Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:31:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083636.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_SRR3083636 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083636.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:31:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083636.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,969,795
Mapped reads	1,594,462 / 80.95%
Unmapped reads	375,333 / 19.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,246 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	47,625 / 2.42%
Duplication rate	2.57%
Clipped reads	1,027,140 / 52.14%

2.2. ACGT Content

Number/percentage of A's	28,753,816 / 29.43%
Number/percentage of C's	18,510,425 / 18.95%
Number/percentage of T's	29,399,247 / 30.09%
Number/percentage of G's	21,022,220 / 21.52%
Number/percentage of N's	13,830 / 0.01%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0316

Standard Deviation	0.2399

2.4. Mapping Quality

Mean Mapping Quality	46.04

2.5. Mismatches and indels

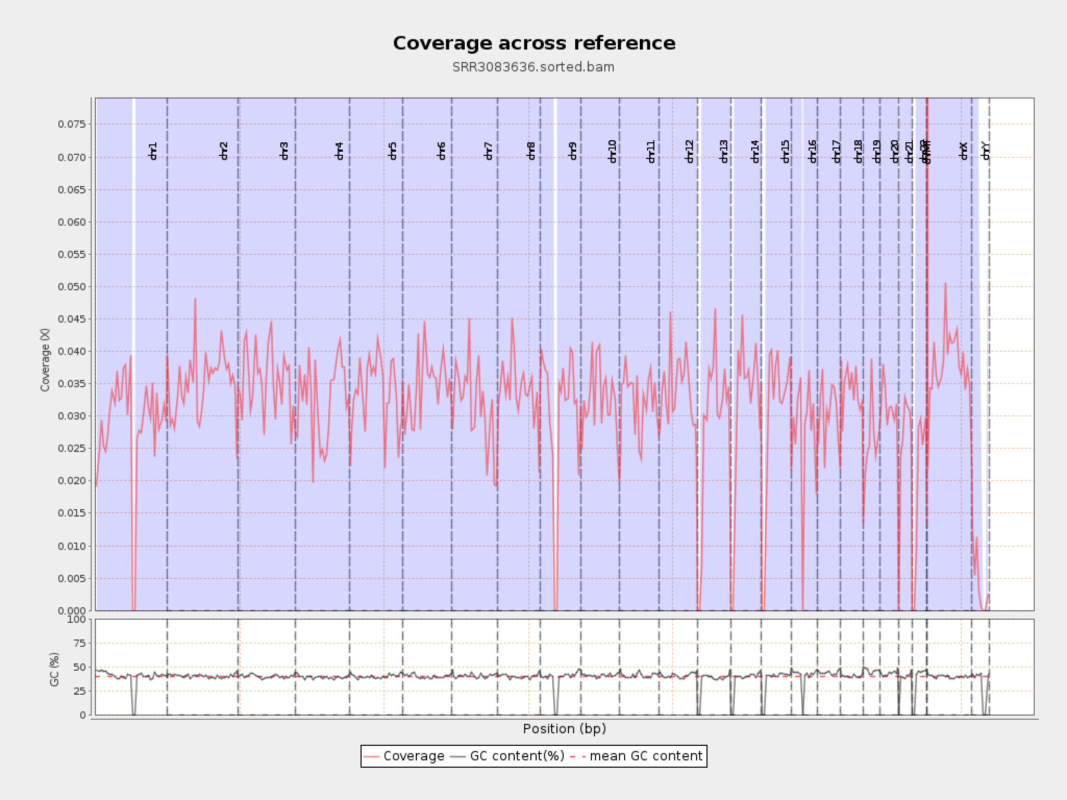
General error rate	0.83%
Mismatches	801,697
Insertions	7,000
Mapped reads with at least one insertion	0.44%
Deletions	19,836
Mapped reads with at least one deletion	1.23%
Homopolymer indels	46.64%

2.6. Chromosome stats

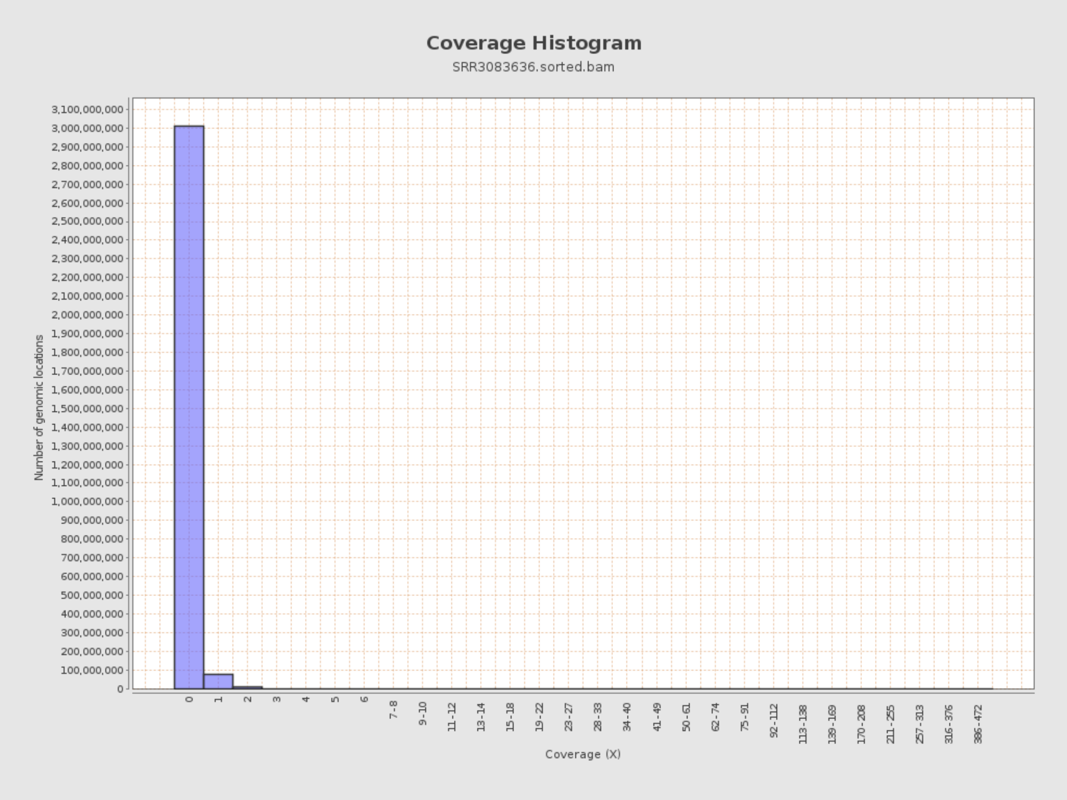
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7127778	0.0286	0.3566
chr2	243199373	8559091	0.0352	0.2567
chr3	198022430	7021908	0.0355	0.205
chr4	191154276	6204870	0.0325	0.2013
chr5	180915260	6133952	0.0339	0.2009
chr6	171115067	5945564	0.0347	0.2135
chr7	159138663	5033440	0.0316	0.2614

chr8	146364022	5008204	0.0342	0.3516
chr9	141213431	4268839	0.0302	0.2241
chr10	135534747	4376318	0.0323	0.2381
chr11	135006516	4411924	0.0327	0.2072
chr12	133851895	4559985	0.0341	0.2023
chr13	115169878	3295623	0.0286	0.1848
chr14	107349540	3284518	0.0306	0.1958
chr15	102531392	3040808	0.0297	0.1881
chr16	90354753	2427853	0.0269	0.1894
chr17	81195210	2456429	0.0303	0.2103
chr18	78077248	2656759	0.034	0.3228
chr19	59128983	1562983	0.0264	0.2654
chr20	63025520	1993130	0.0316	0.1973
chr21	48129895	1258368	0.0261	0.1825
chr22	51304566	974986	0.019	0.1496
chrMT	16571	19138	1.1549	1.2634
chrX	155270560	5870135	0.0378	0.2234
chrY	59373566	238999	0.004	0.085

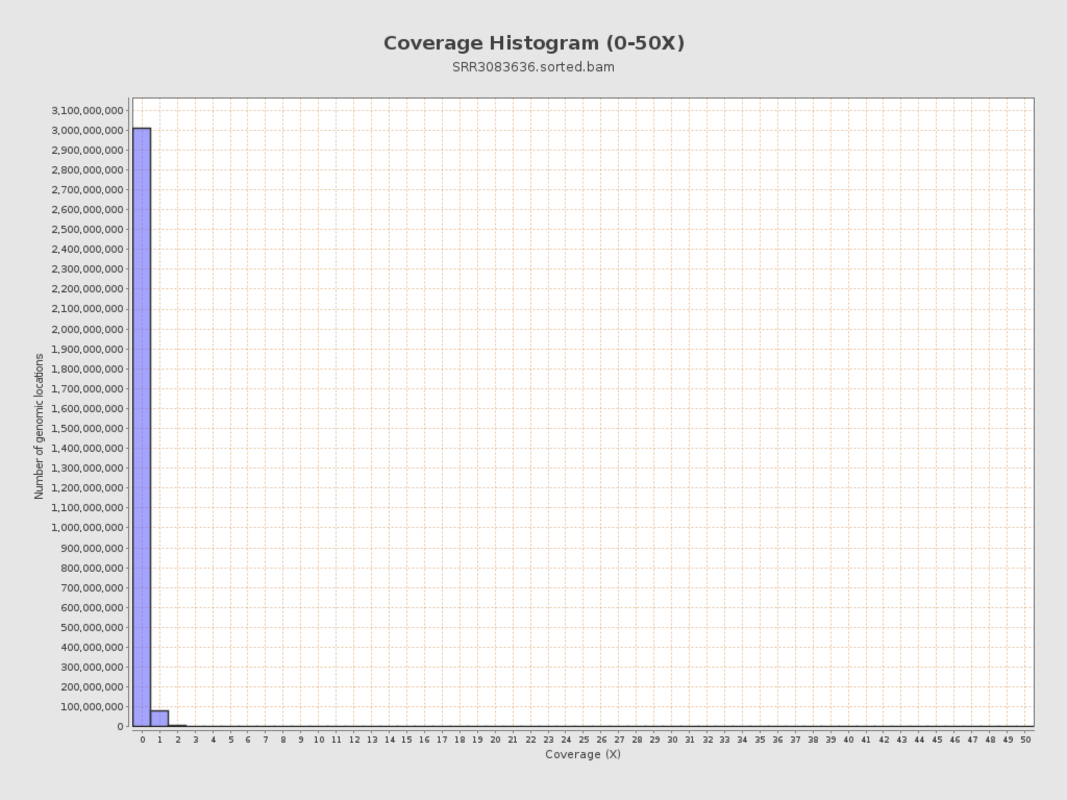
3. Results : Coverage across reference



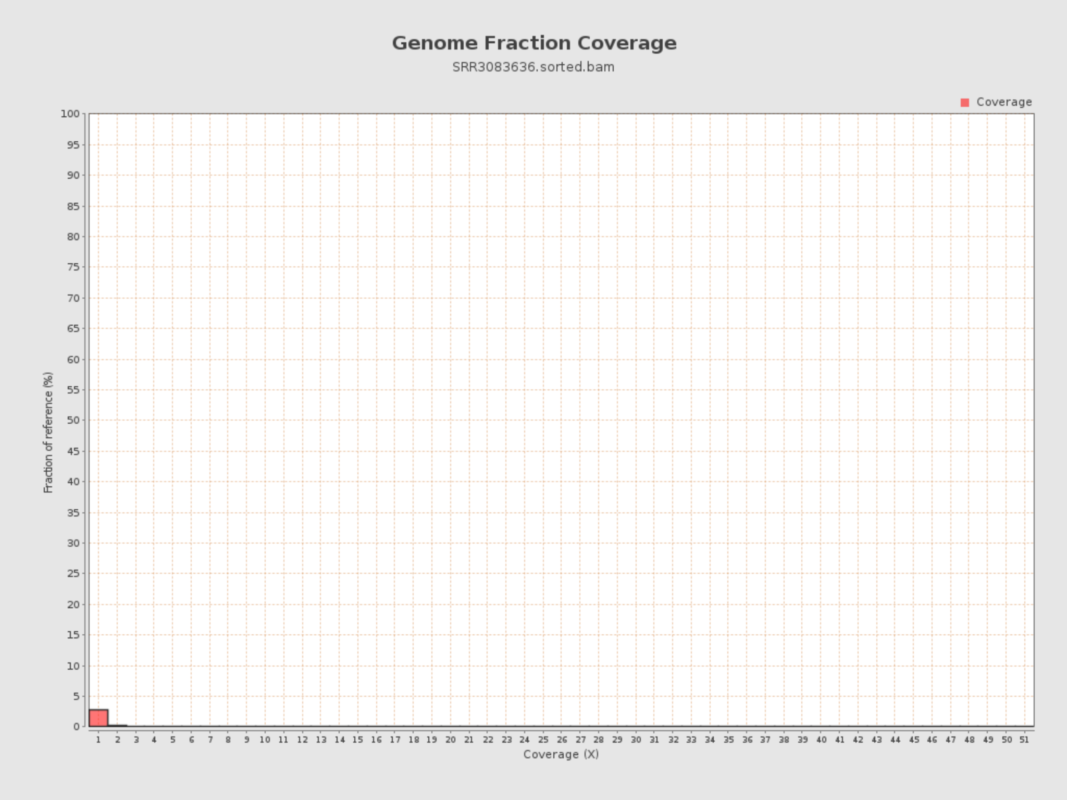
4. Results : Coverage Histogram



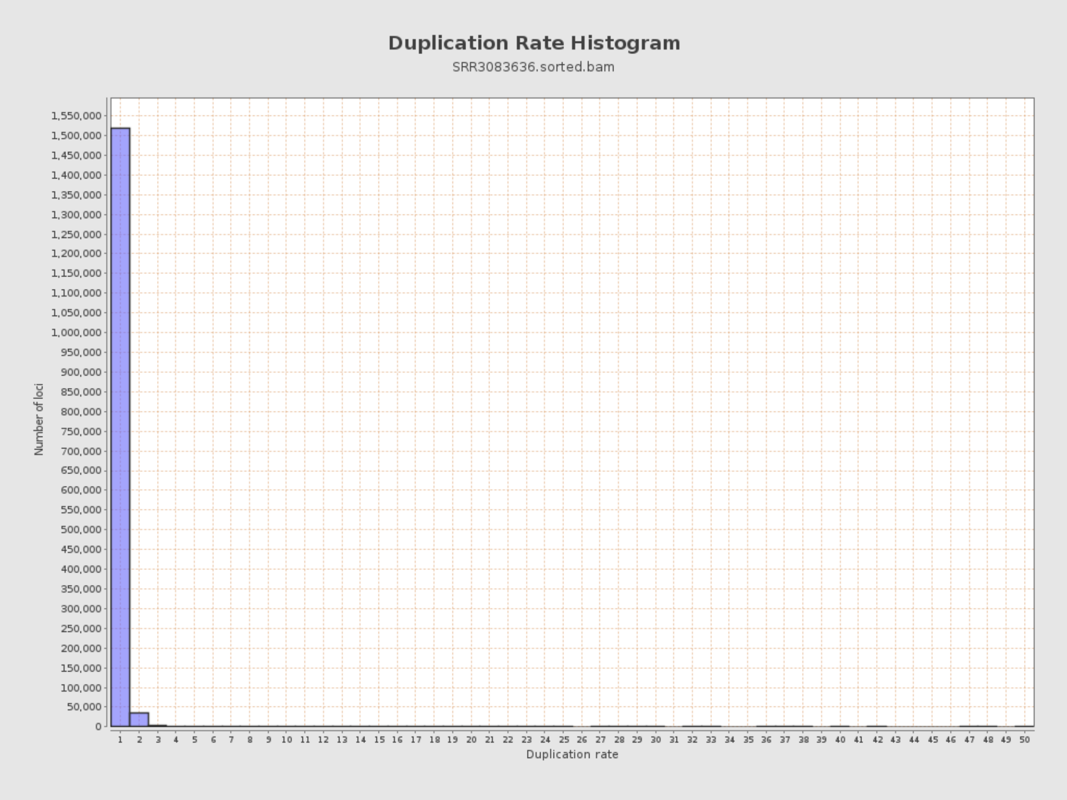
5. Results : Coverage Histogram (0-50X)



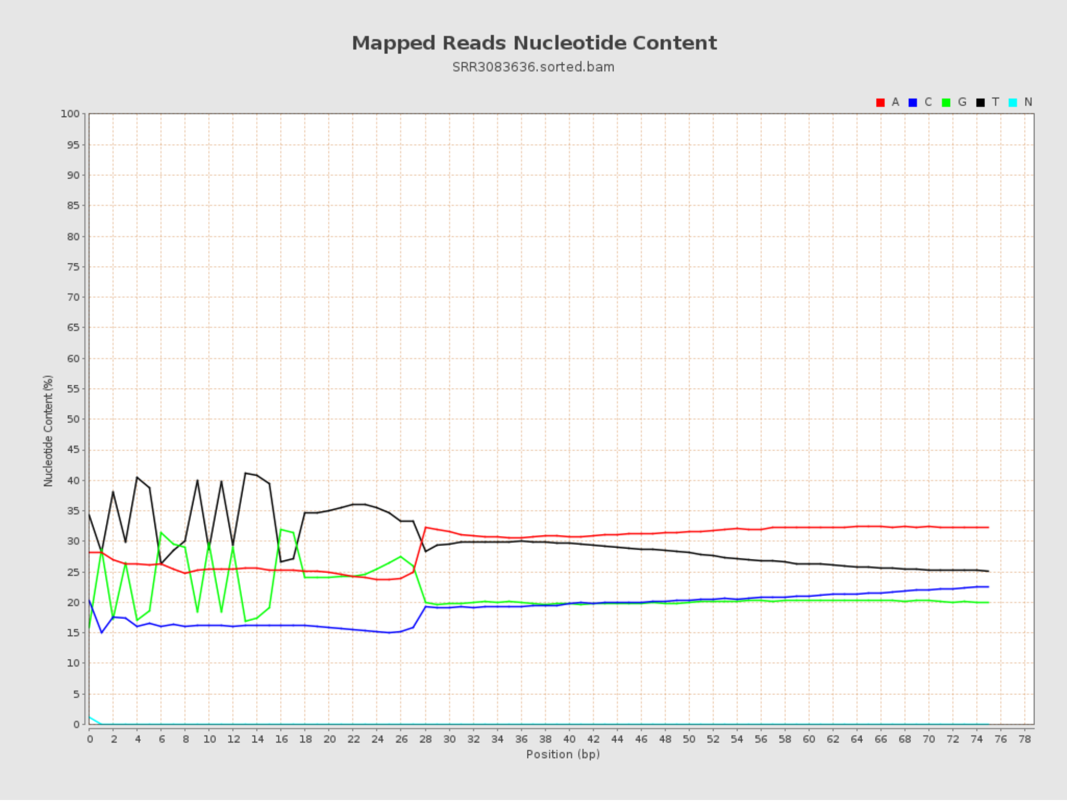
6. Results : Genome Fraction Coverage



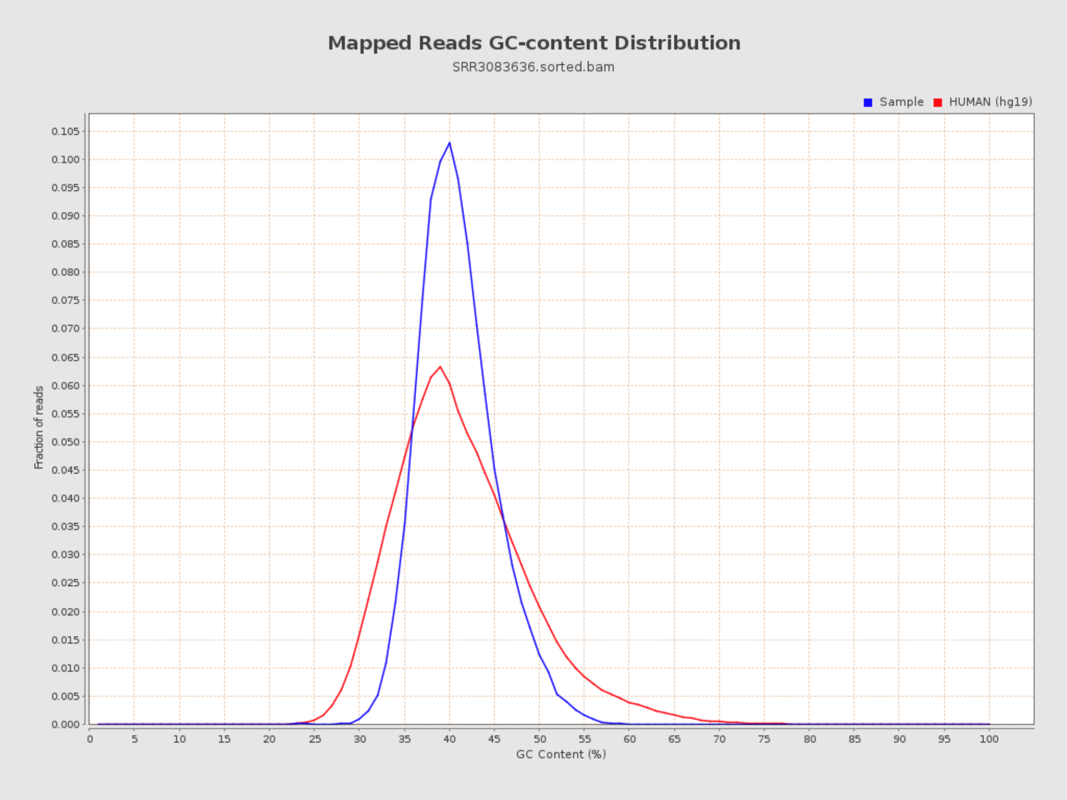
7. Results : Duplication Rate Histogram



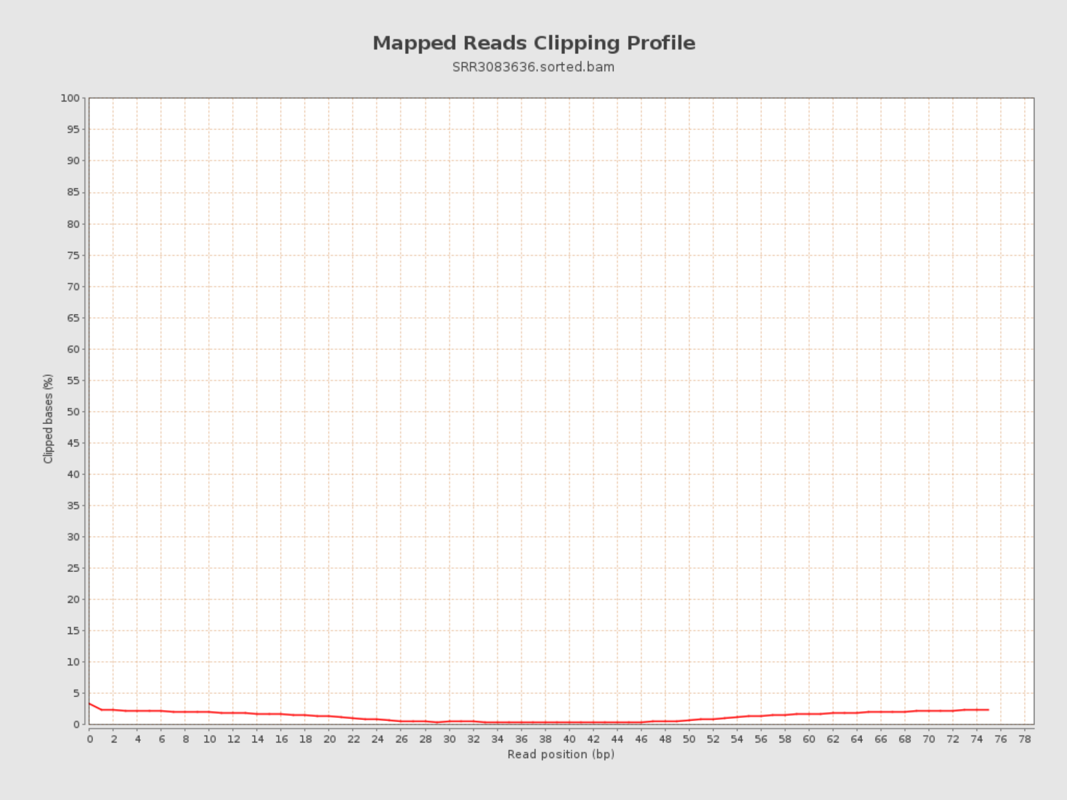
8. Results : Mapped Reads Nucleotide Content



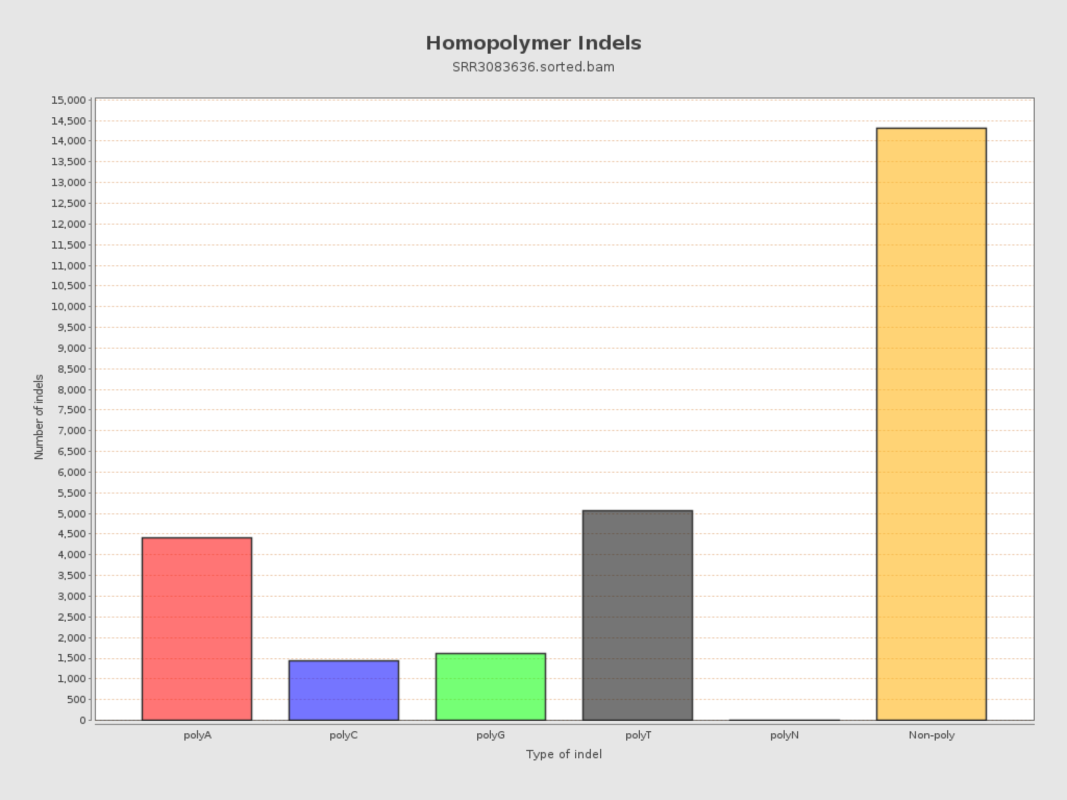
9. Results : Mapped Reads GC-content Distribution



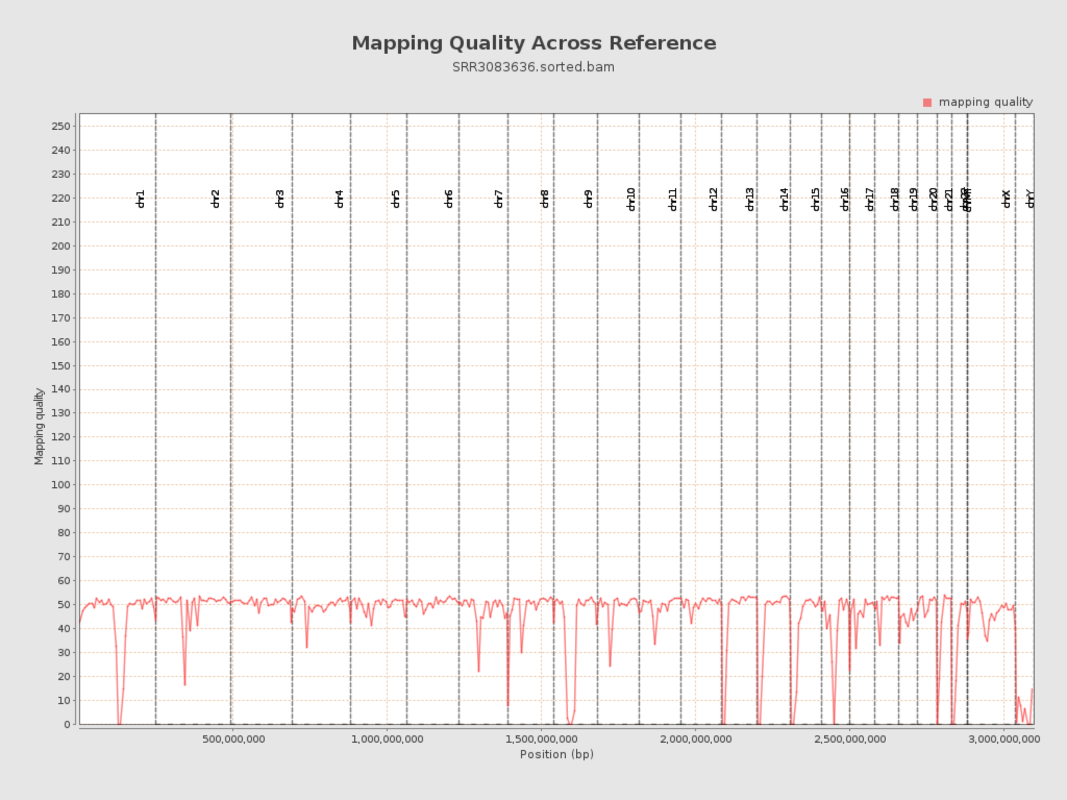
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram