Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:38:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080660.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_SRR3080660 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080660.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:38:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080660.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,464,046
Mapped reads	1,327,314 / 90.66%
Unmapped reads	136,732 / 9.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,915 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	49,282 / 3.37%
Duplication rate	3.23%
Clipped reads	619,140 / 42.29%

2.2. ACGT Content

Number/percentage of A's	23,538,822 / 26.84%
Number/percentage of C's	16,283,746 / 18.57%
Number/percentage of T's	27,647,917 / 31.52%
Number/percentage of G's	20,227,518 / 23.06%
Number/percentage of N's	3,767 / 0%
GC Percentage	41.63%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.2346

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

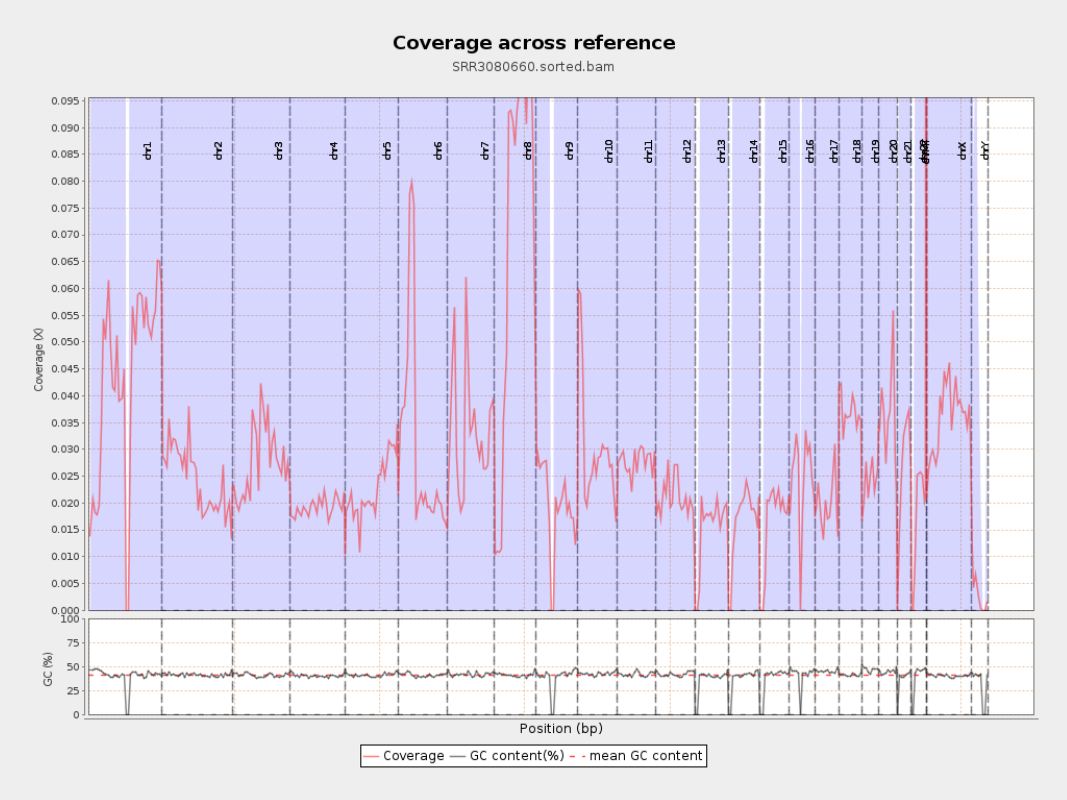
General error rate	0.7%
Mismatches	598,472
Insertions	6,582
Mapped reads with at least one insertion	0.49%
Deletions	19,649
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.6%

2.6. Chromosome stats

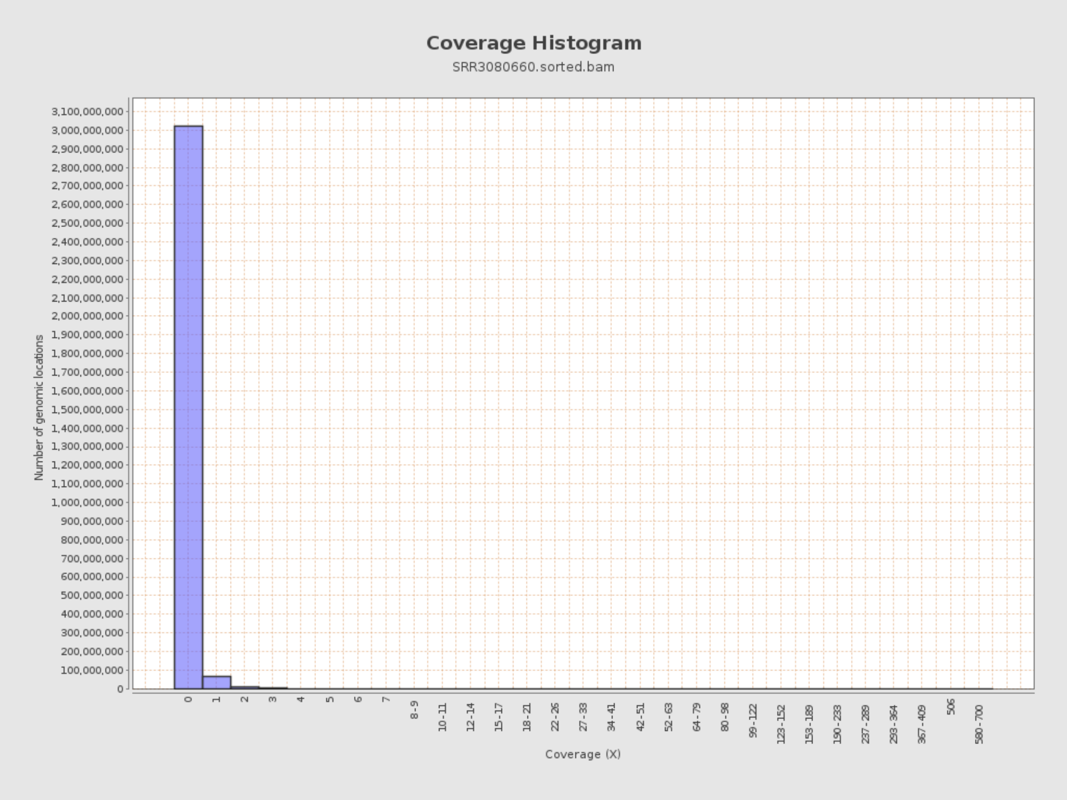
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10695854	0.0429	0.2493
chr2	243199373	5944036	0.0244	0.3462
chr3	198022430	5529341	0.0279	0.1866
chr4	191154276	3671780	0.0192	0.1571
chr5	180915260	4086468	0.0226	0.1685
chr6	171115067	5287012	0.0309	0.2264
chr7	159138663	5438715	0.0342	0.464

chr8	146364022	10241993	0.07	0.3224
chr9	141213431	2704813	0.0192	0.1745
chr10	135534747	4143673	0.0306	0.2037
chr11	135006516	3724959	0.0276	0.1953
chr12	133851895	2797863	0.0209	0.1629
chr13	115169878	1759108	0.0153	0.1392
chr14	107349540	1752197	0.0163	0.1446
chr15	102531392	1675998	0.0163	0.1545
chr16	90354753	2218080	0.0245	0.1778
chr17	81195210	1582977	0.0195	0.1591
chr18	78077248	2887952	0.037	0.243
chr19	59128983	1446233	0.0245	0.1858
chr20	63025520	2290797	0.0363	0.2157
chr21	48129895	1258972	0.0262	0.1831
chr22	51304566	863947	0.0168	0.1452
chrMT	16571	10022	0.6048	0.9253
chrX	155270560	5547281	0.0357	0.2167
chrY	59373566	173220	0.0029	0.0654

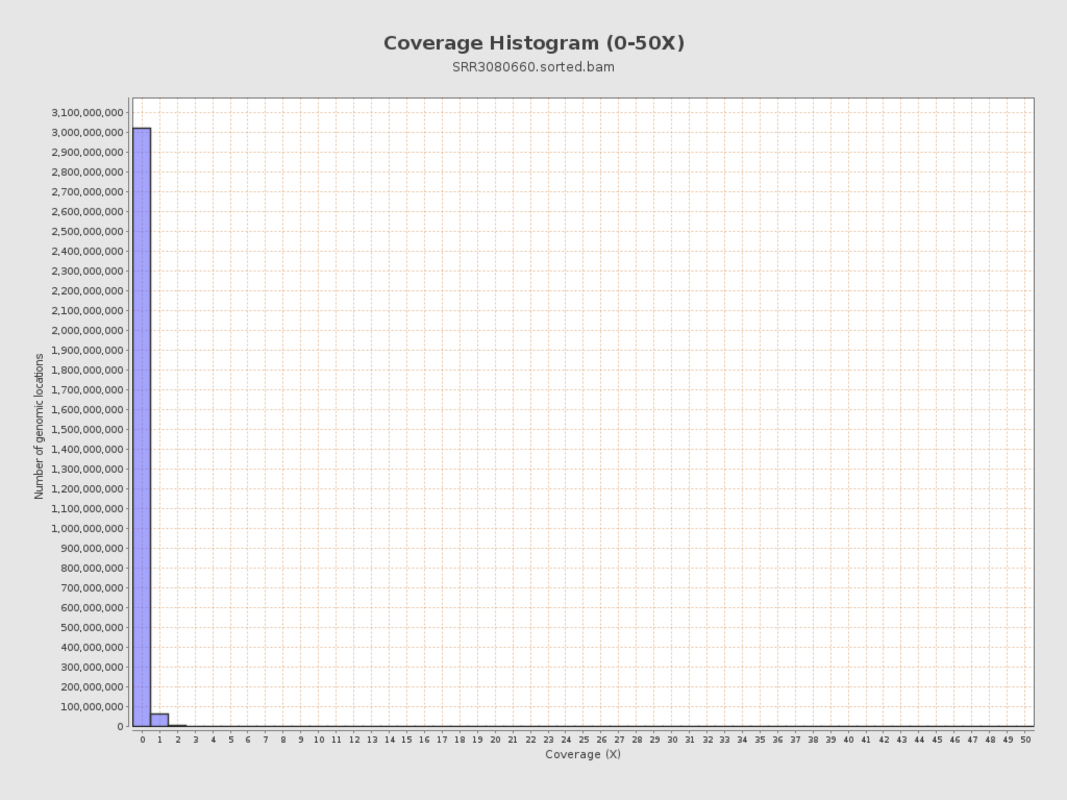
3. Results : Coverage across reference



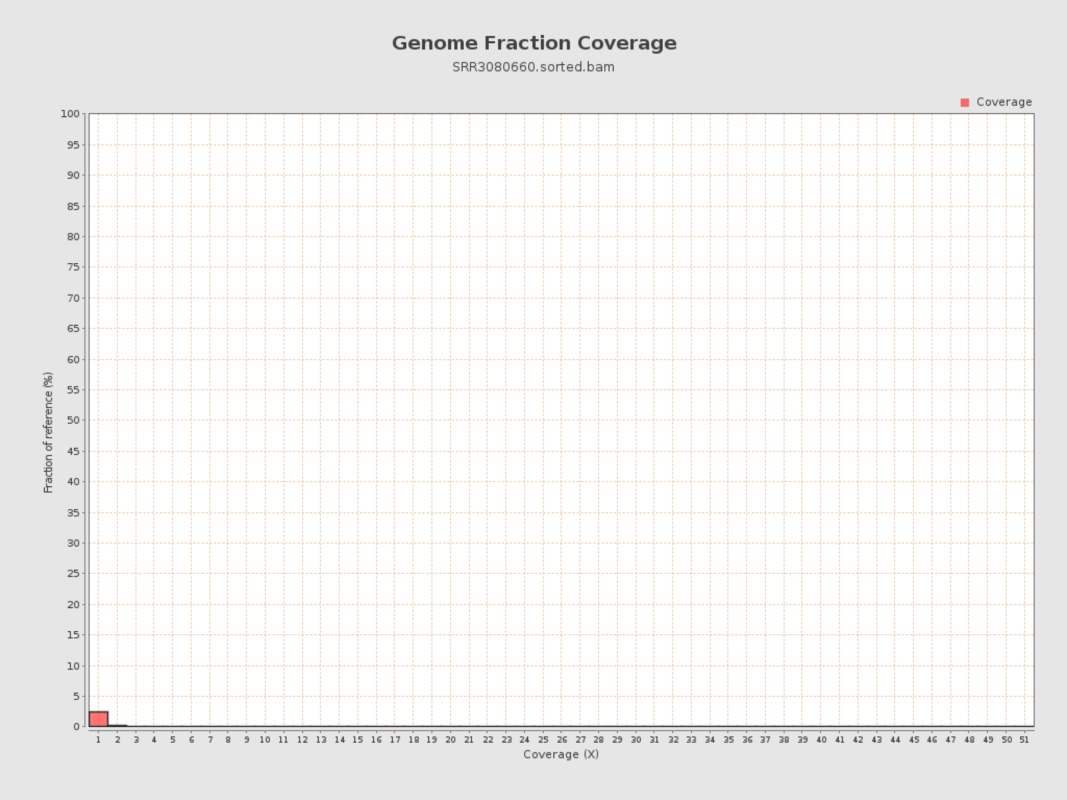
4. Results : Coverage Histogram



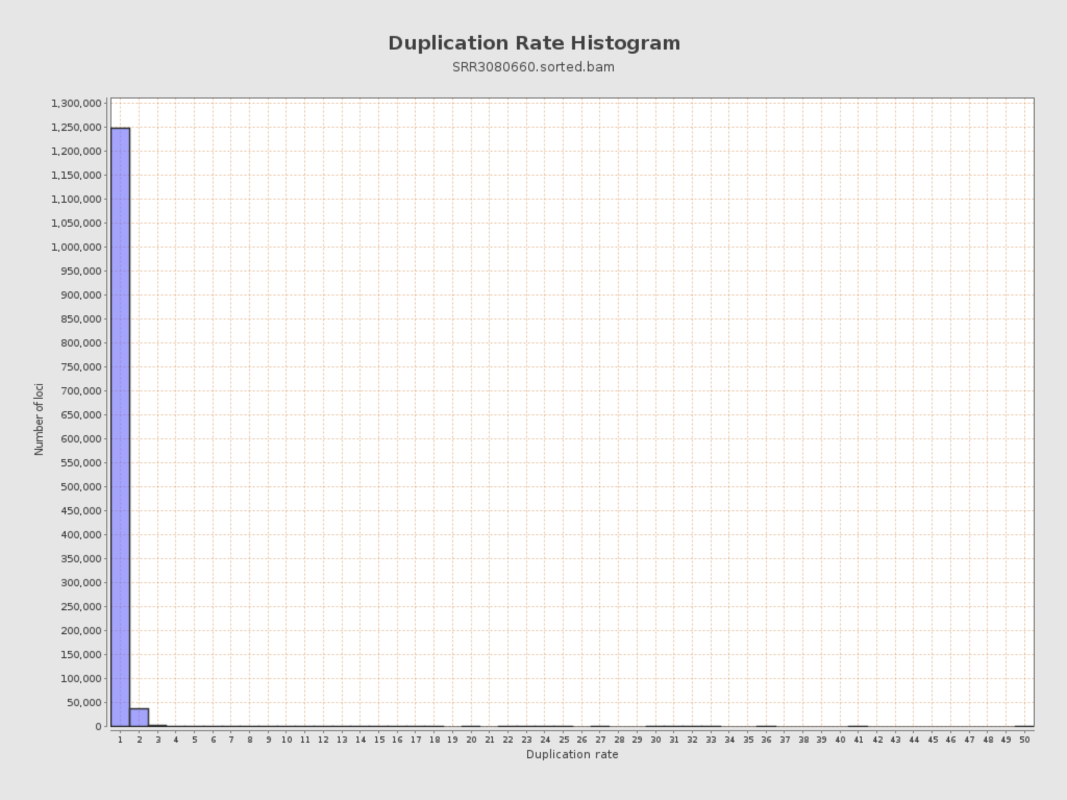
5. Results : Coverage Histogram (0-50X)



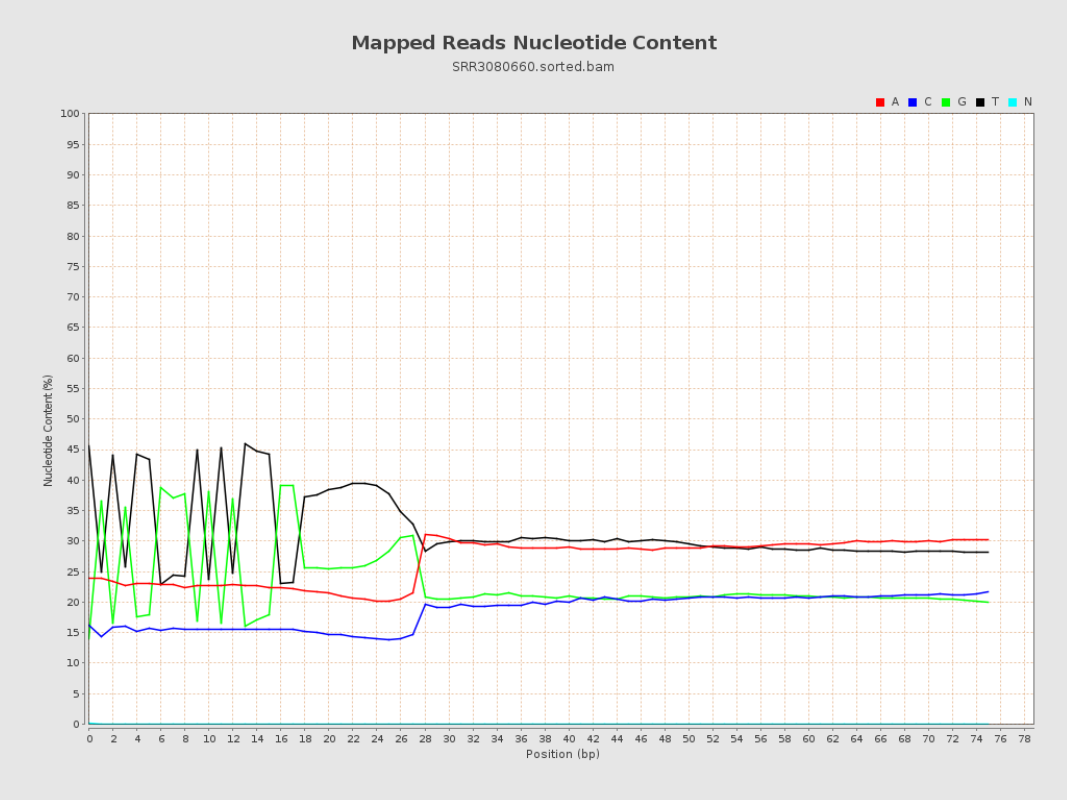
6. Results : Genome Fraction Coverage



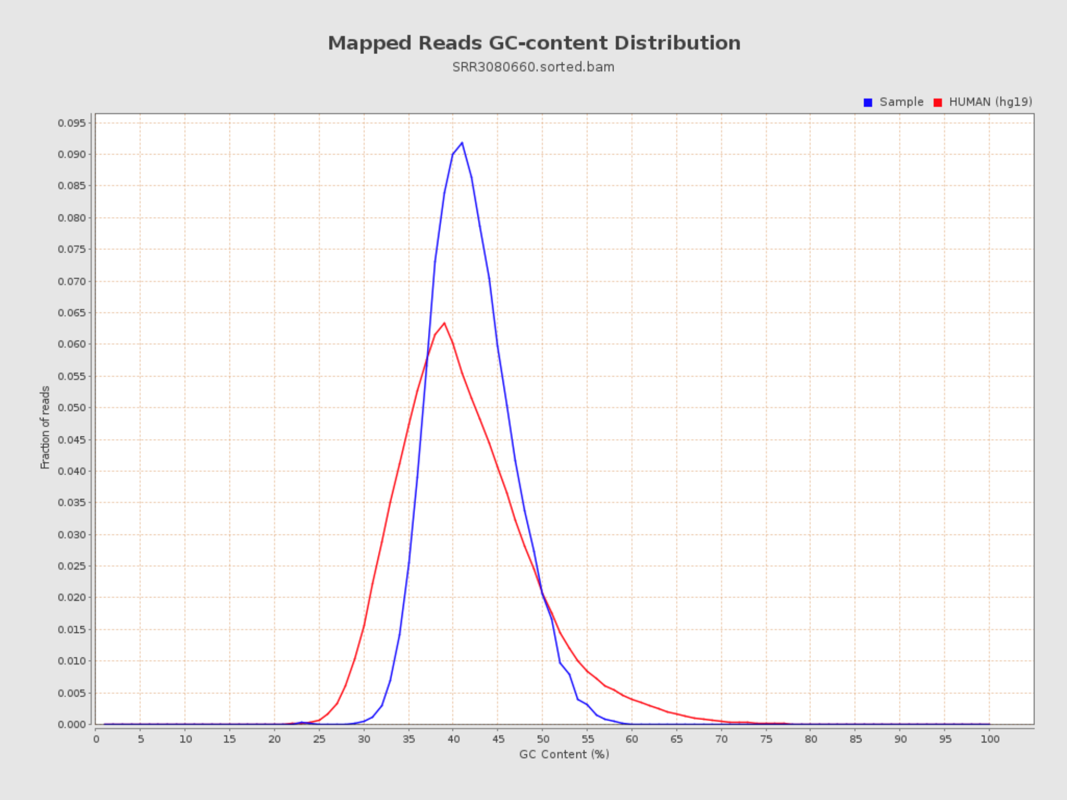
7. Results : Duplication Rate Histogram



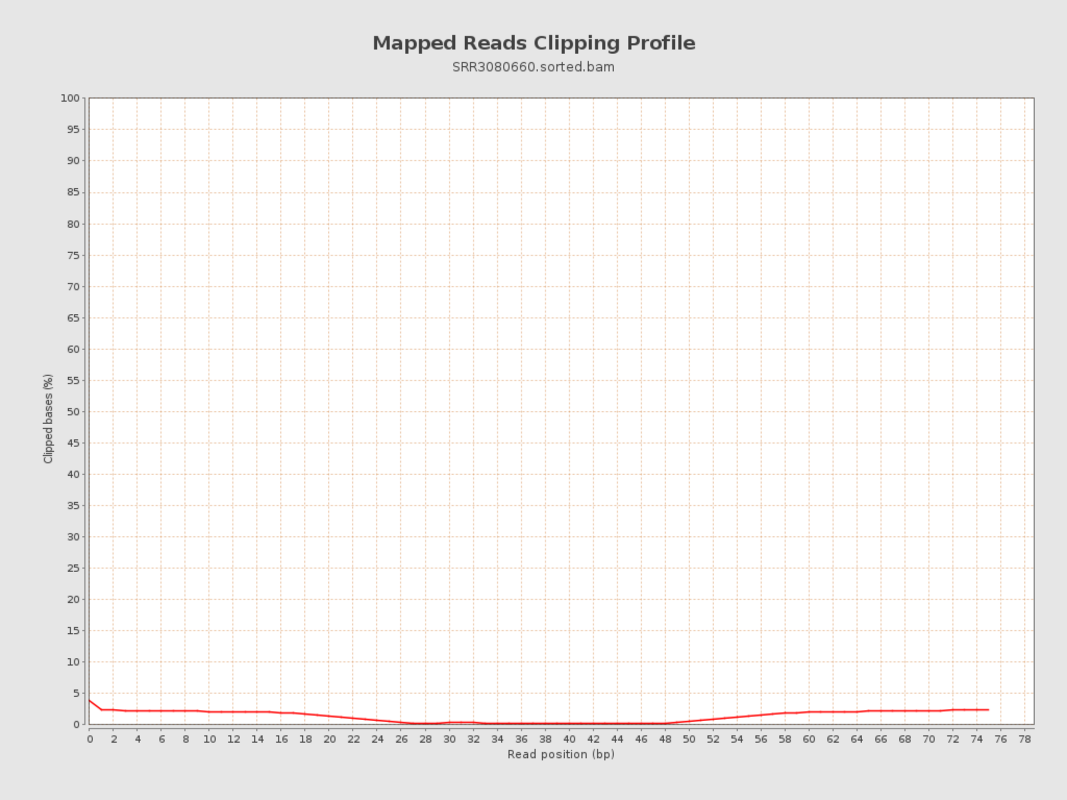
8. Results : Mapped Reads Nucleotide Content



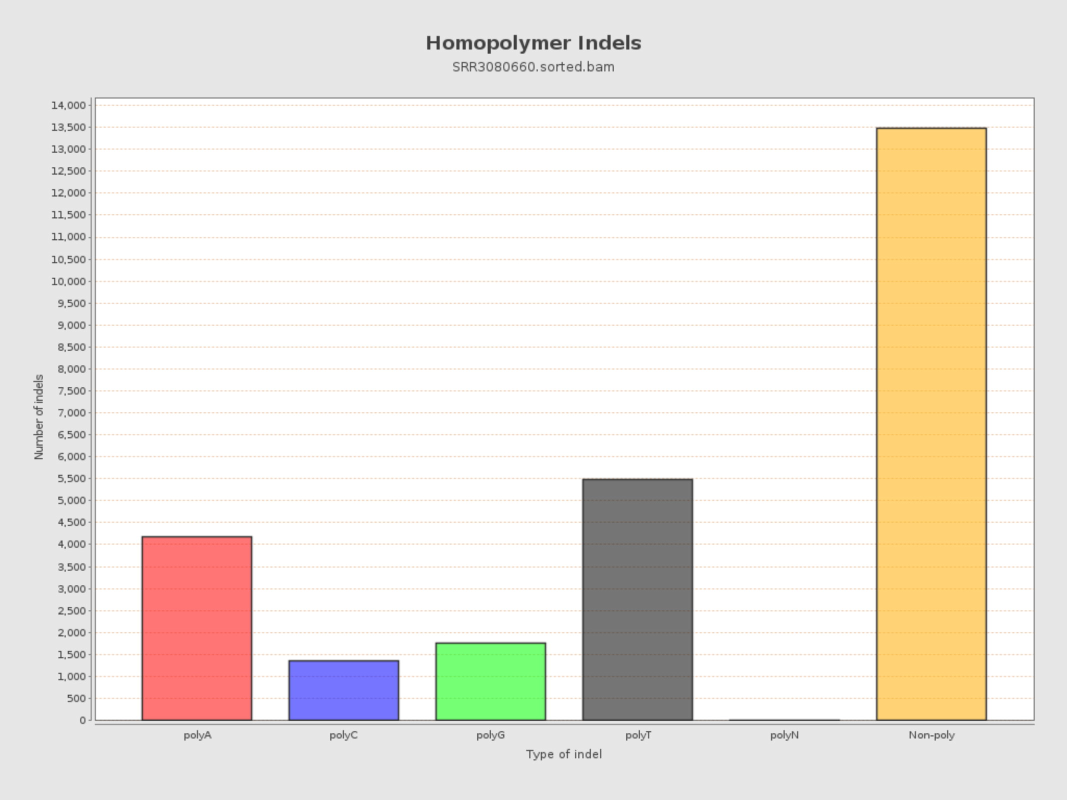
9. Results : Mapped Reads GC-content Distribution



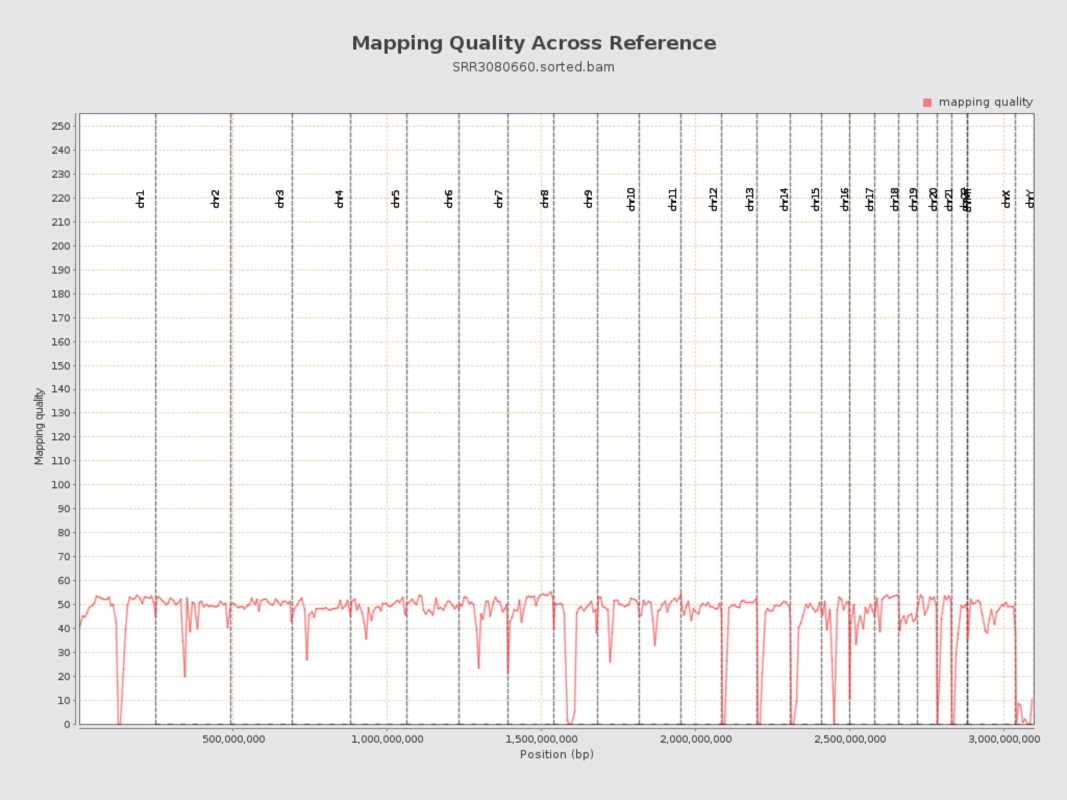
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram