Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:50:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080616.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_SRR3080616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080616.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:50:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,076,218
Mapped reads	5,139,313 / 84.58%
Unmapped reads	936,905 / 15.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,239 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	286,373 / 4.71%
Duplication rate	4.53%
Clipped reads	2,461,609 / 40.51%

2.2. ACGT Content

Number/percentage of A's	93,815,050 / 27.56%
Number/percentage of C's	59,724,993 / 17.54%
Number/percentage of T's	111,726,419 / 32.82%
Number/percentage of G's	74,894,013 / 22%
Number/percentage of N's	277,162 / 0.08%
GC Percentage	39.54%

2.3. Coverage

Mean	0.11

Standard Deviation	0.6869

2.4. Mapping Quality

Mean Mapping Quality	47.18

2.5. Mismatches and indels

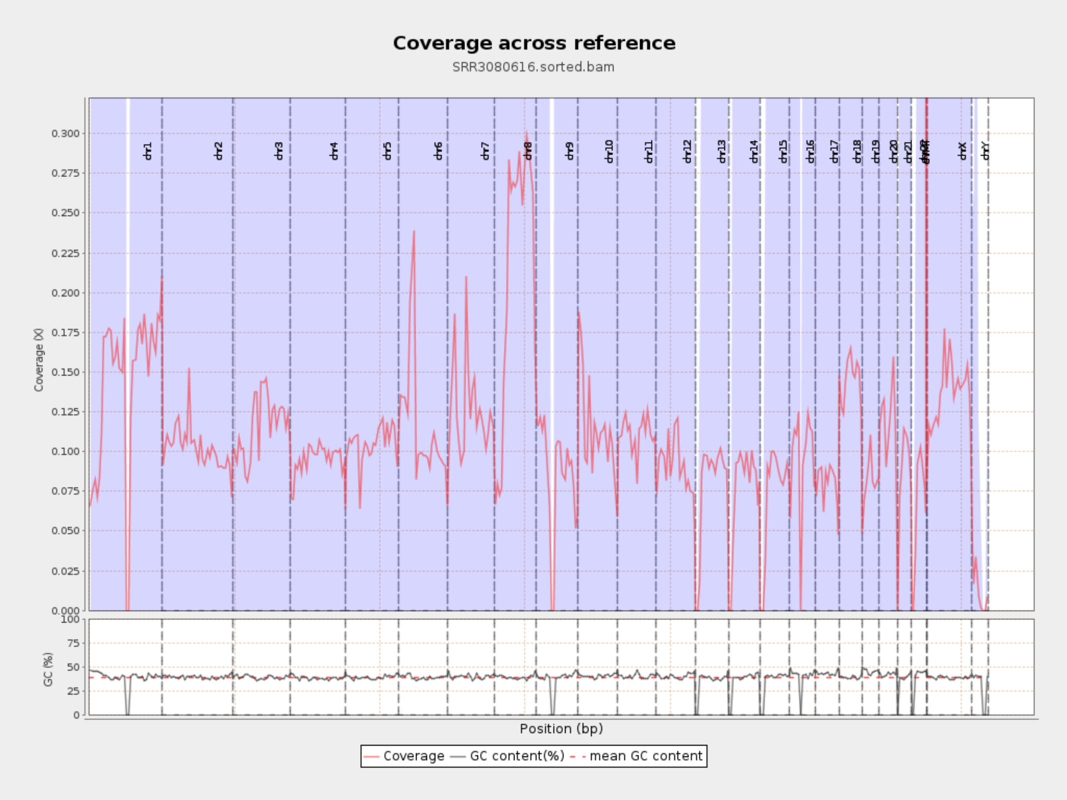
General error rate	0.9%
Mismatches	3,009,322
Insertions	27,801
Mapped reads with at least one insertion	0.54%
Deletions	82,942
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.6%

2.6. Chromosome stats

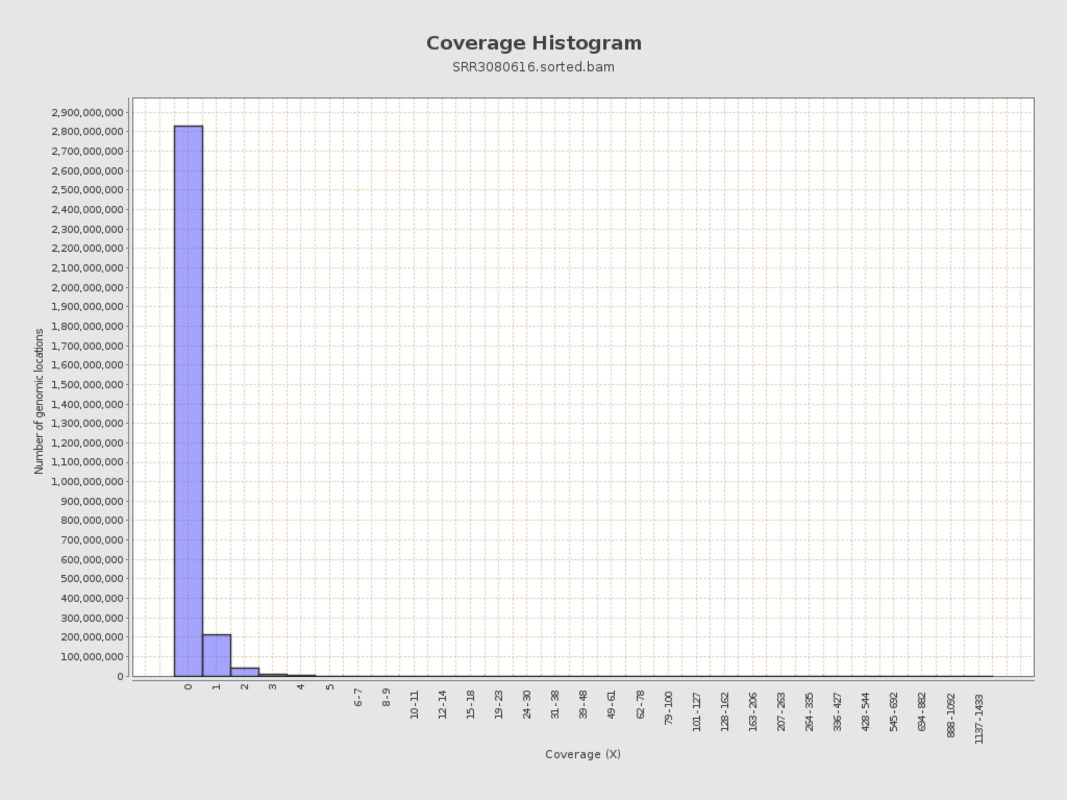
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	35226246	0.1413	0.9941
chr2	243199373	24900924	0.1024	0.7103
chr3	198022430	23096626	0.1166	0.4128
chr4	191154276	18171118	0.0951	0.3909
chr5	180915260	19036505	0.1052	0.3896
chr6	171115067	20404808	0.1192	0.6492
chr7	159138663	20386222	0.1281	1.4462

chr8	146364022	31606508	0.2159	1.1043
chr9	141213431	12115396	0.0858	0.5794
chr10	135534747	15772488	0.1164	0.6564
chr11	135006516	14894531	0.1103	0.5306
chr12	133851895	12163753	0.0909	0.3758
chr13	115169878	8905656	0.0773	0.3315
chr14	107349540	8094215	0.0754	0.3706
chr15	102531392	7422331	0.0724	0.3275
chr16	90354753	8669855	0.096	0.4199
chr17	81195210	6453915	0.0795	0.389
chr18	78077248	11381928	0.1458	0.9739
chr19	59128983	4895762	0.0828	0.7373
chr20	63025520	7467134	0.1185	0.4377
chr21	48129895	4137455	0.086	0.3921
chr22	51304566	3193670	0.0622	0.2974
chrMT	16571	245558	14.8185	20.5585
chrX	155270560	21210355	0.1366	0.5154
chrY	59373566	719518	0.0121	0.2178

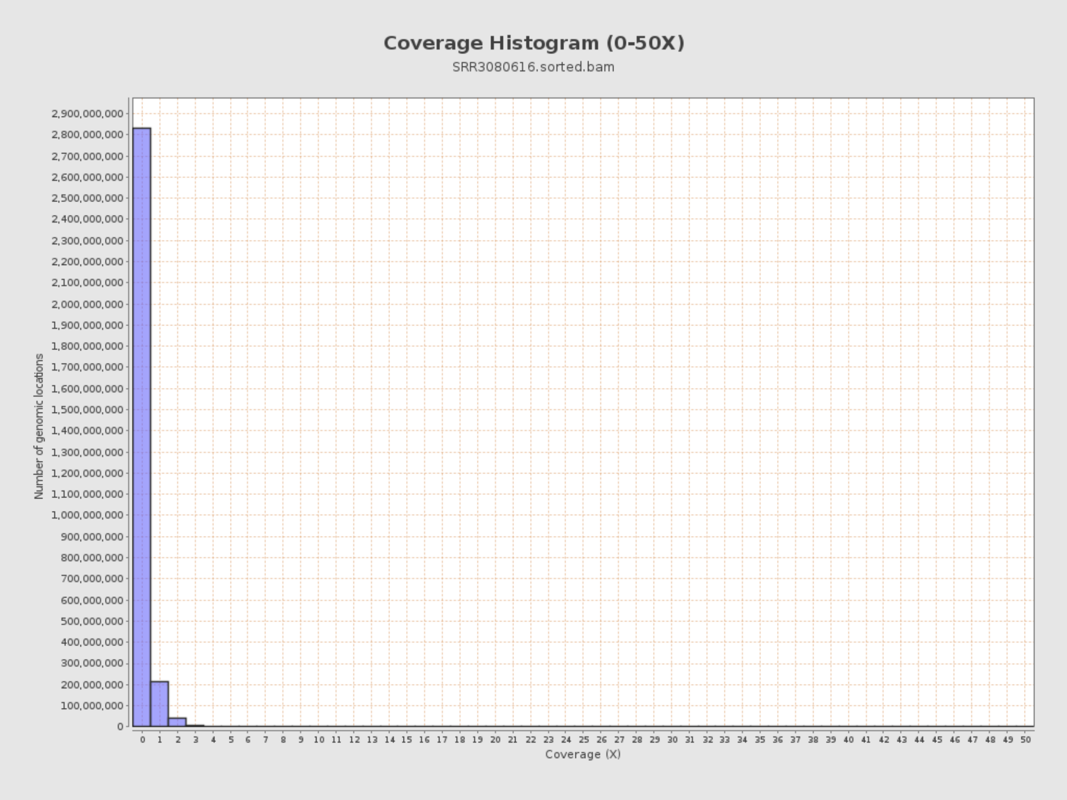
3. Results : Coverage across reference



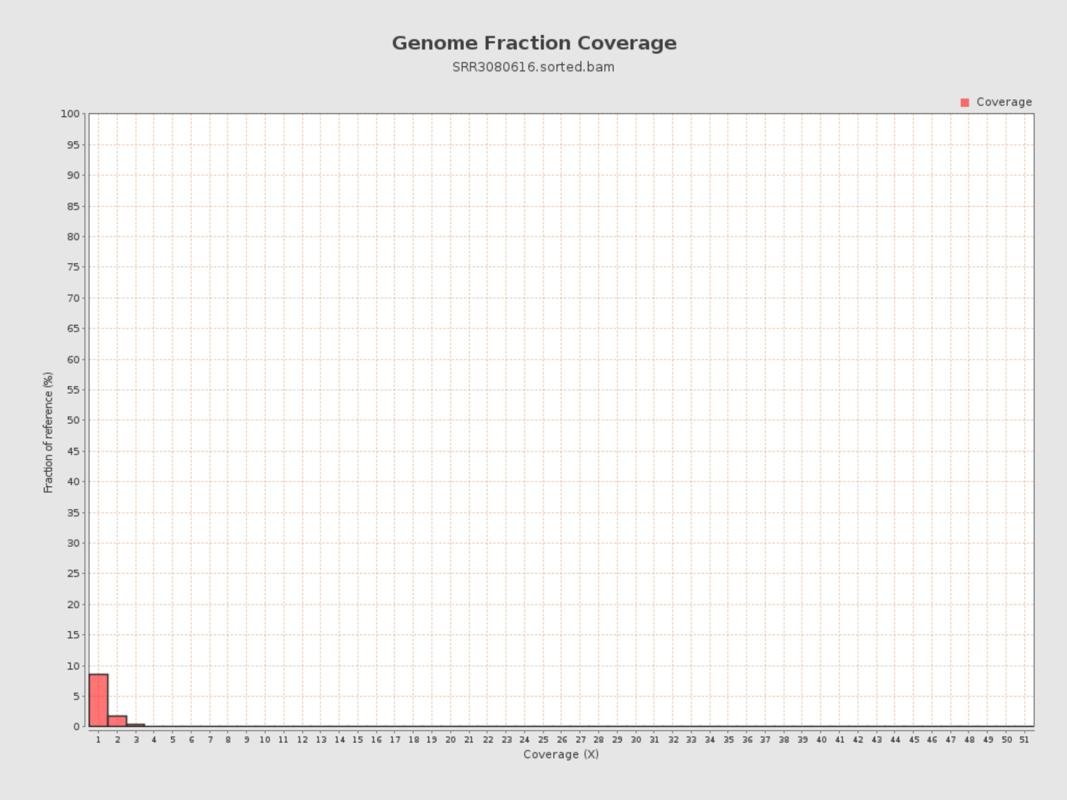
4. Results : Coverage Histogram



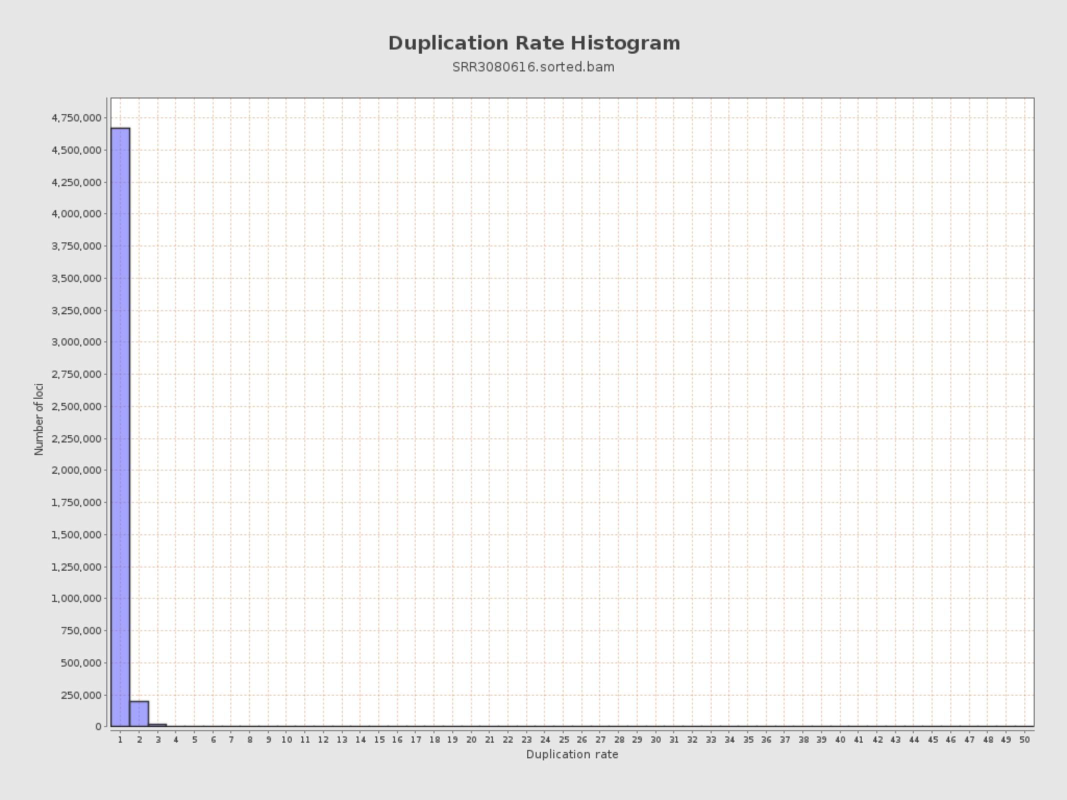
5. Results : Coverage Histogram (0-50X)



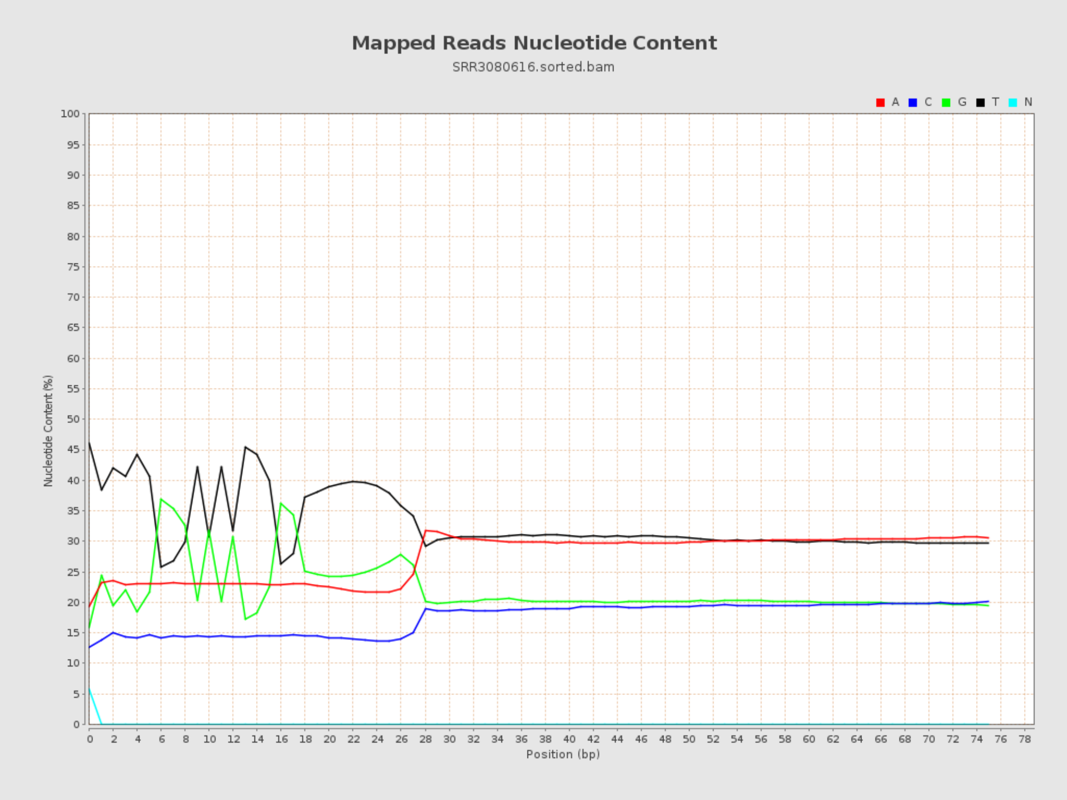
6. Results : Genome Fraction Coverage



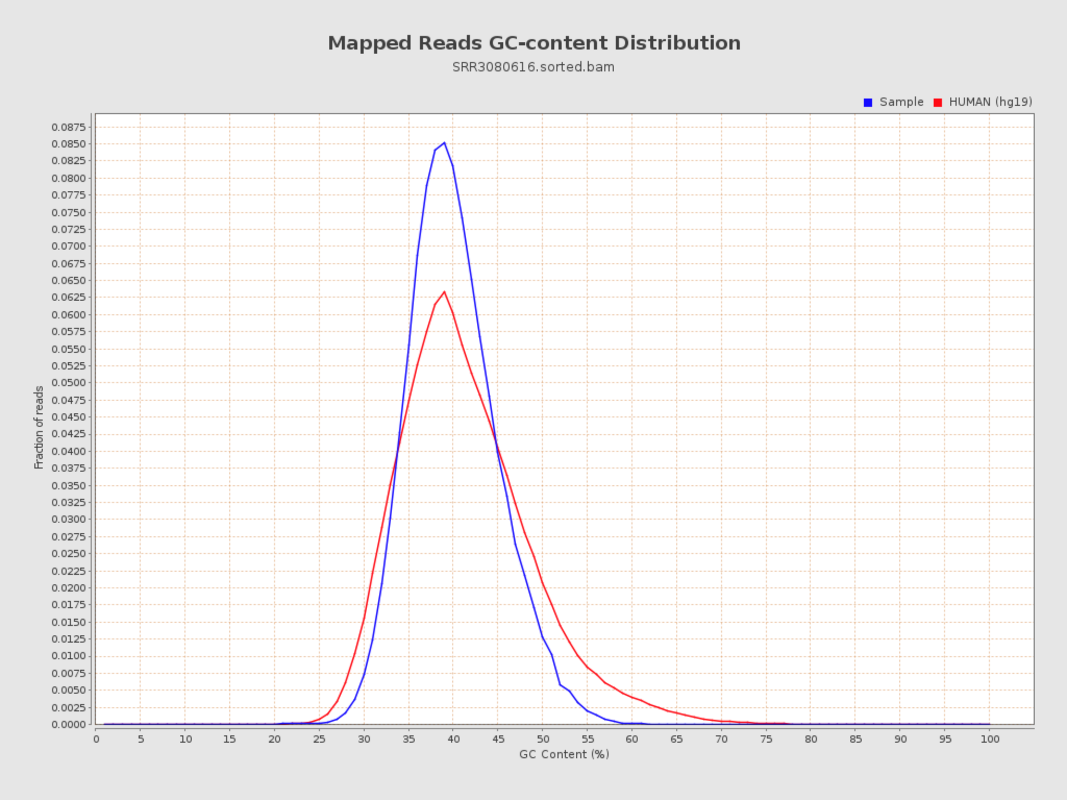
7. Results : Duplication Rate Histogram



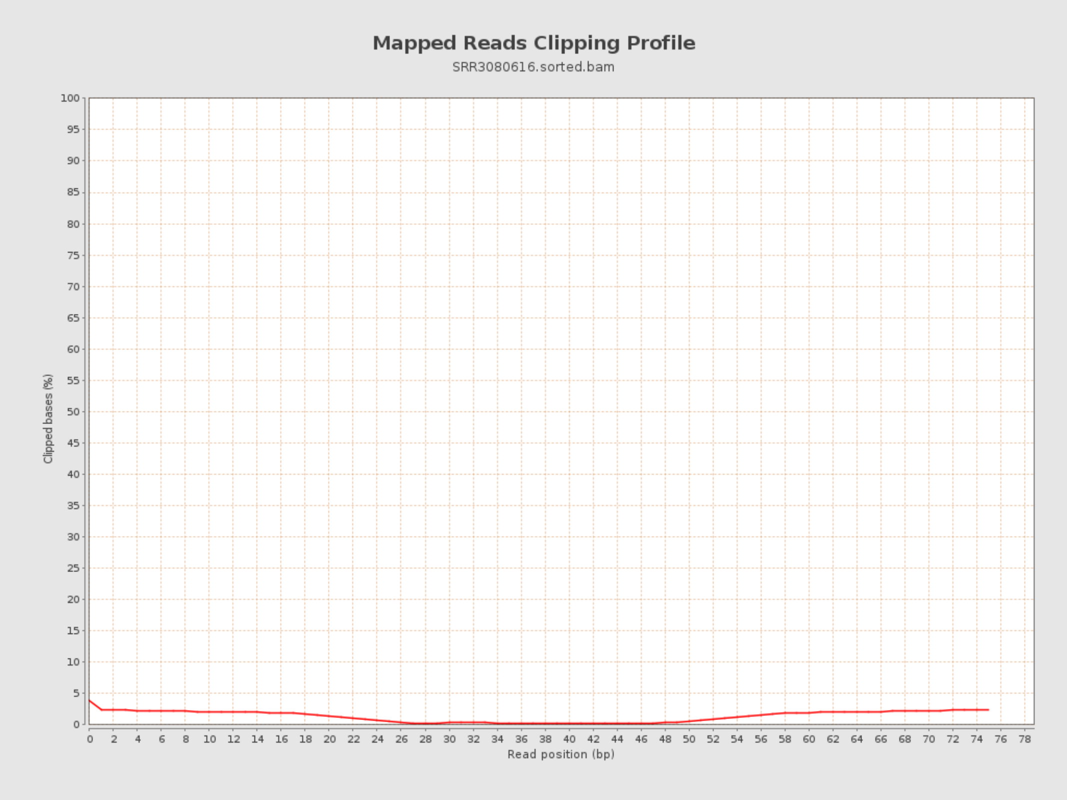
8. Results : Mapped Reads Nucleotide Content



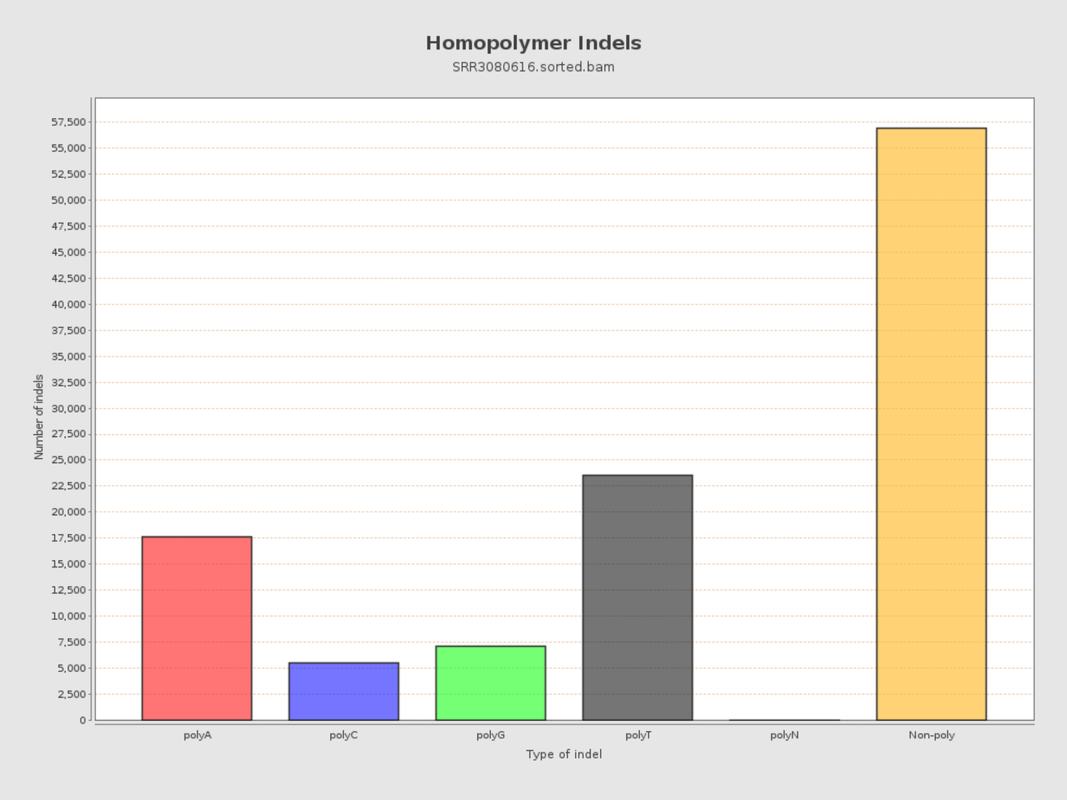
9. Results : Mapped Reads GC-content Distribution



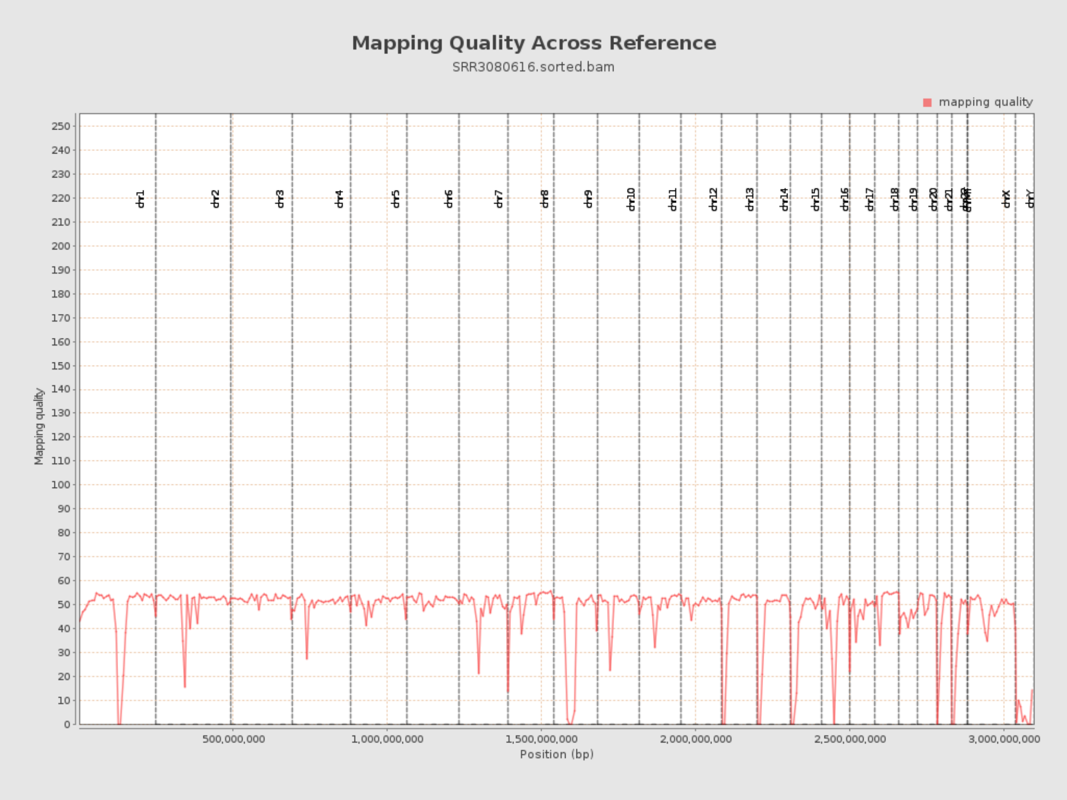
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram