Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:32:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080653.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_SRR3080653 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080653.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:32:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080653.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,216,468
Mapped reads	1,116,066 / 91.75%
Unmapped reads	100,402 / 8.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,961 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	31,686 / 2.6%
Duplication rate	2.5%
Clipped reads	468,901 / 38.55%

2.2. ACGT Content

Number/percentage of A's	20,857,011 / 27.84%
Number/percentage of C's	13,738,178 / 18.34%
Number/percentage of T's	23,742,753 / 31.69%
Number/percentage of G's	16,578,894 / 22.13%
Number/percentage of N's	3,298 / 0%
GC Percentage	40.47%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.1958

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

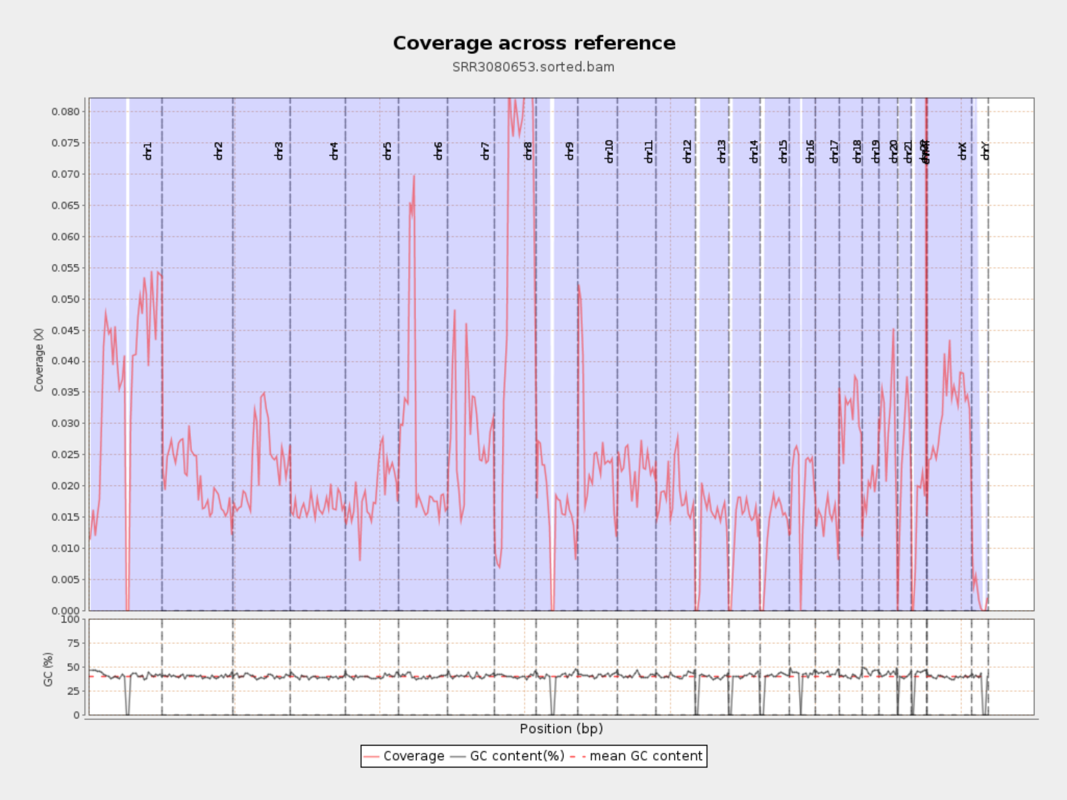
General error rate	0.69%
Mismatches	509,947
Insertions	5,815
Mapped reads with at least one insertion	0.52%
Deletions	17,663
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.82%

2.6. Chromosome stats

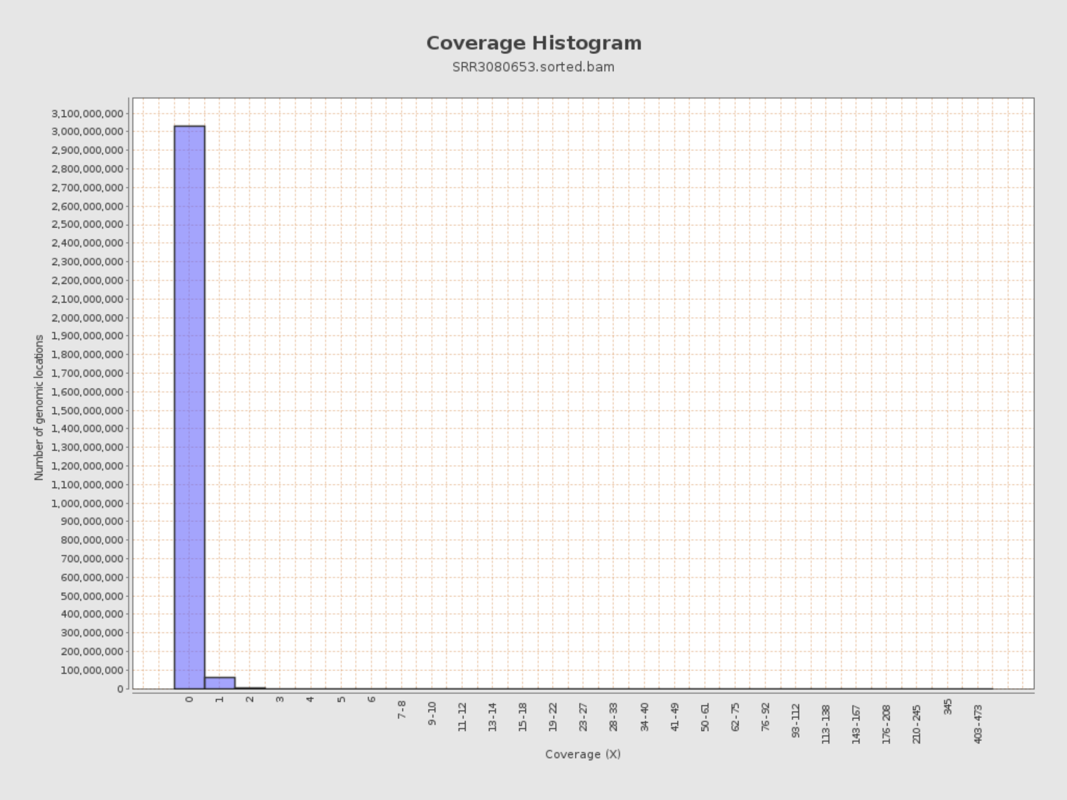
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9197403	0.0369	0.2351
chr2	243199373	5123187	0.0211	0.2575
chr3	198022430	4677038	0.0236	0.1673
chr4	191154276	3212909	0.0168	0.1428
chr5	180915260	3404783	0.0188	0.149
chr6	171115067	4537905	0.0265	0.1996
chr7	159138663	4616582	0.029	0.3071

chr8	146364022	8934549	0.061	0.2927
chr9	141213431	2288189	0.0162	0.1537
chr10	135534747	3526499	0.026	0.183
chr11	135006516	3075031	0.0228	0.1714
chr12	133851895	2448174	0.0183	0.1483
chr13	115169878	1565376	0.0136	0.1275
chr14	107349540	1422938	0.0133	0.1262
chr15	102531392	1307591	0.0128	0.1256
chr16	90354753	1845096	0.0204	0.1593
chr17	81195210	1186868	0.0146	0.1317
chr18	78077248	2509900	0.0321	0.2337
chr19	59128983	1181431	0.02	0.1685
chr20	63025520	1912507	0.0303	0.1909
chr21	48129895	1142159	0.0237	0.1705
chr22	51304566	714233	0.0139	0.1276
chrMT	16571	19684	1.1879	1.3329
chrX	155270560	4953702	0.0319	0.2004
chrY	59373566	145544	0.0025	0.056

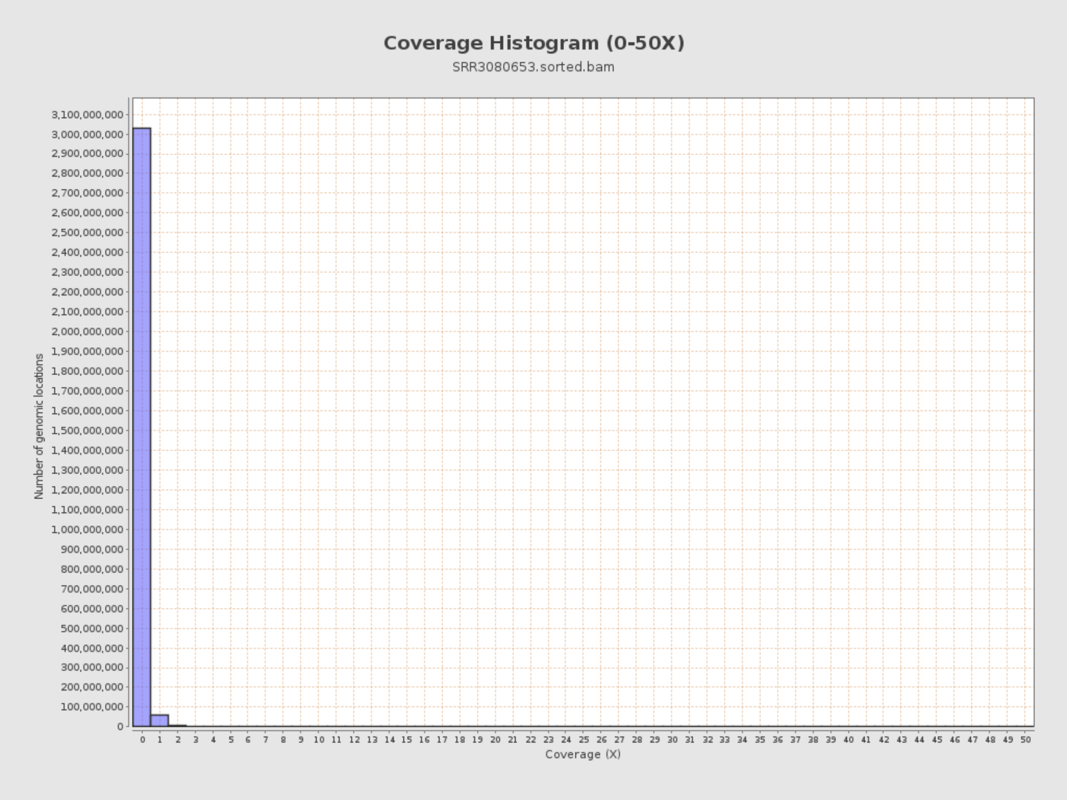
3. Results : Coverage across reference



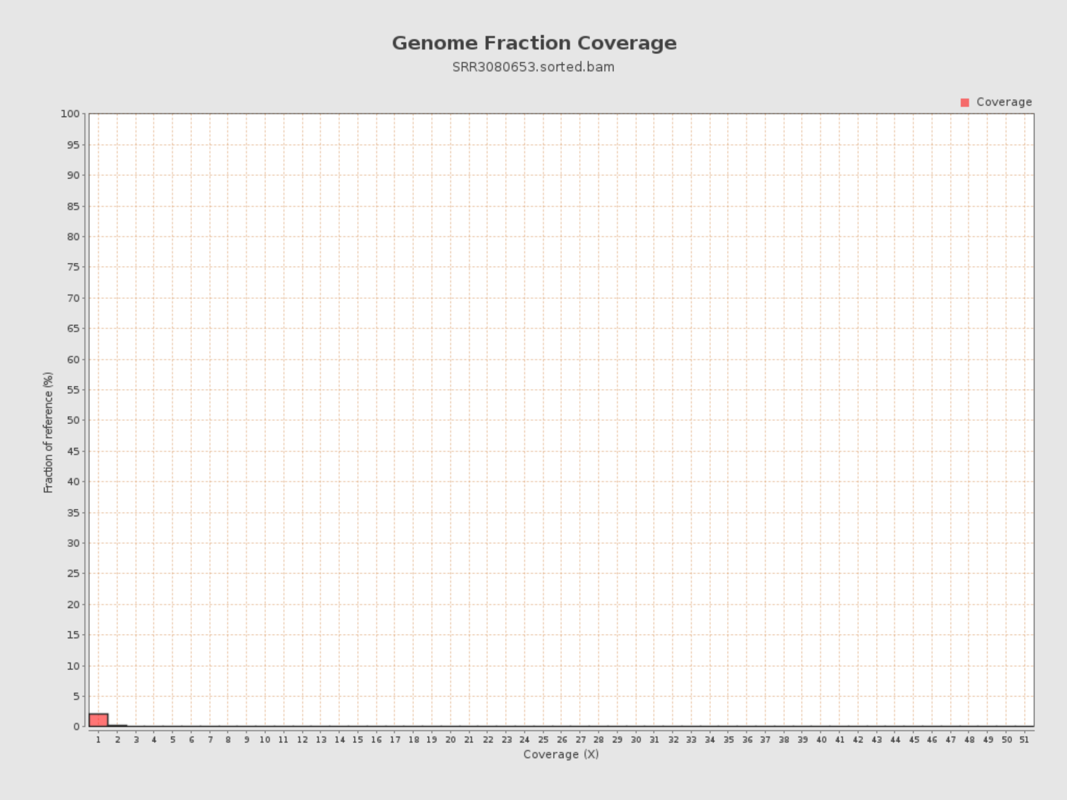
4. Results : Coverage Histogram



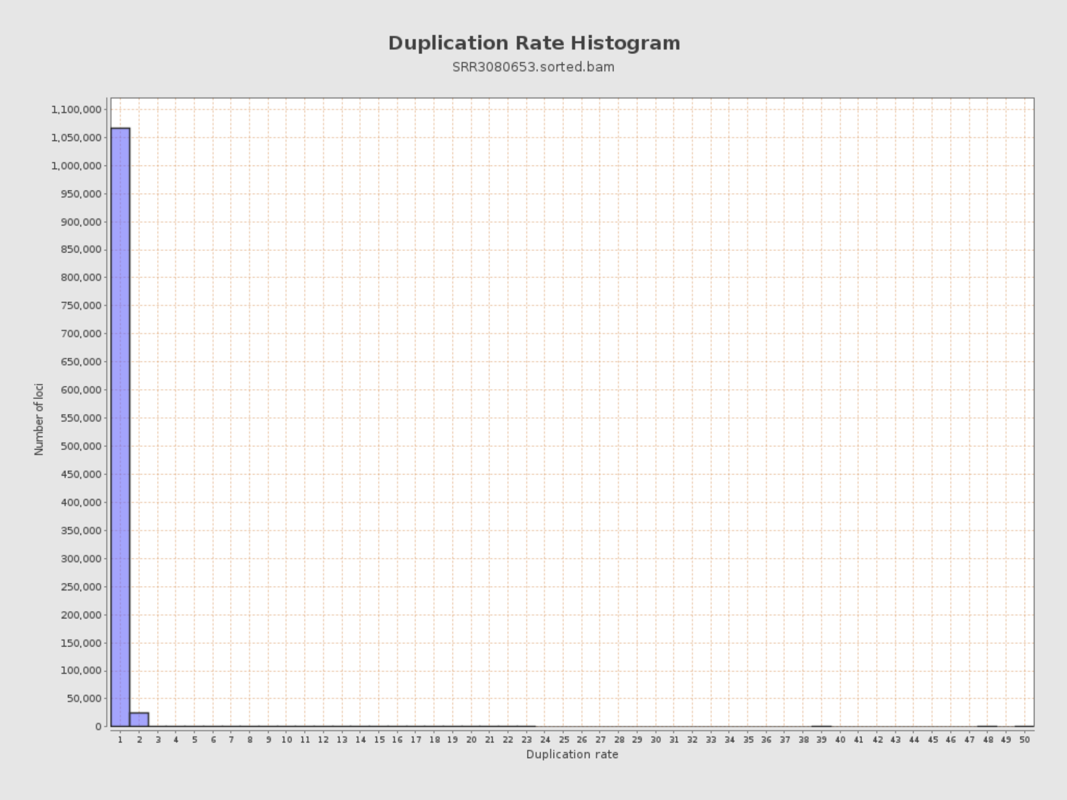
5. Results : Coverage Histogram (0-50X)



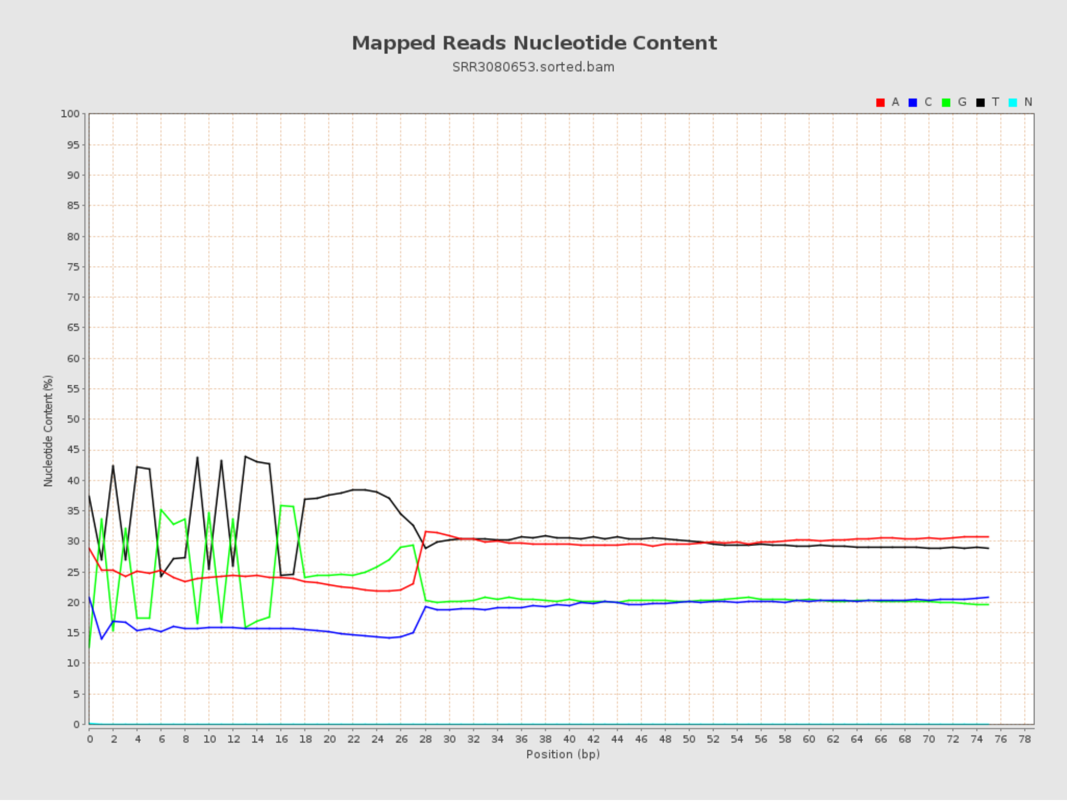
6. Results : Genome Fraction Coverage



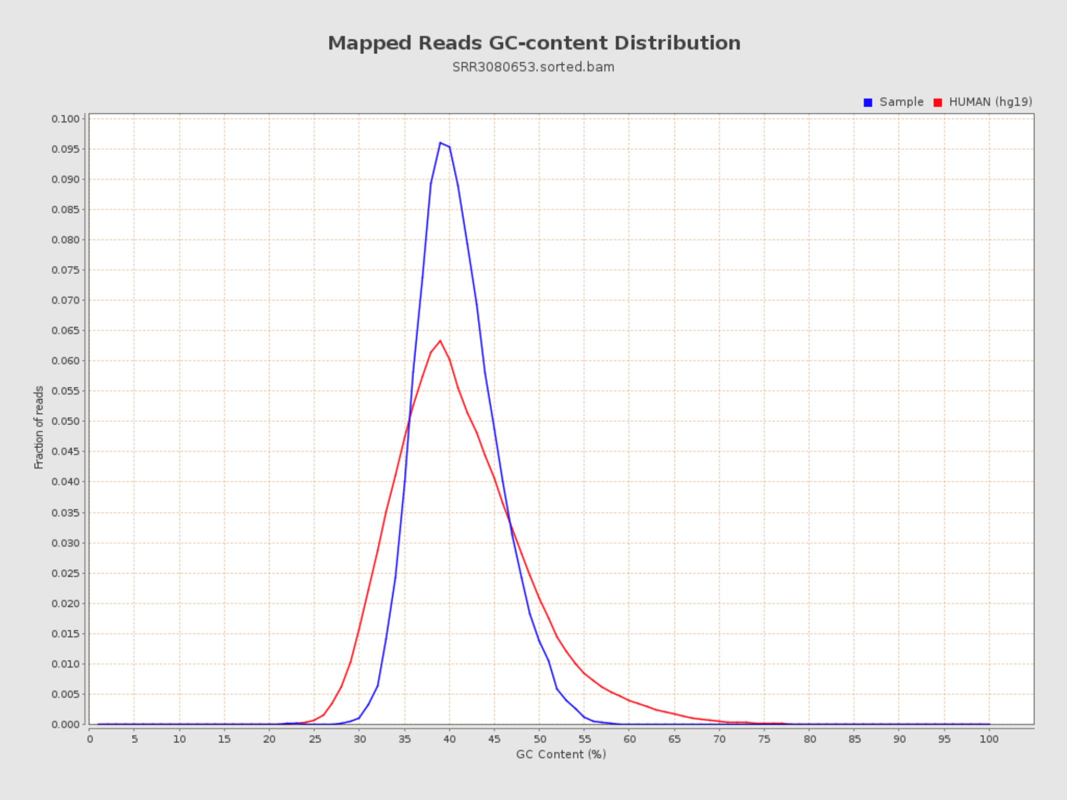
7. Results : Duplication Rate Histogram



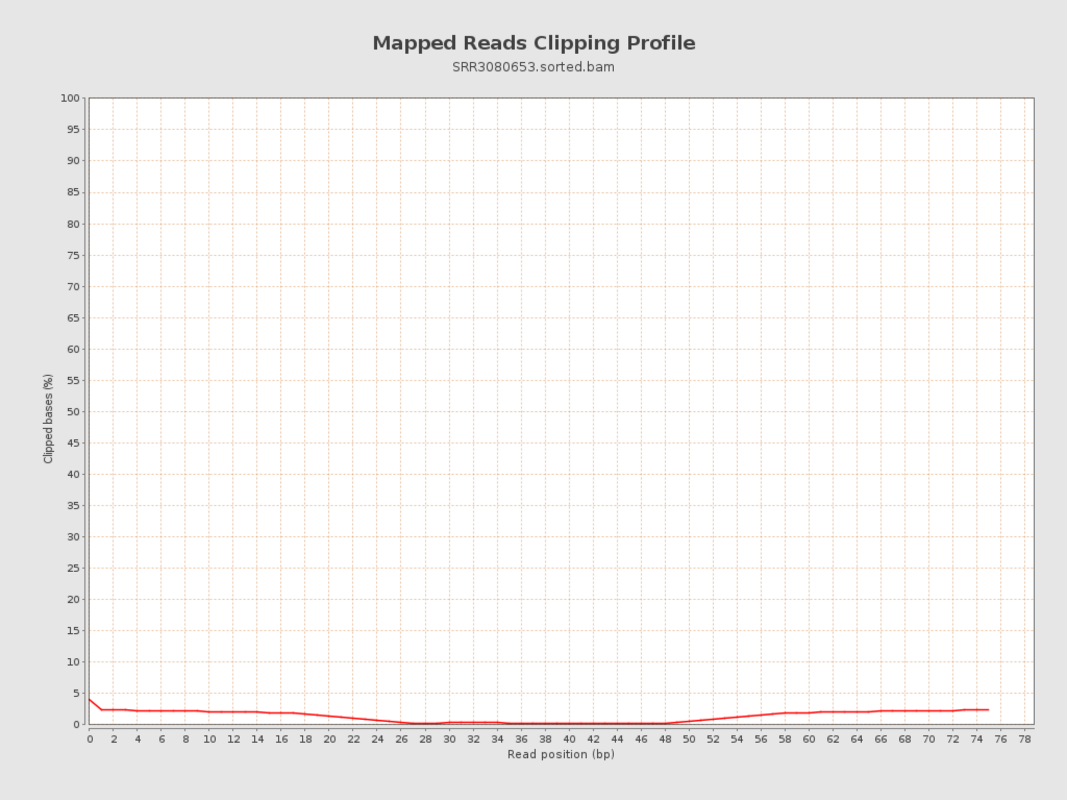
8. Results : Mapped Reads Nucleotide Content



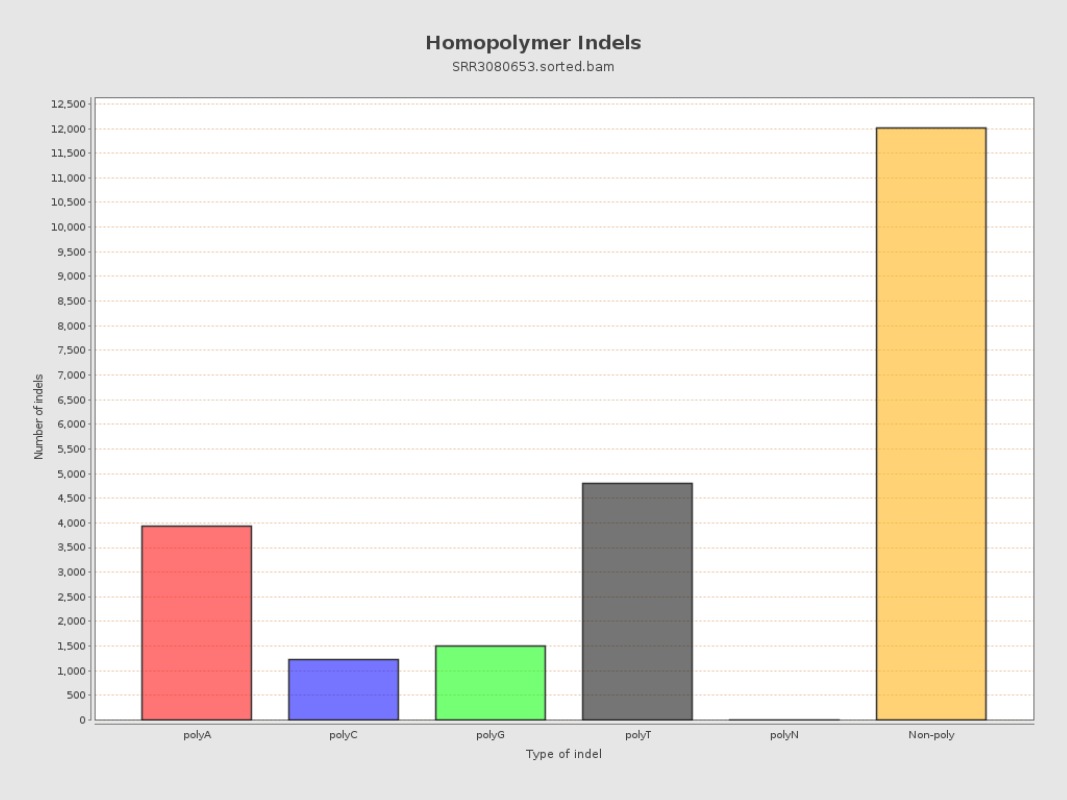
9. Results : Mapped Reads GC-content Distribution



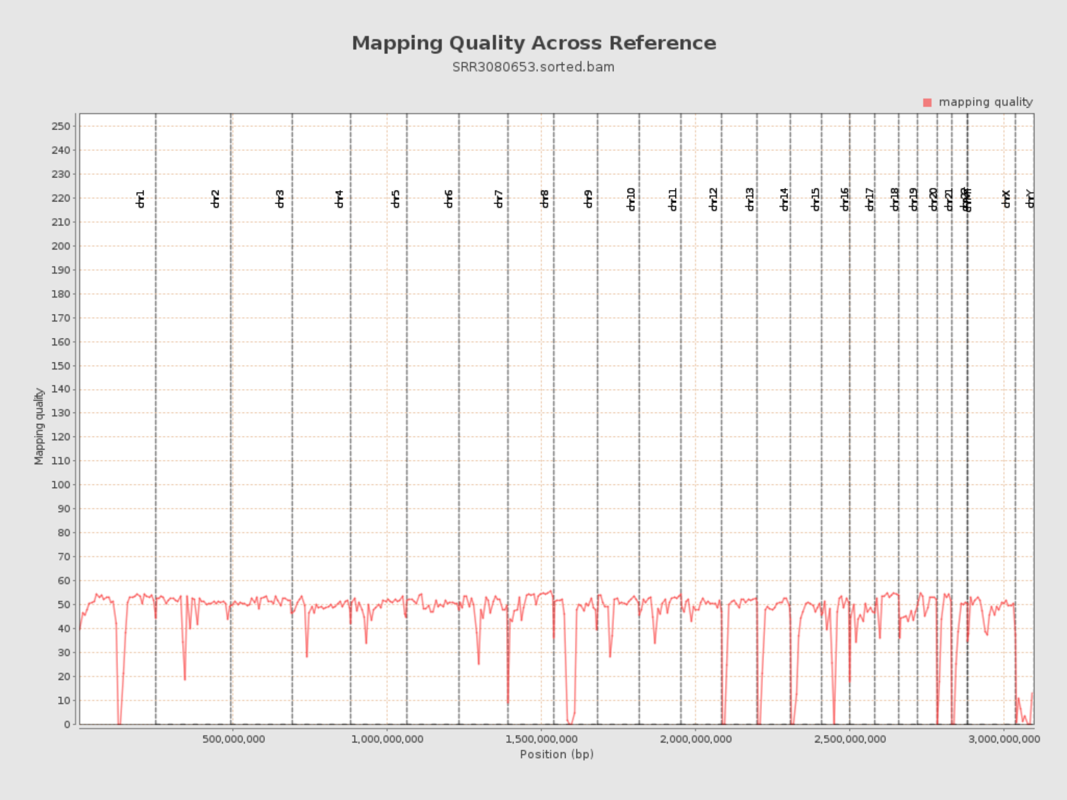
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram