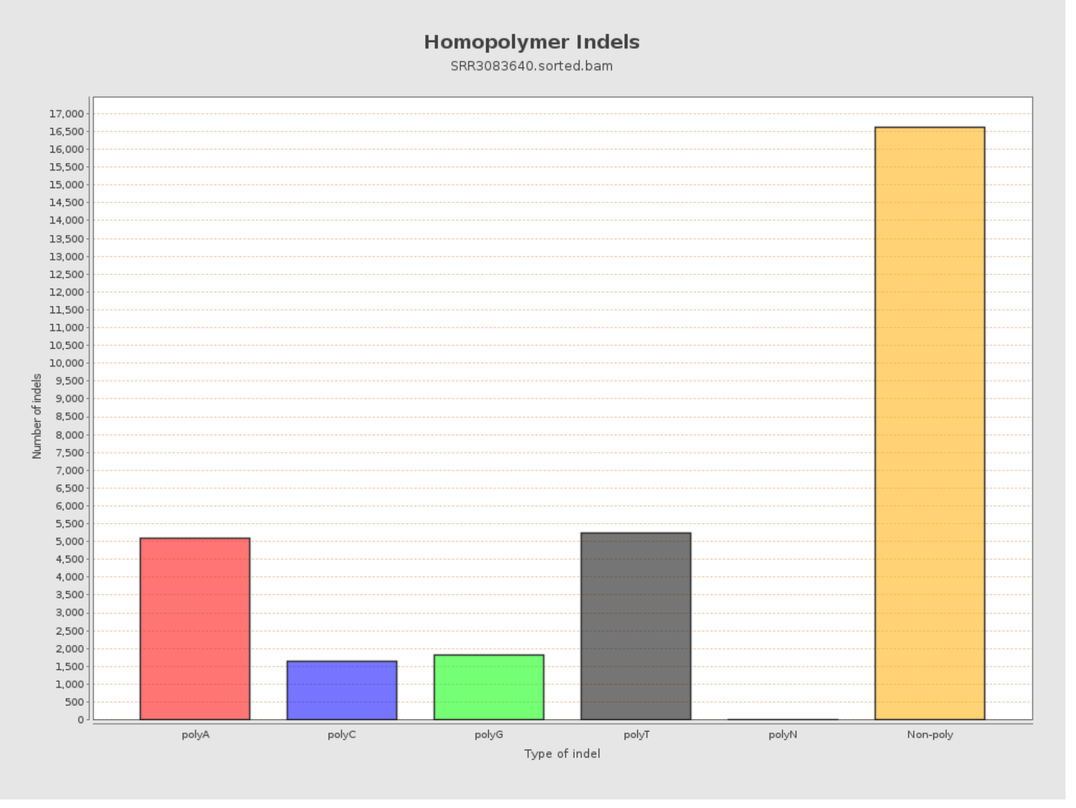
9. Results : Mapped Reads GC-content Distribution



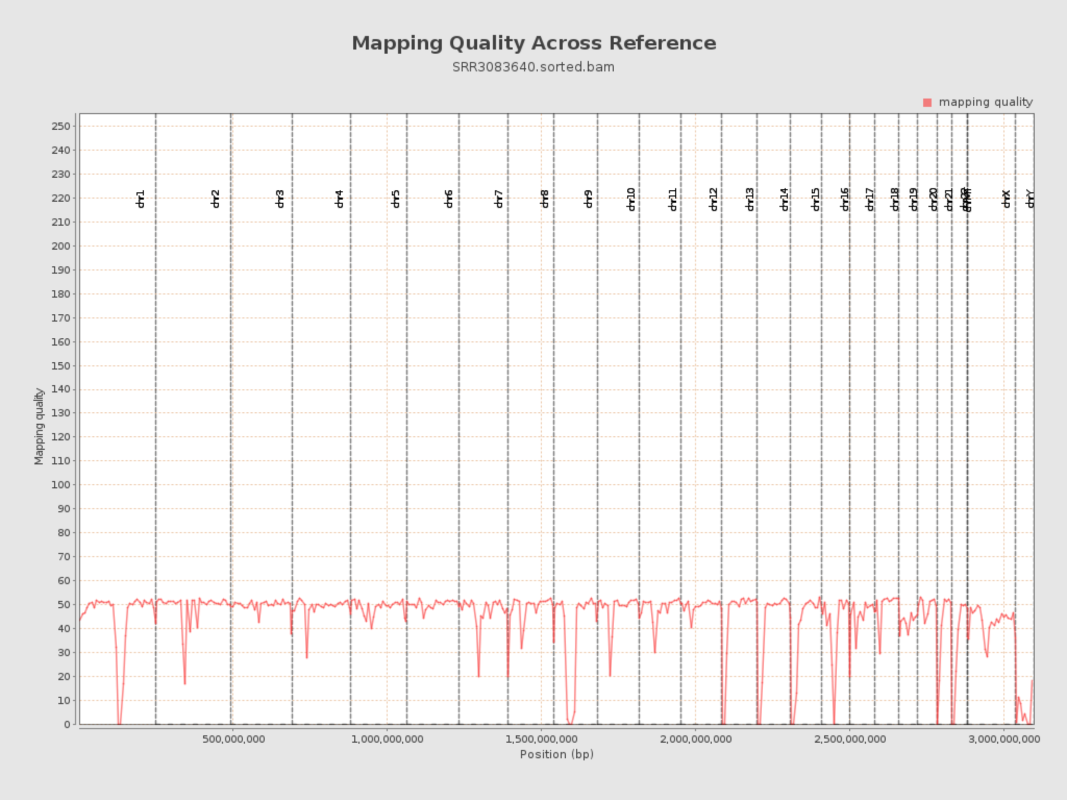
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram