Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:00:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083646.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_SRR3083646 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083646.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:00:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083646.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,618,404
Mapped reads	1,240,782 / 76.67%
Unmapped reads	377,622 / 23.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,242 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	28,781 / 1.78%
Duplication rate	1.96%
Clipped reads	802,843 / 49.61%

2.2. ACGT Content

Number/percentage of A's	21,943,233 / 29.2%
Number/percentage of C's	14,336,715 / 19.08%
Number/percentage of T's	21,674,498 / 28.85%
Number/percentage of G's	17,170,312 / 22.85%
Number/percentage of N's	10,458 / 0.01%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2126

2.4. Mapping Quality

Mean Mapping Quality	44.37

2.5. Mismatches and indels

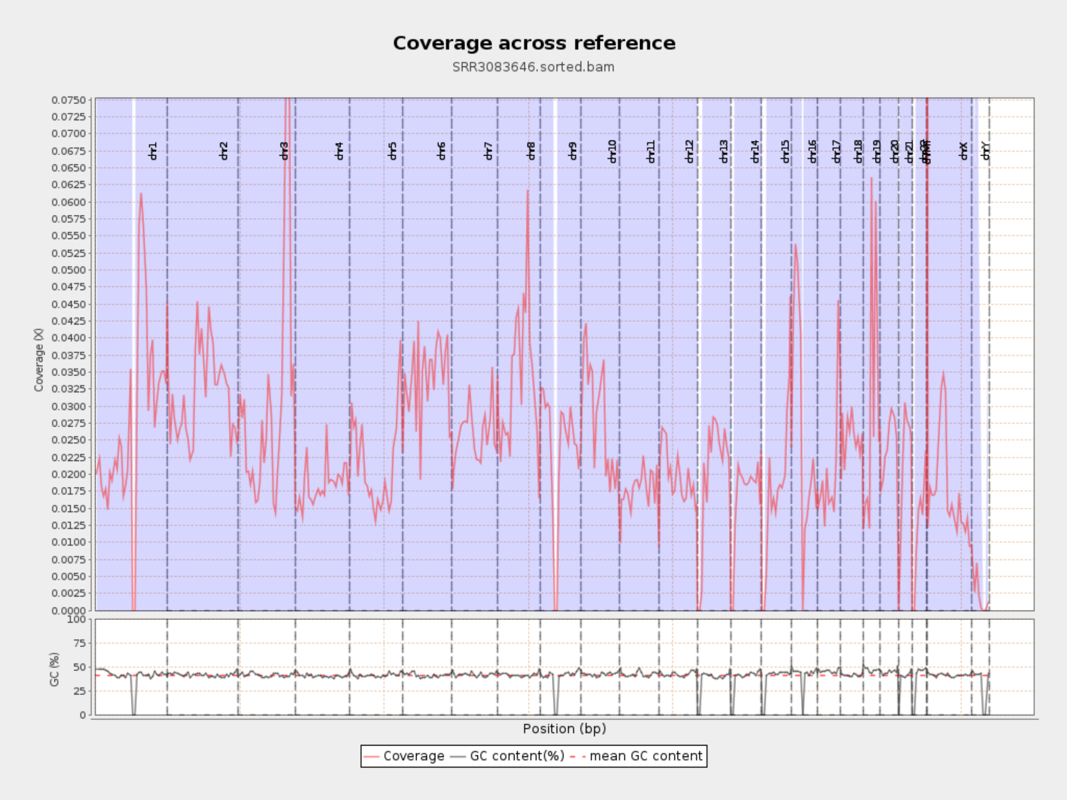
General error rate	0.85%
Mismatches	632,841
Insertions	4,957
Mapped reads with at least one insertion	0.4%
Deletions	14,875
Mapped reads with at least one deletion	1.19%
Homopolymer indels	45.51%

2.6. Chromosome stats

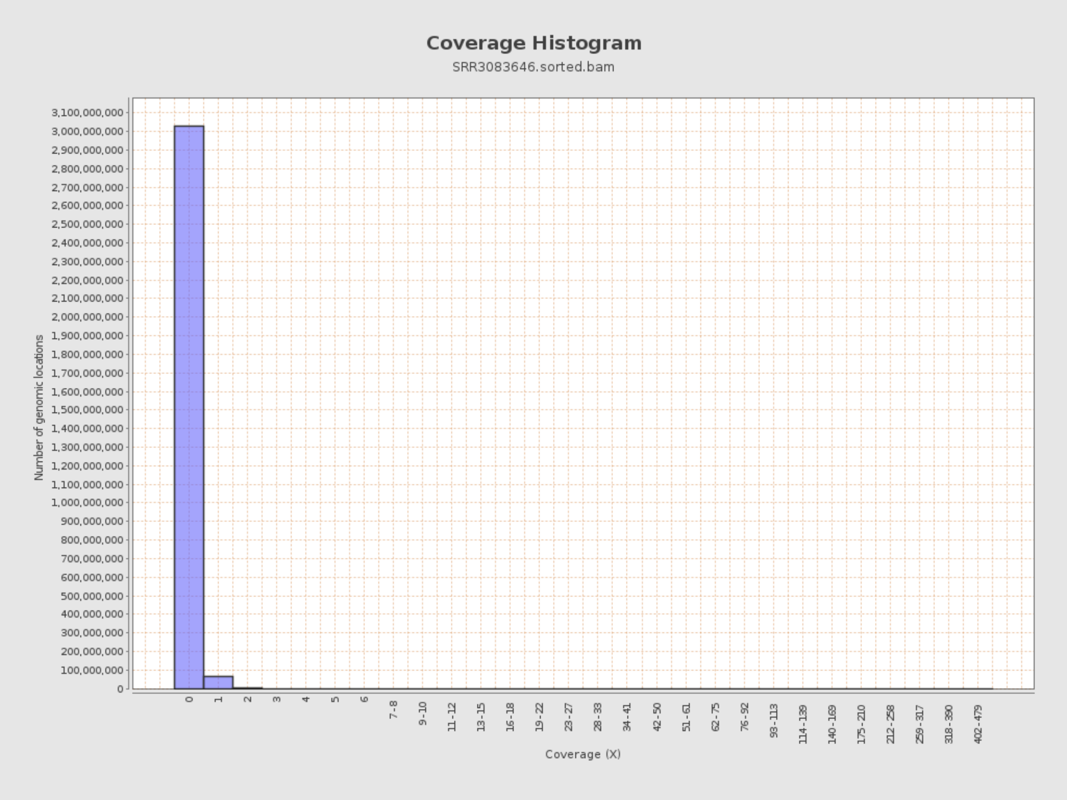
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6931682	0.0278	0.4131
chr2	243199373	7794685	0.0321	0.2124
chr3	198022430	6018309	0.0304	0.1868
chr4	191154276	3521298	0.0184	0.1446
chr5	180915260	3910872	0.0216	0.1565
chr6	171115067	5827509	0.0341	0.224
chr7	159138663	4127290	0.0259	0.2254

chr8	146364022	5011916	0.0342	0.246
chr9	141213431	3349560	0.0237	0.178
chr10	135534747	3853928	0.0284	0.221
chr11	135006516	2432412	0.018	0.158
chr12	133851895	2670163	0.0199	0.1503
chr13	115169878	2311685	0.0201	0.1496
chr14	107349540	1758854	0.0164	0.136
chr15	102531392	1773435	0.0173	0.1394
chr16	90354753	2345407	0.026	0.1752
chr17	81195210	1679711	0.0207	0.1543
chr18	78077248	1998417	0.0256	0.2343
chr19	59128983	1780351	0.0301	0.2947
chr20	63025520	1513700	0.024	0.1654
chr21	48129895	1036771	0.0215	0.1578
chr22	51304566	628369	0.0122	0.1169
chrMT	16571	8087	0.488	0.8533
chrX	155270560	2731079	0.0176	0.1469
chrY	59373566	143109	0.0024	0.058

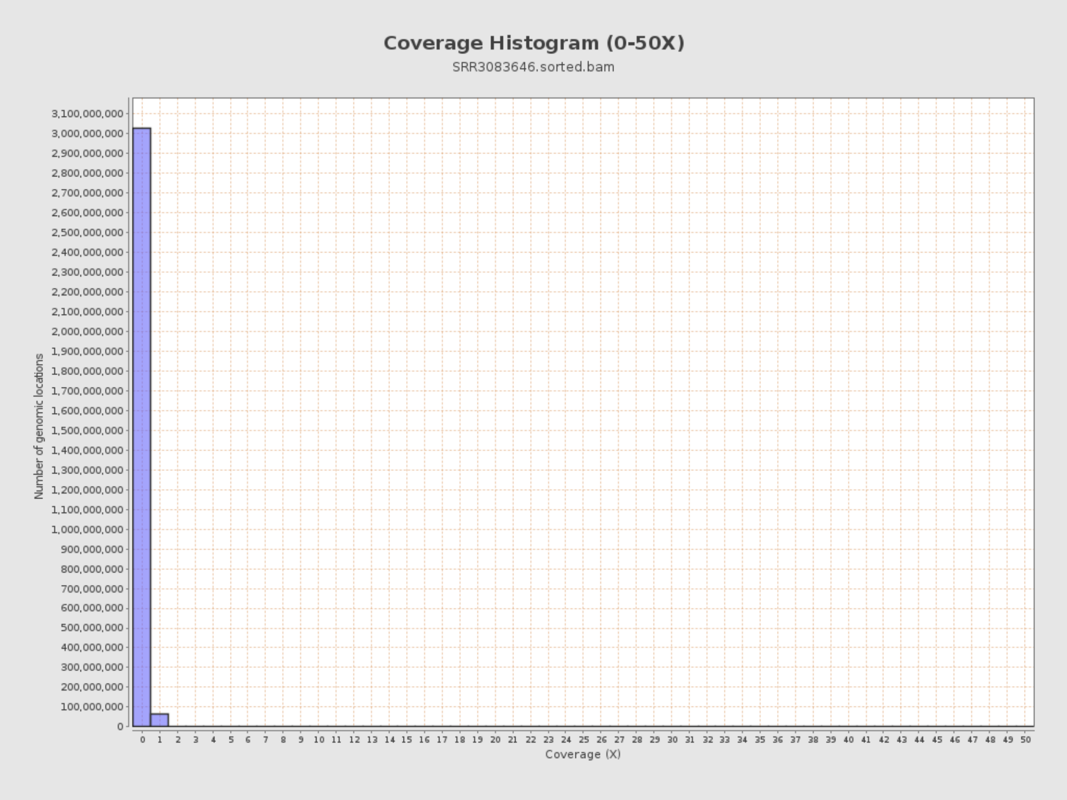
3. Results : Coverage across reference



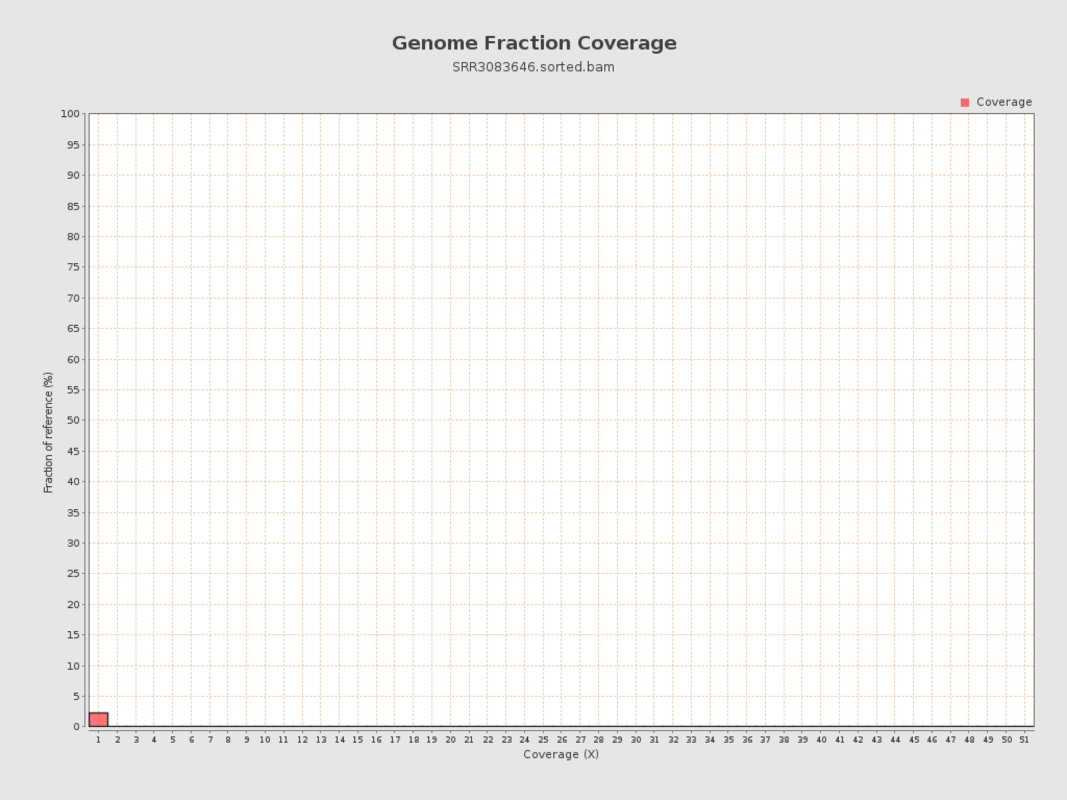
4. Results : Coverage Histogram



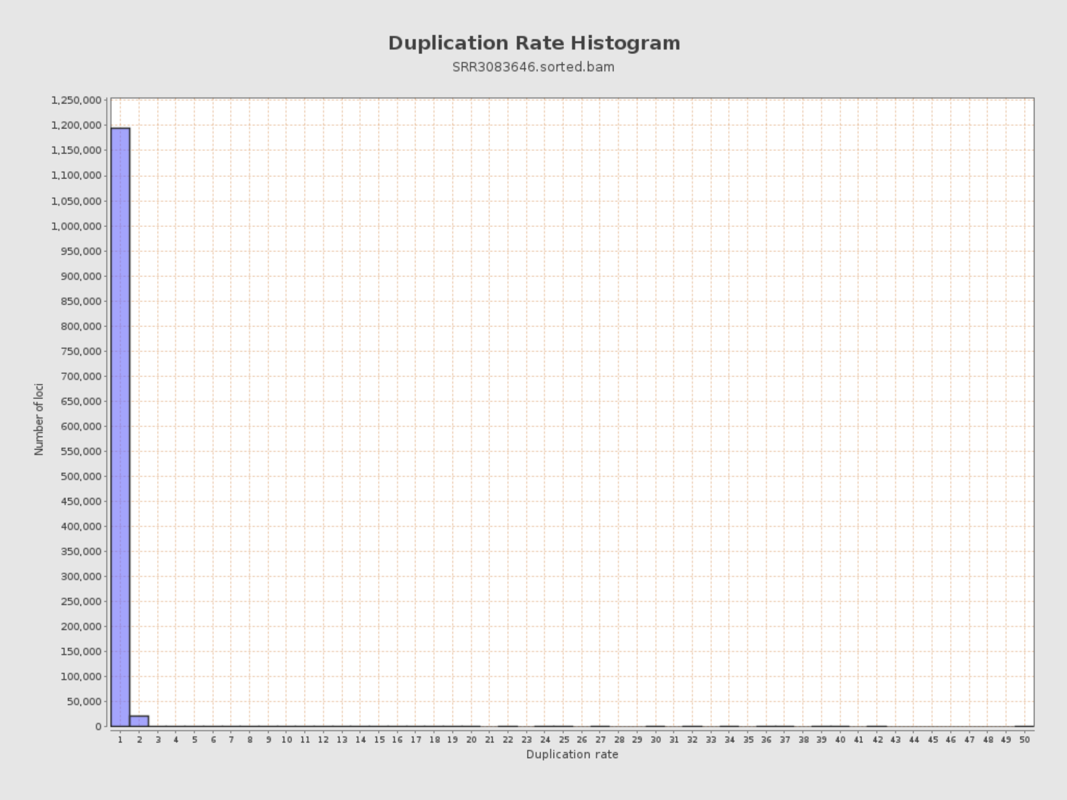
5. Results : Coverage Histogram (0-50X)



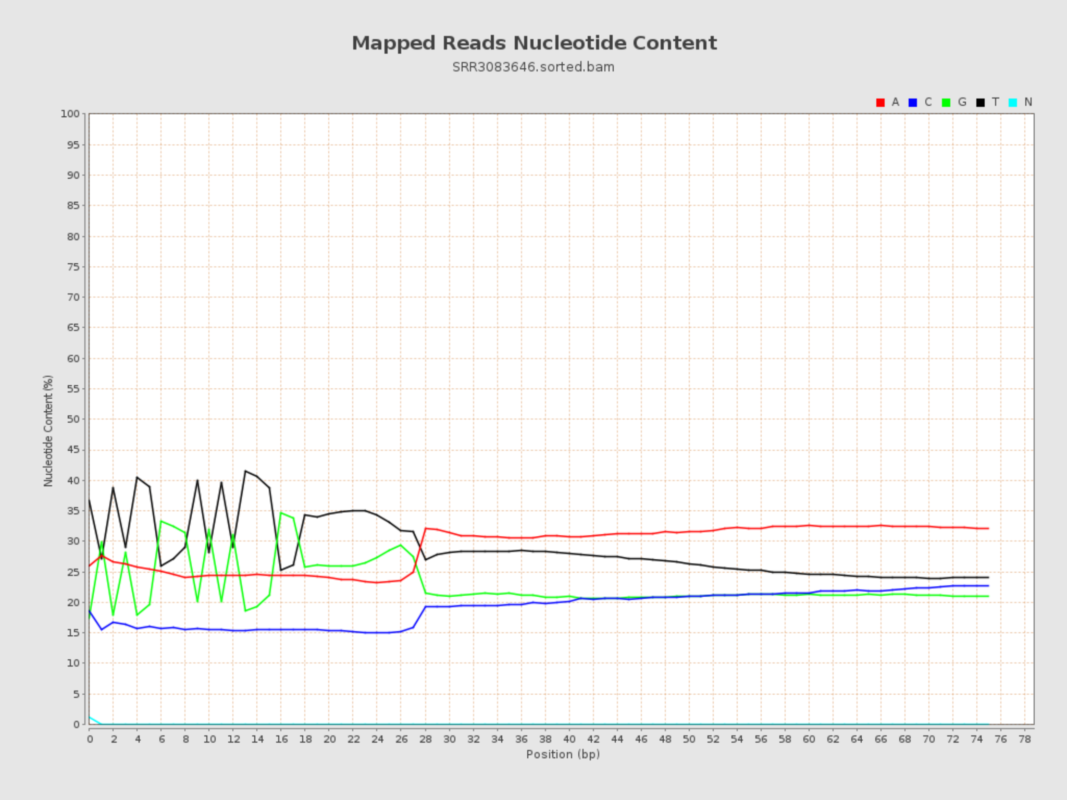
6. Results : Genome Fraction Coverage



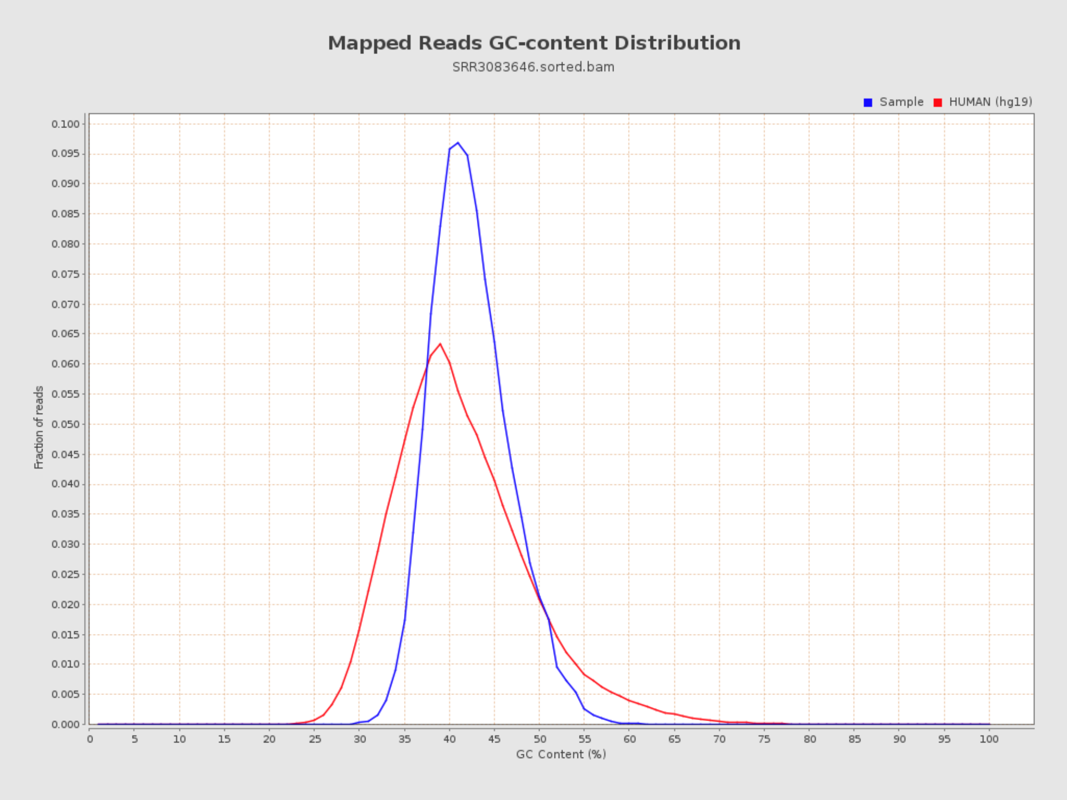
7. Results : Duplication Rate Histogram



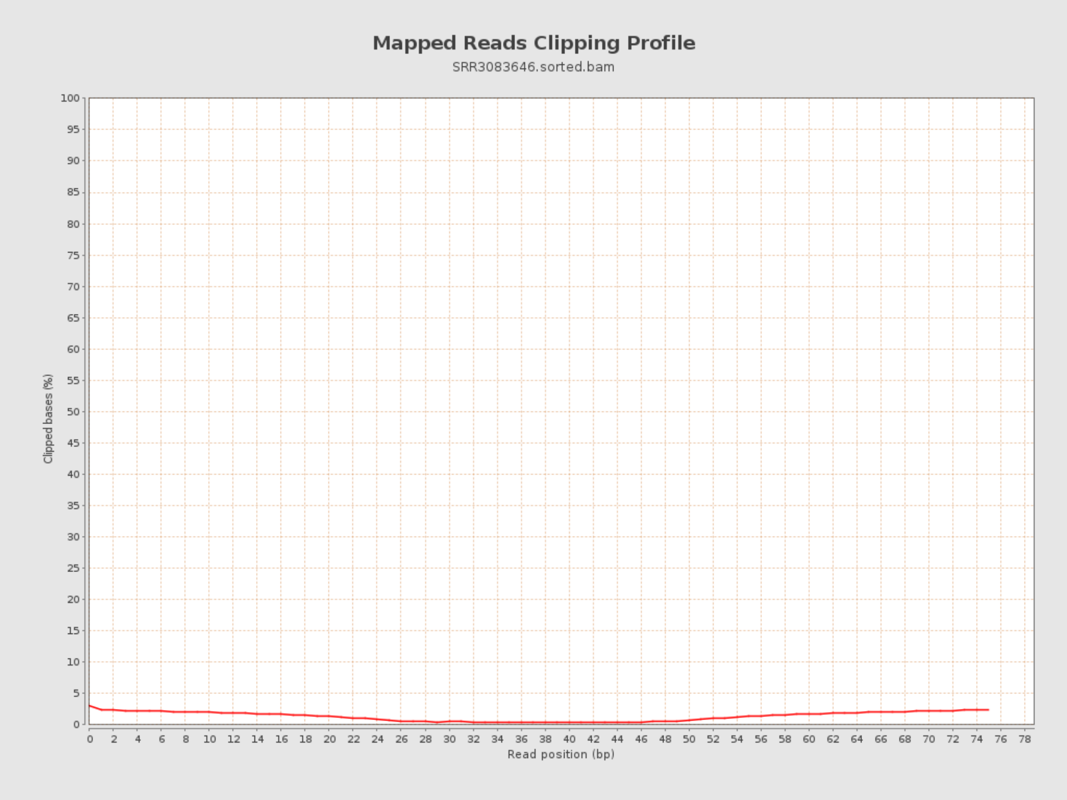
8. Results : Mapped Reads Nucleotide Content



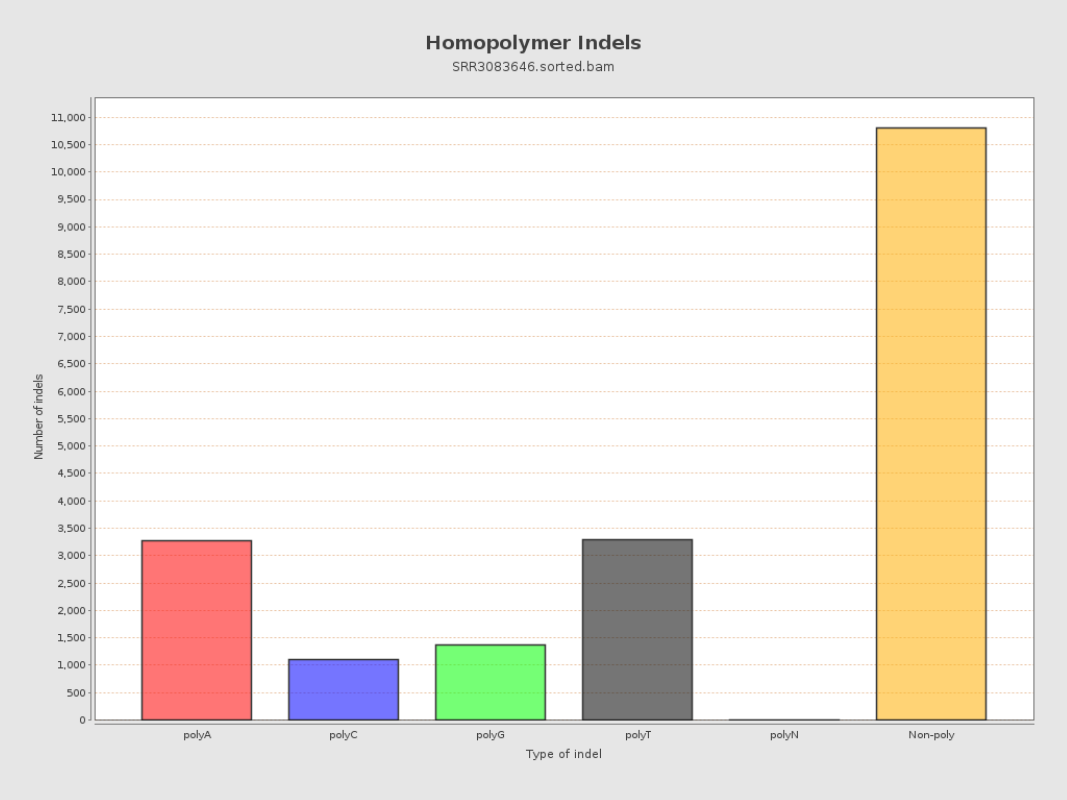
9. Results : Mapped Reads GC-content Distribution



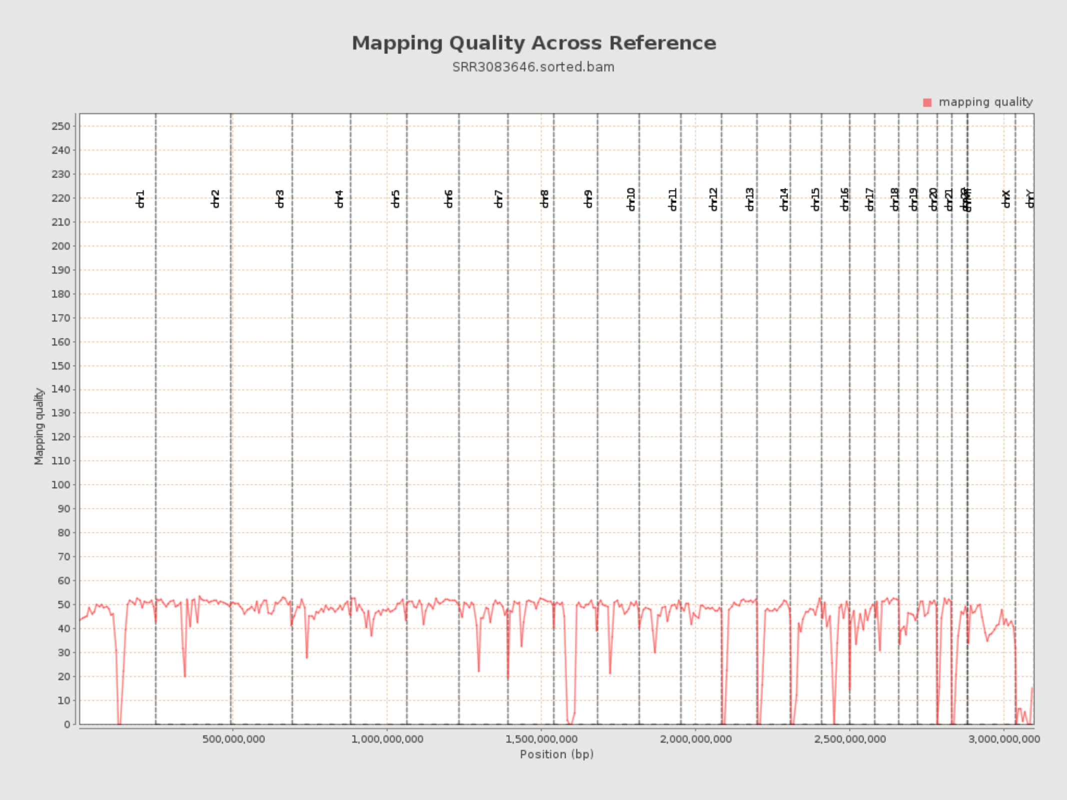
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram