Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:08:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080636.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_SRR3080636 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080636.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:08:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080636.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,190,165
Mapped reads	5,033,647 / 81.32%
Unmapped reads	1,156,518 / 18.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	60,701 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	457,439 / 7.39%
Duplication rate	7.52%
Clipped reads	2,308,870 / 37.3%

2.2. ACGT Content

Number/percentage of A's	95,167,251 / 28.23%
Number/percentage of C's	60,710,913 / 18.01%
Number/percentage of T's	109,190,858 / 32.39%
Number/percentage of G's	71,738,068 / 21.28%
Number/percentage of N's	283,100 / 0.08%
GC Percentage	39.29%

2.3. Coverage

Mean	0.1089

Standard Deviation	0.6238

2.4. Mapping Quality

Mean Mapping Quality	47.09

2.5. Mismatches and indels

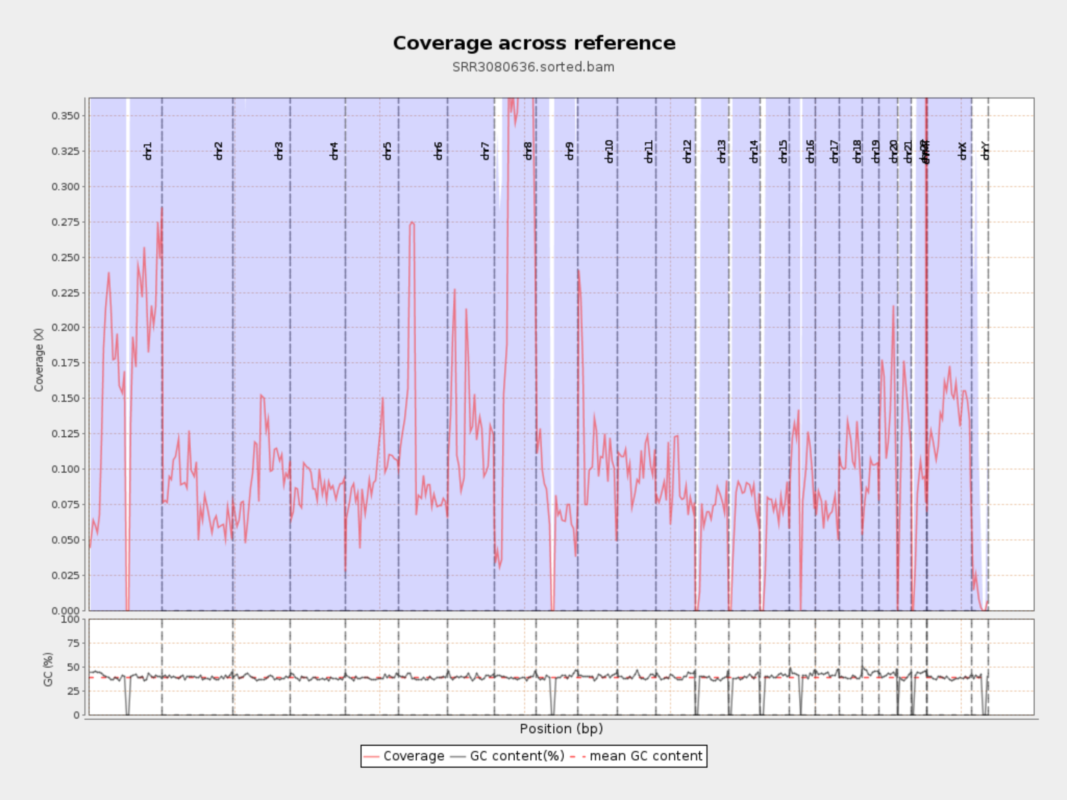
General error rate	0.93%
Mismatches	3,074,449
Insertions	27,331
Mapped reads with at least one insertion	0.54%
Deletions	81,462
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.66%

2.6. Chromosome stats

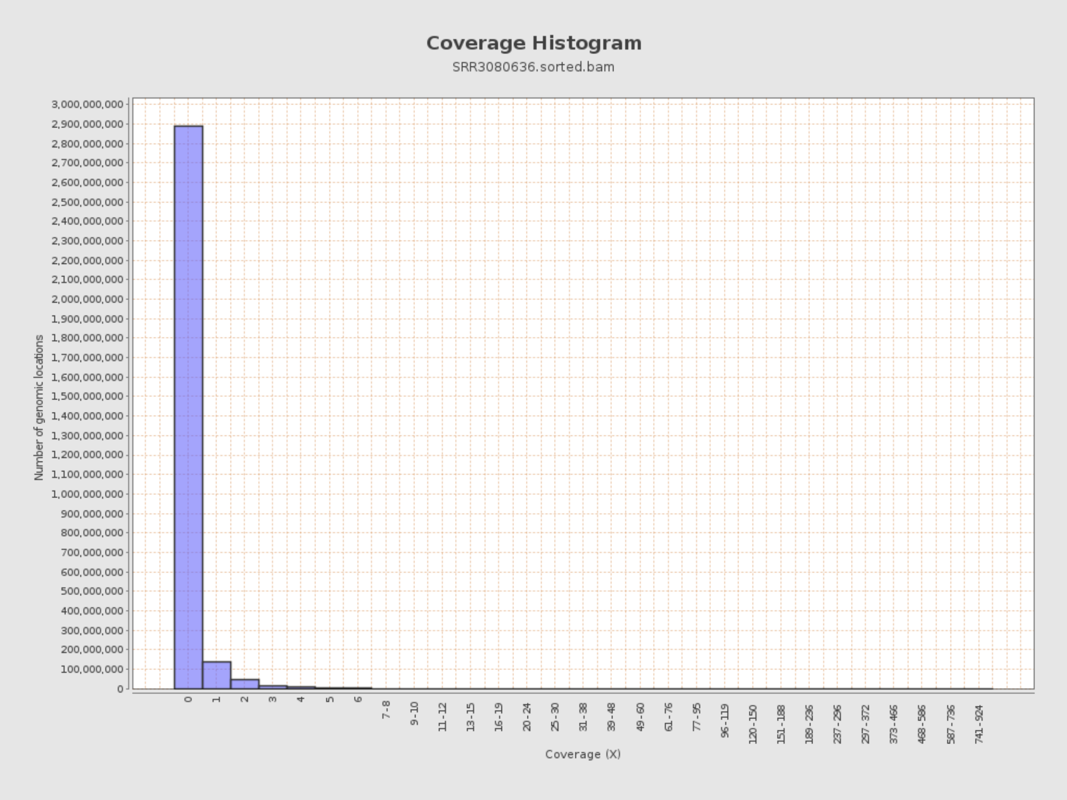
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	41666183	0.1672	0.7879
chr2	243199373	19435869	0.0799	0.6049
chr3	198022430	19360679	0.0978	0.4565
chr4	191154276	16575435	0.0867	0.4382
chr5	180915260	16861367	0.0932	0.445
chr6	171115067	19894137	0.1163	0.6405
chr7	159138663	21316232	0.1339	1.1421

chr8	146364022	40804962	0.2788	1.0336
chr9	141213431	9738453	0.069	0.4893
chr10	135534747	16319865	0.1204	0.6039
chr11	135006516	13730612	0.1017	0.5244
chr12	133851895	11483286	0.0858	0.4327
chr13	115169878	7113652	0.0618	0.3632
chr14	107349540	7460576	0.0695	0.4093
chr15	102531392	6305657	0.0615	0.3678
chr16	90354753	9081831	0.1005	0.4813
chr17	81195210	5666360	0.0698	0.3965
chr18	78077248	8616392	0.1104	0.7986
chr19	59128983	5440497	0.092	0.6024
chr20	63025520	9103560	0.1444	0.5738
chr21	48129895	5629483	0.117	0.5141
chr22	51304566	3316725	0.0646	0.3693
chrMT	16571	275941	16.652	26.3447
chrX	155270560	21407415	0.1379	0.5677
chrY	59373566	617337	0.0104	0.1648

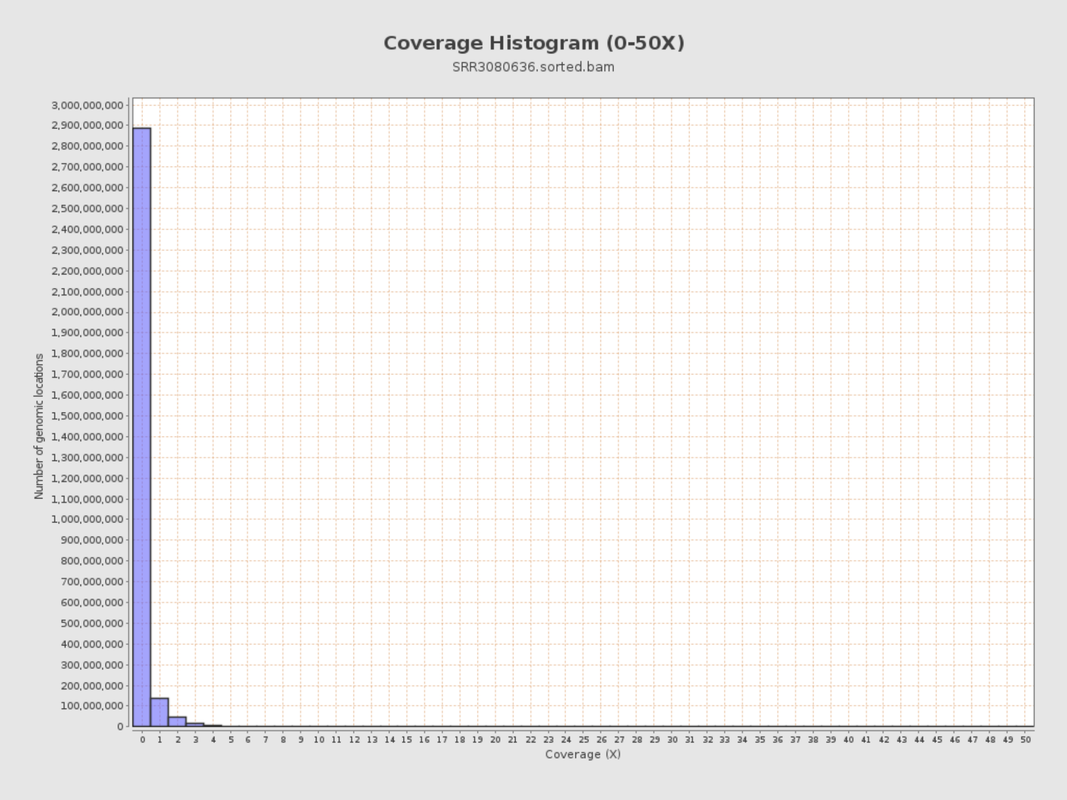
3. Results : Coverage across reference



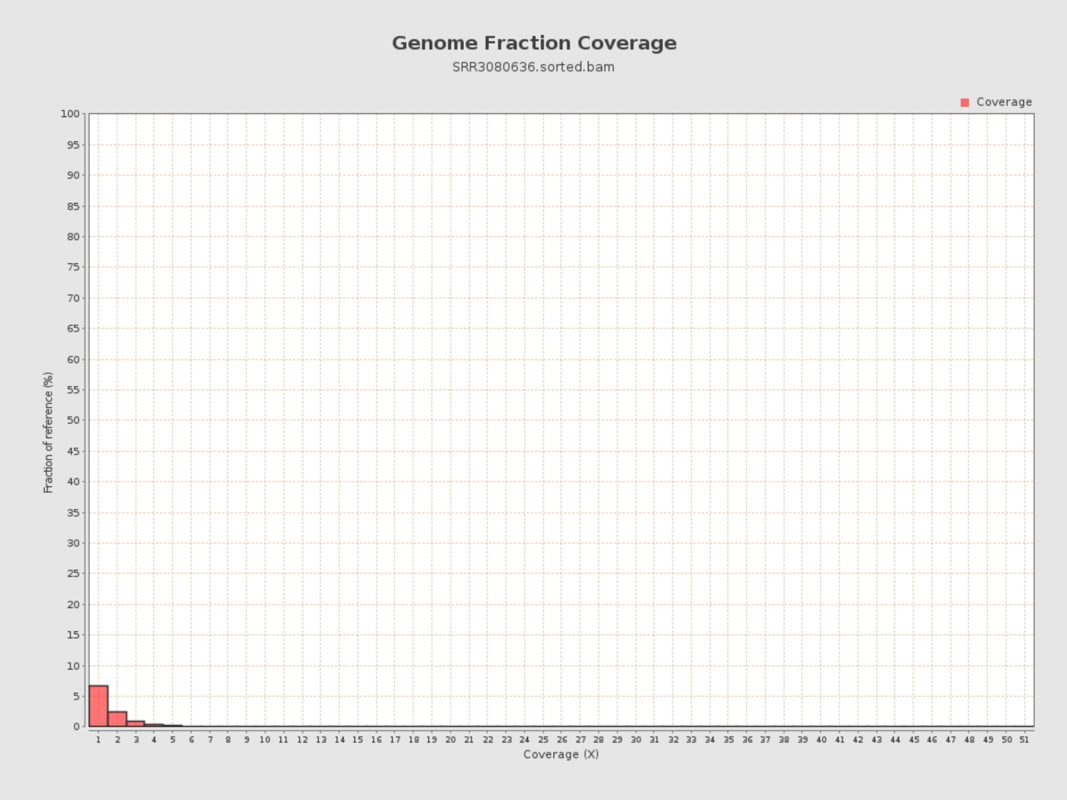
4. Results : Coverage Histogram



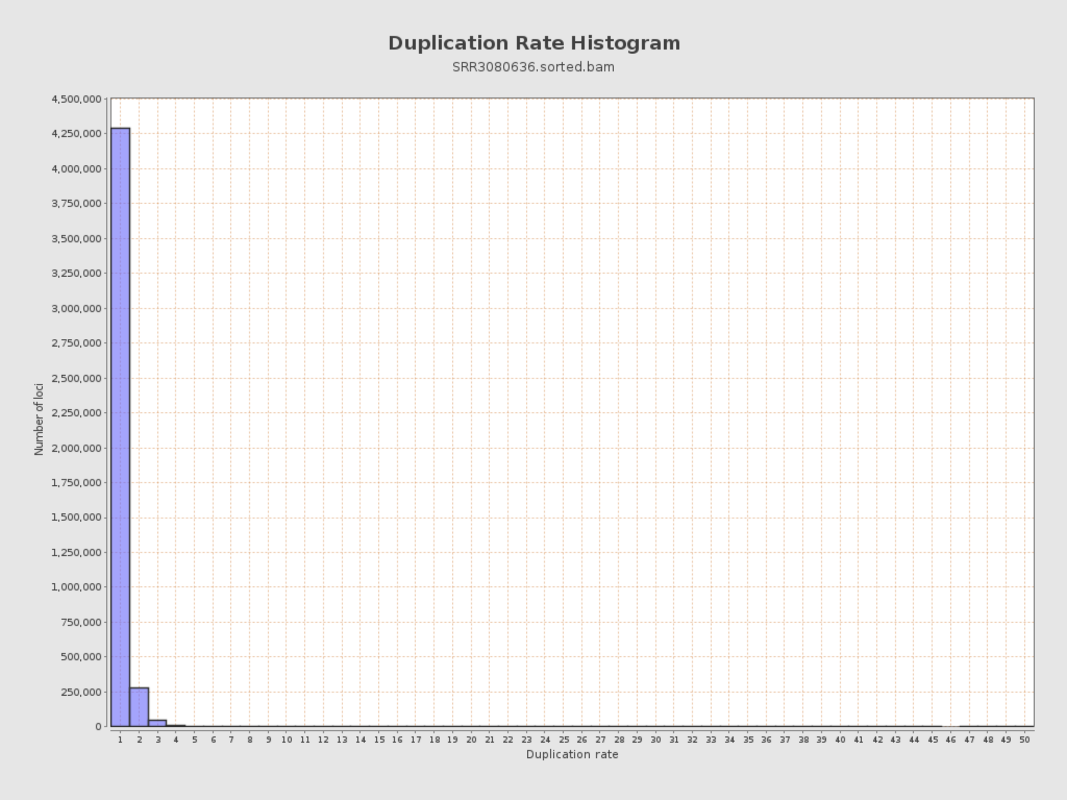
5. Results : Coverage Histogram (0-50X)



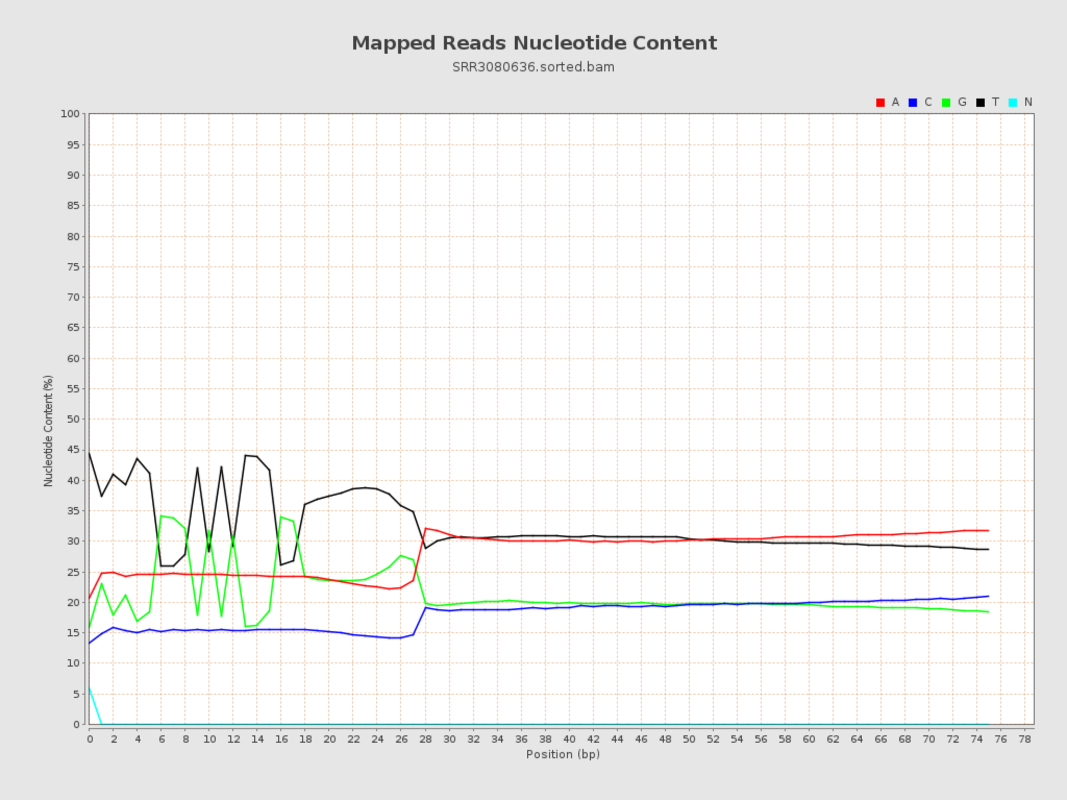
6. Results : Genome Fraction Coverage



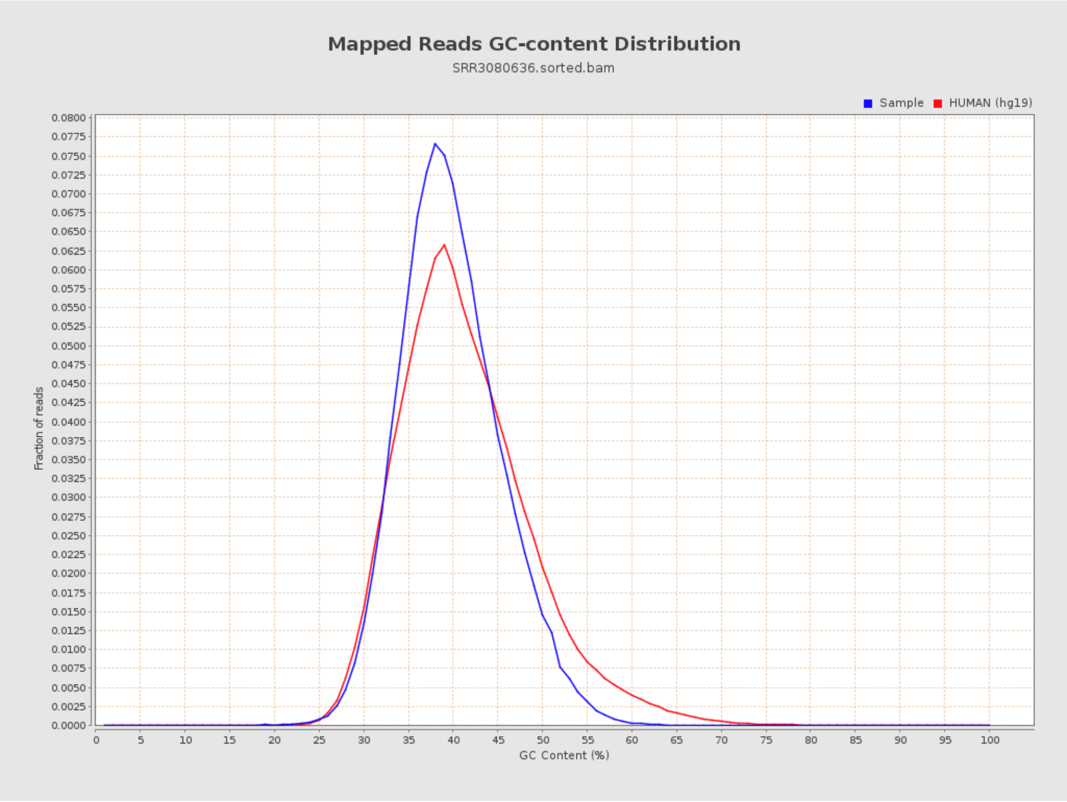
7. Results : Duplication Rate Histogram



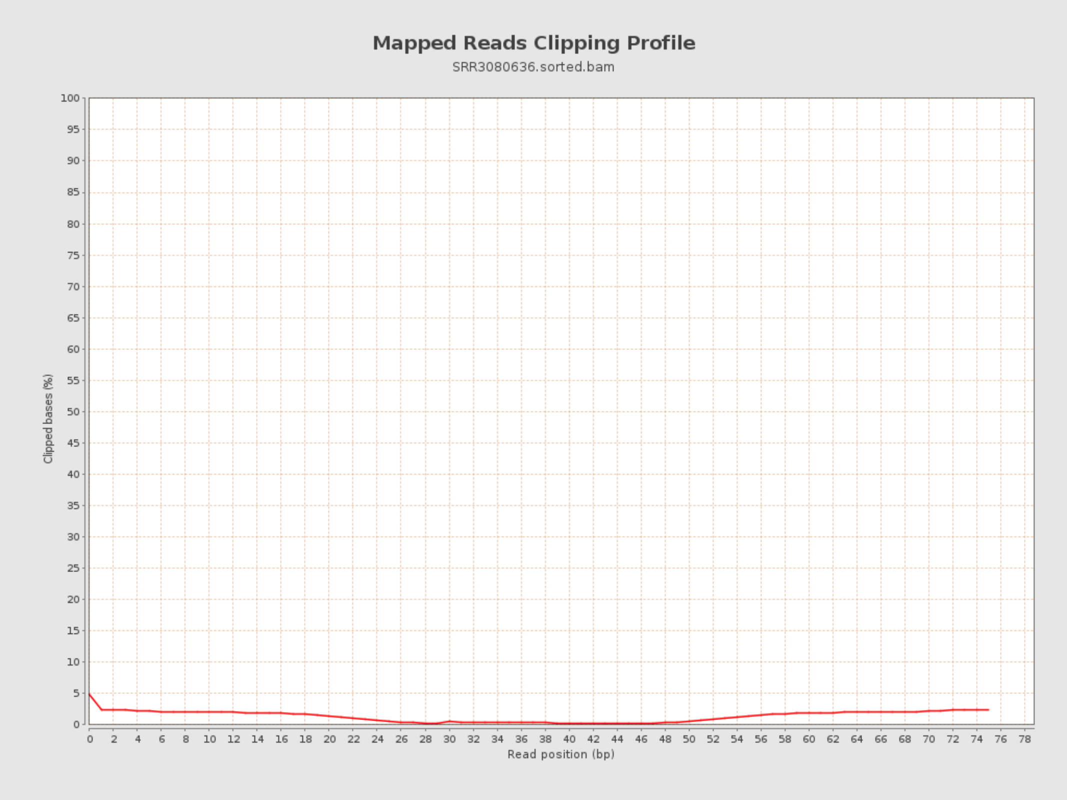
8. Results : Mapped Reads Nucleotide Content



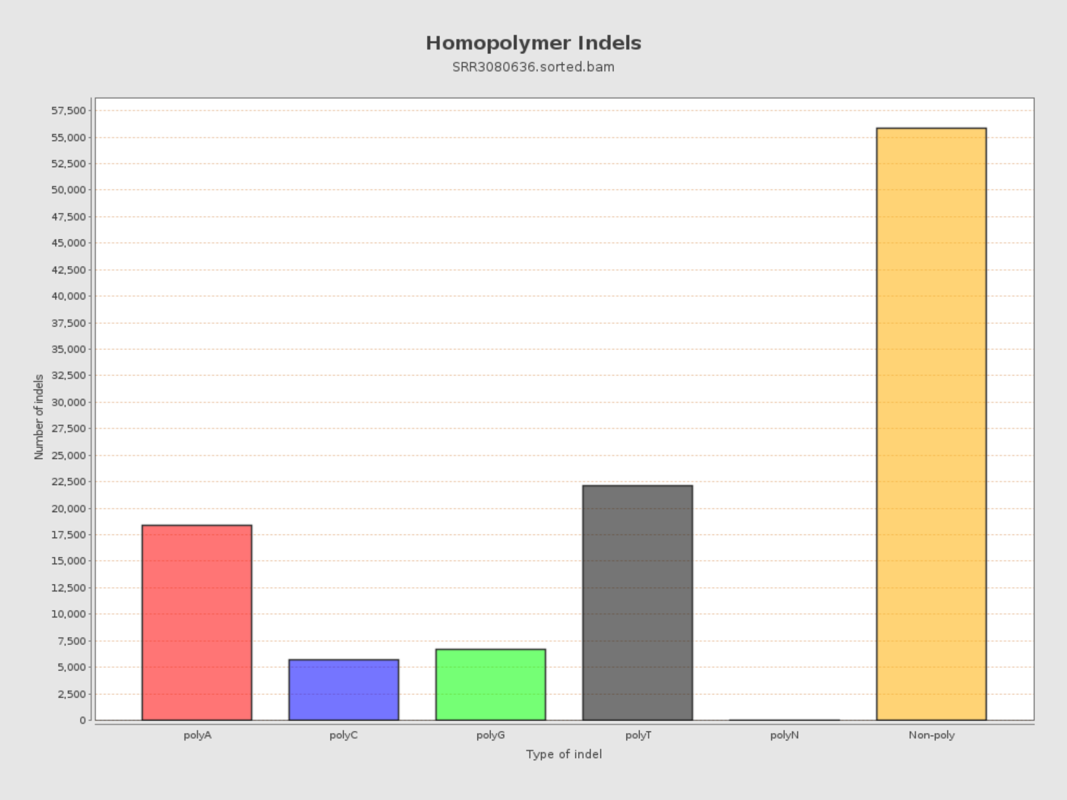
9. Results : Mapped Reads GC-content Distribution



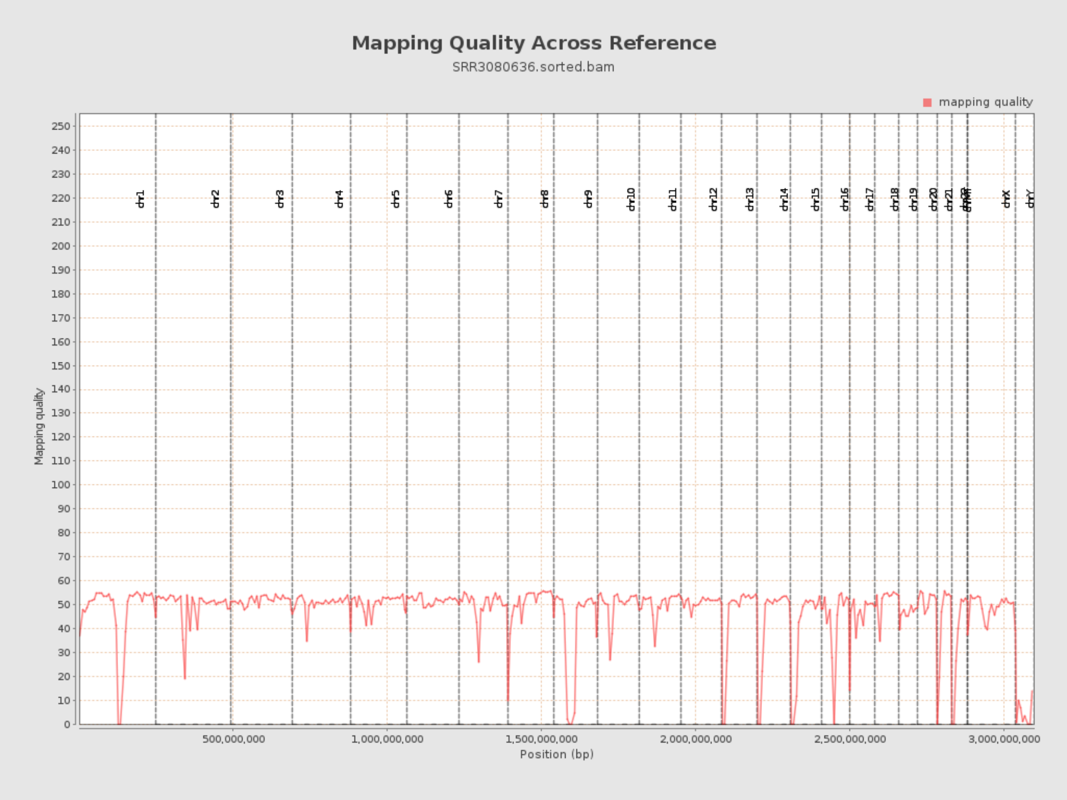
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram