Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:48:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013329.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_SRR6013329 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013329.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:48:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013329.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,249,229
Mapped reads	1,015,350 / 81.28%
Unmapped reads	233,879 / 18.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,319 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	16,882 / 1.35%
Duplication rate	1.43%
Clipped reads	382,545 / 30.62%

2.2. ACGT Content

Number/percentage of A's	21,269,159 / 30.71%
Number/percentage of C's	11,531,144 / 16.65%
Number/percentage of T's	21,163,101 / 30.56%
Number/percentage of G's	15,264,867 / 22.04%
Number/percentage of N's	27,032 / 0.04%
GC Percentage	38.69%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.181

2.4. Mapping Quality

Mean Mapping Quality	49.33

2.5. Mismatches and indels

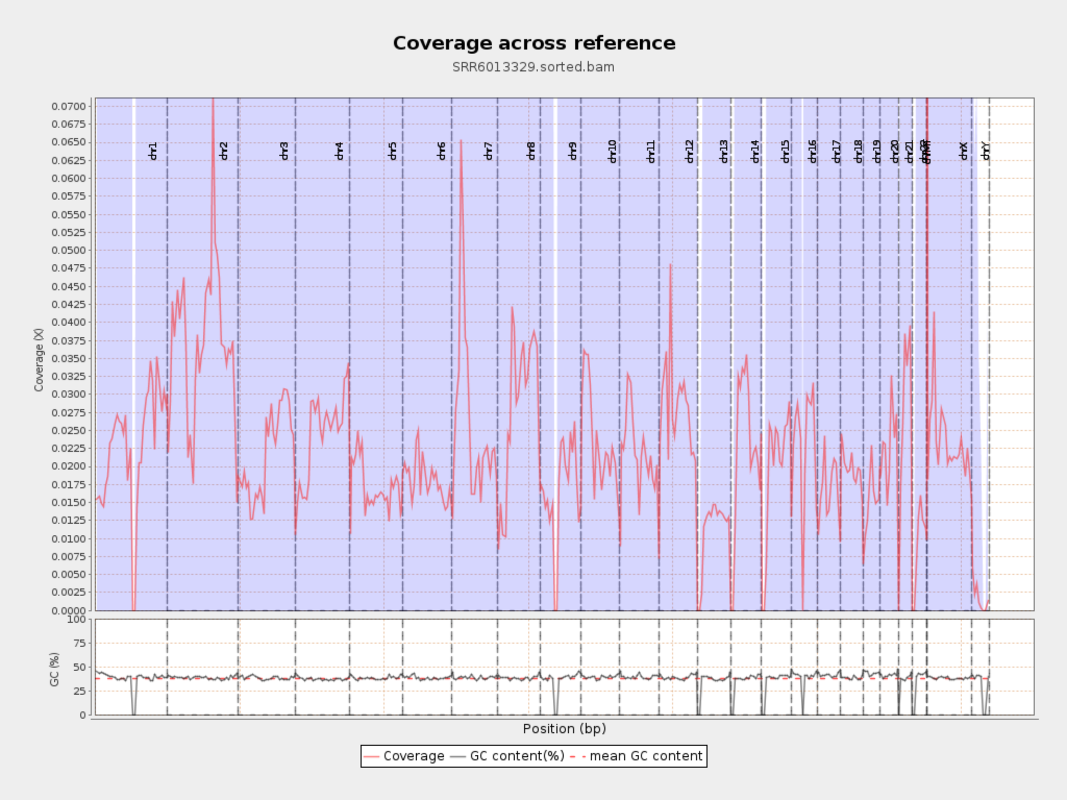
General error rate	1.13%
Mismatches	778,564
Insertions	4,381
Mapped reads with at least one insertion	0.43%
Deletions	19,986
Mapped reads with at least one deletion	1.94%
Homopolymer indels	49.79%

2.6. Chromosome stats

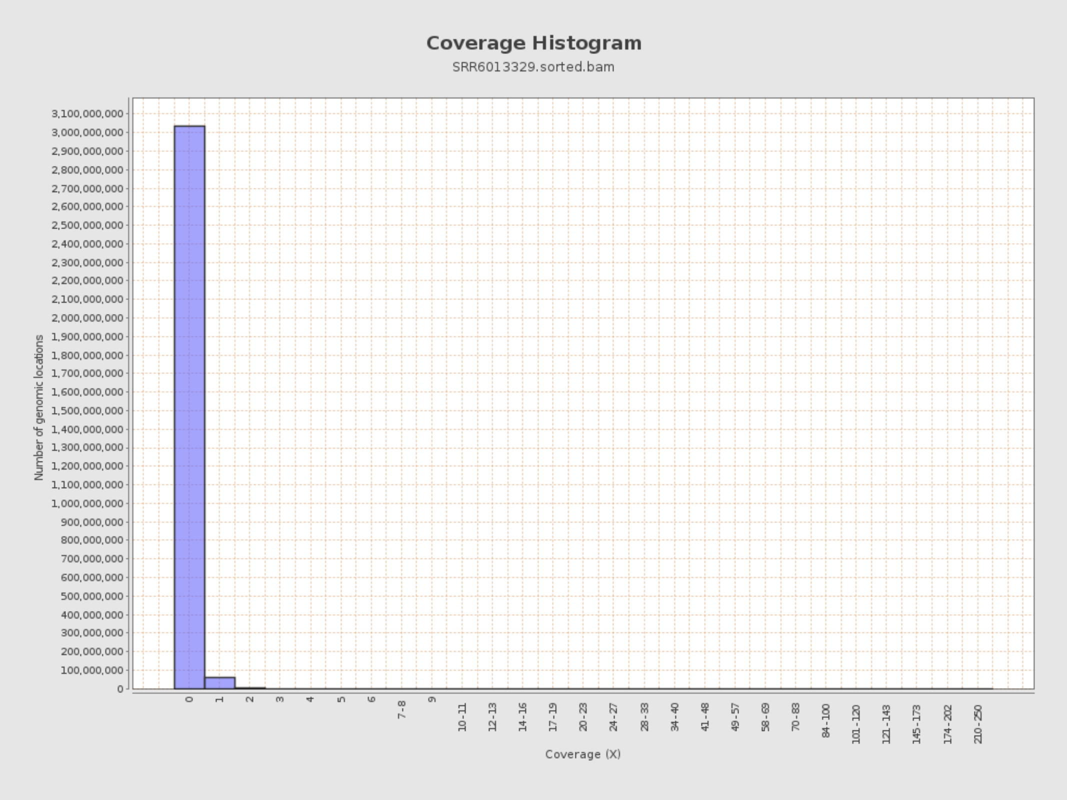
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5668848	0.0227	0.2393
chr2	243199373	9167125	0.0377	0.2253
chr3	198022430	4302433	0.0217	0.1583
chr4	191154276	4663231	0.0244	0.1696
chr5	180915260	3131983	0.0173	0.1406
chr6	171115067	3121654	0.0182	0.1531
chr7	159138663	4214658	0.0265	0.2254

chr8	146364022	4158376	0.0284	0.2406
chr9	141213431	2336515	0.0165	0.1468
chr10	135534747	3213277	0.0237	0.1817
chr11	135006516	2961873	0.0219	0.1738
chr12	133851895	3797854	0.0284	0.1837
chr13	115169878	1267814	0.011	0.1112
chr14	107349540	2418710	0.0225	0.1642
chr15	102531392	1996329	0.0195	0.1524
chr16	90354753	2041277	0.0226	0.1643
chr17	81195210	1355693	0.0167	0.1457
chr18	78077248	1554307	0.0199	0.2043
chr19	59128983	912730	0.0154	0.1511
chr20	63025520	1423989	0.0226	0.1626
chr21	48129895	1338296	0.0278	0.185
chr22	51304566	479942	0.0094	0.1036
chrMT	16571	6548	0.3951	0.781
chrX	155270560	3656238	0.0235	0.17
chrY	59373566	99539	0.0017	0.0457

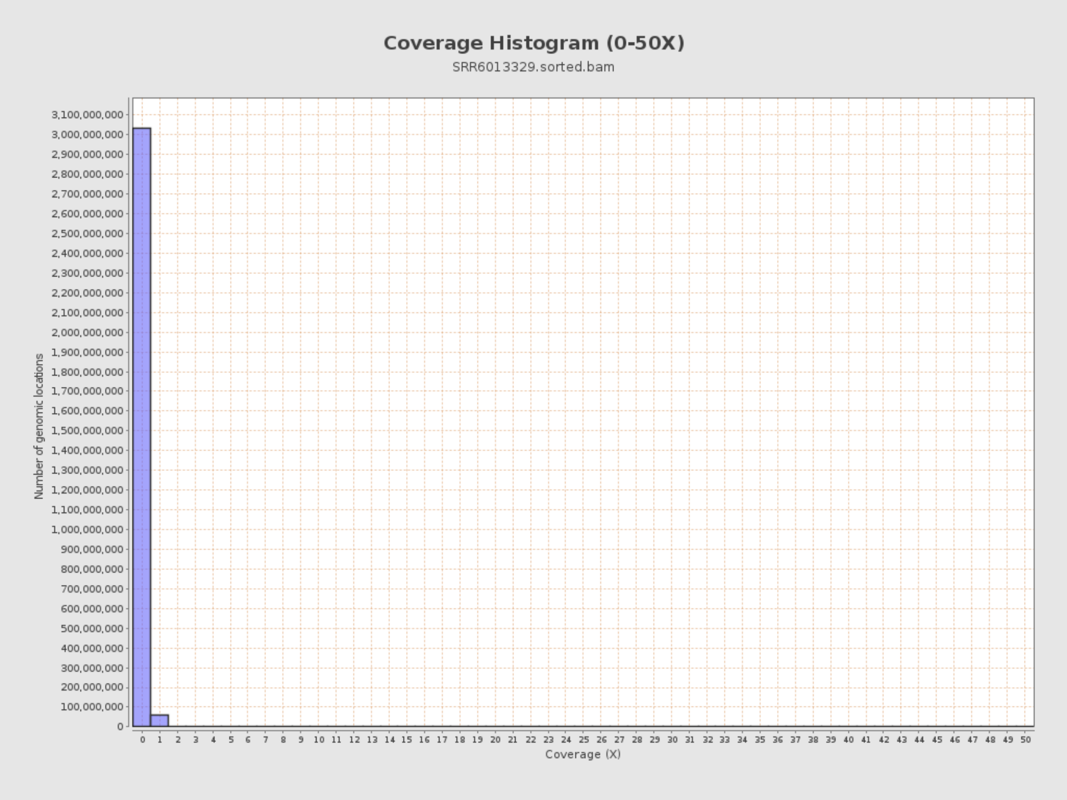
3. Results : Coverage across reference



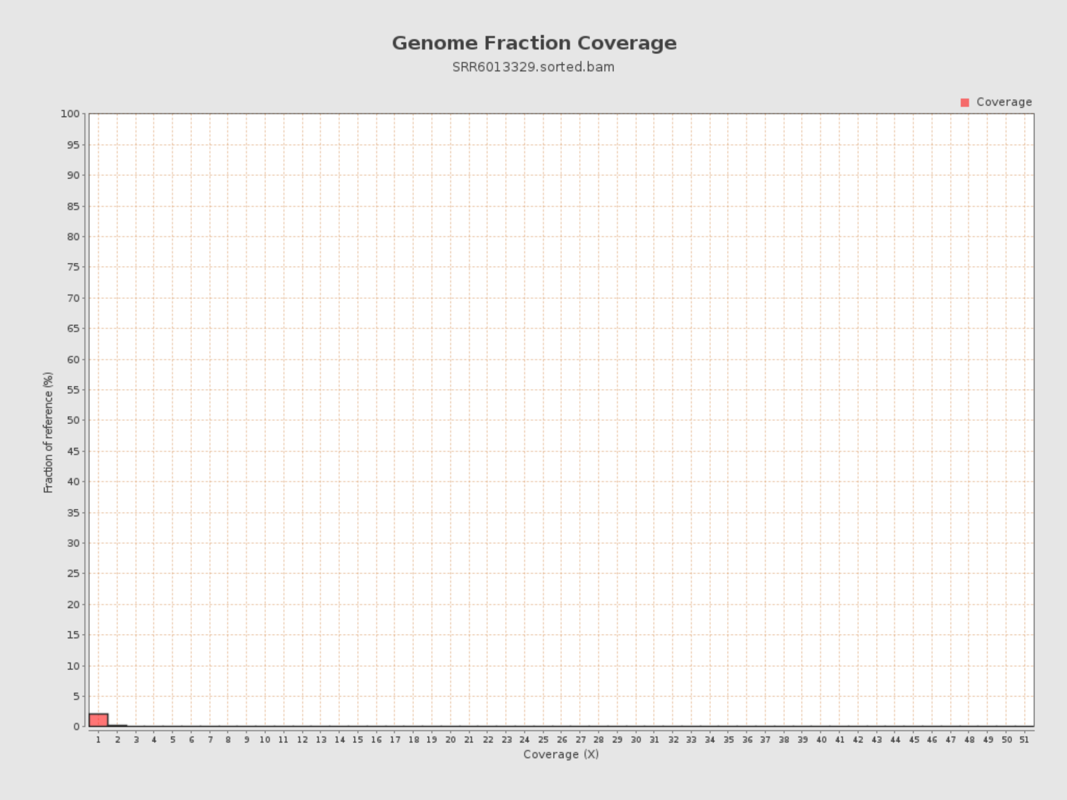
4. Results : Coverage Histogram



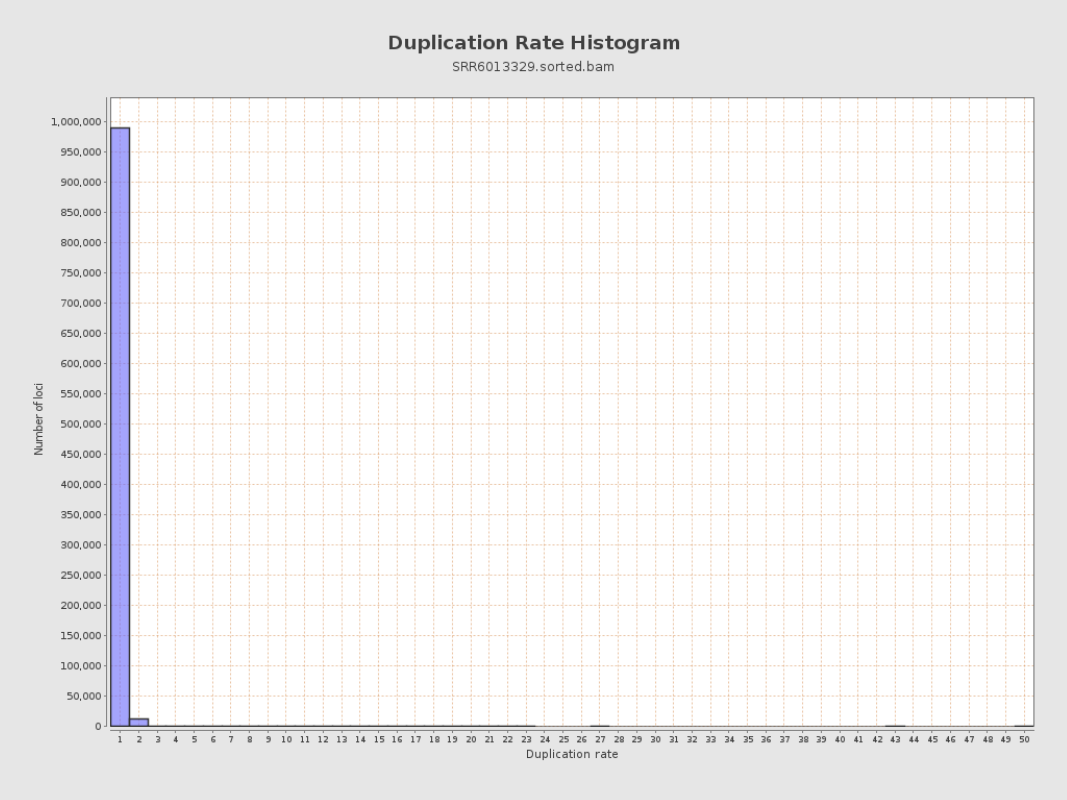
5. Results : Coverage Histogram (0-50X)



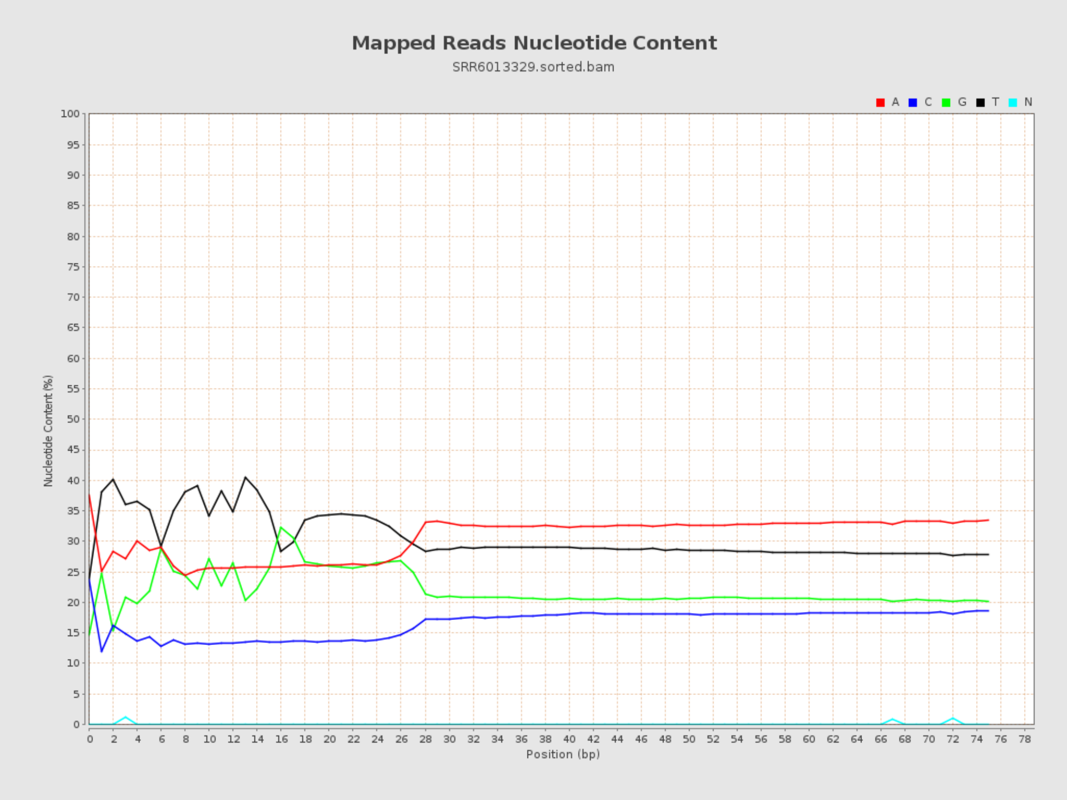
6. Results : Genome Fraction Coverage



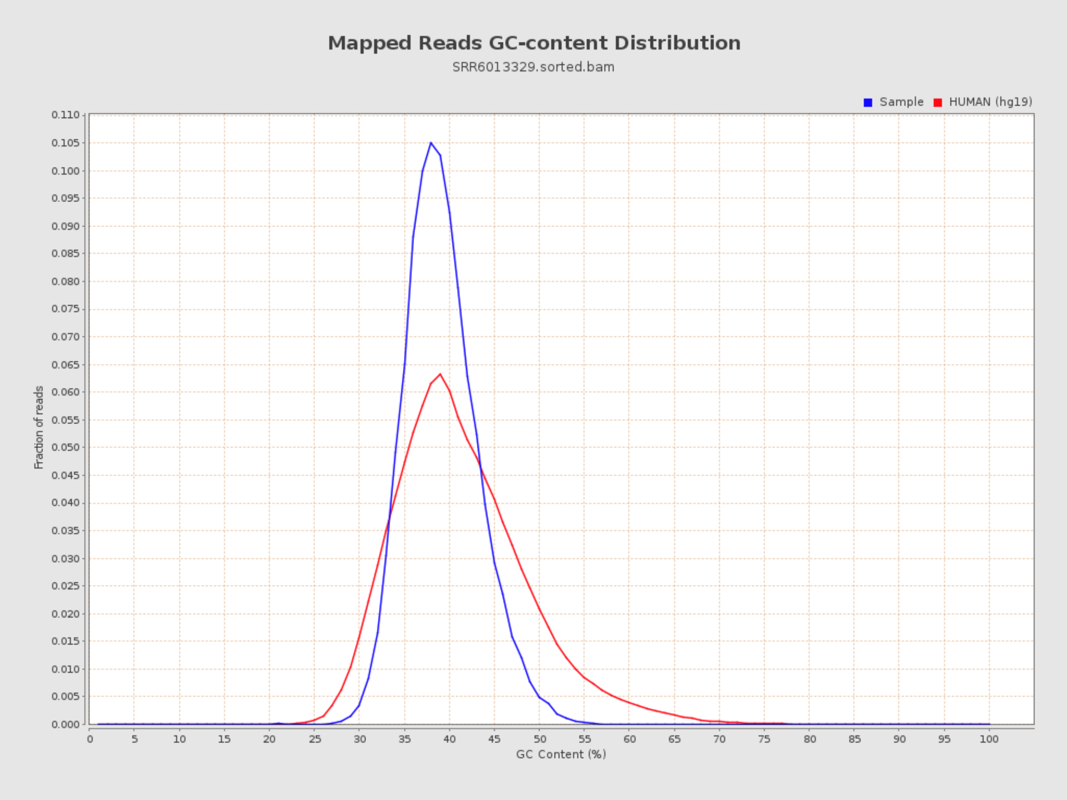
7. Results : Duplication Rate Histogram



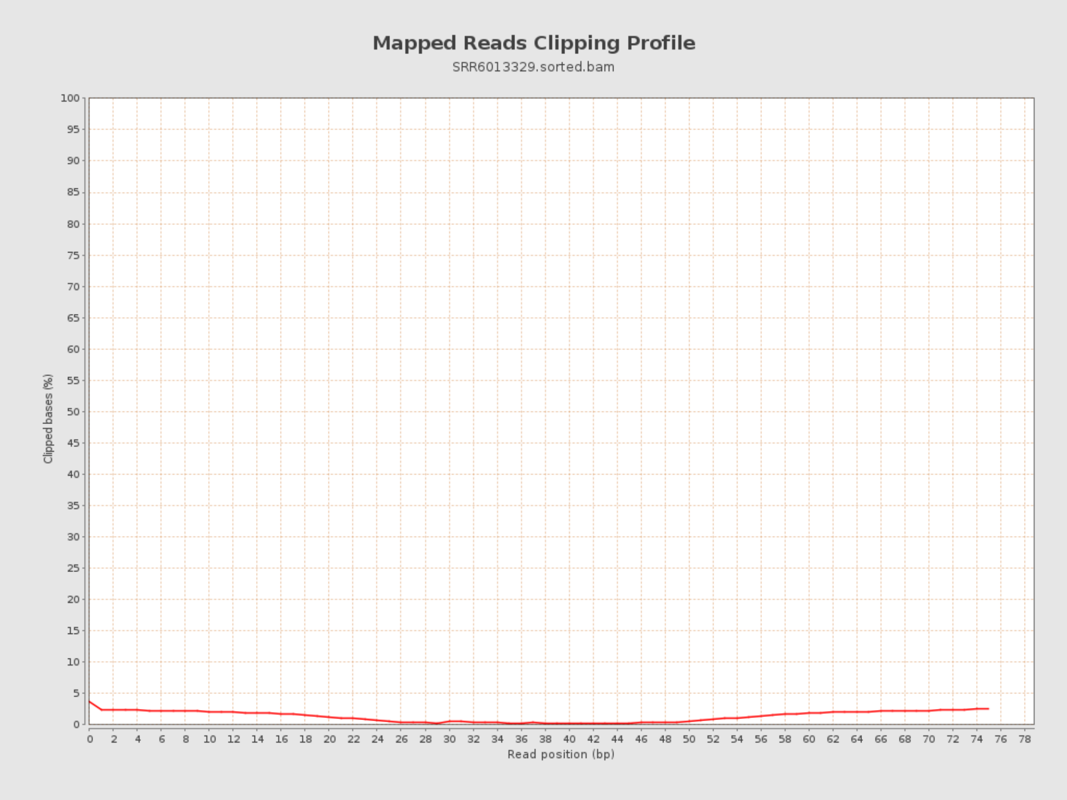
8. Results : Mapped Reads Nucleotide Content



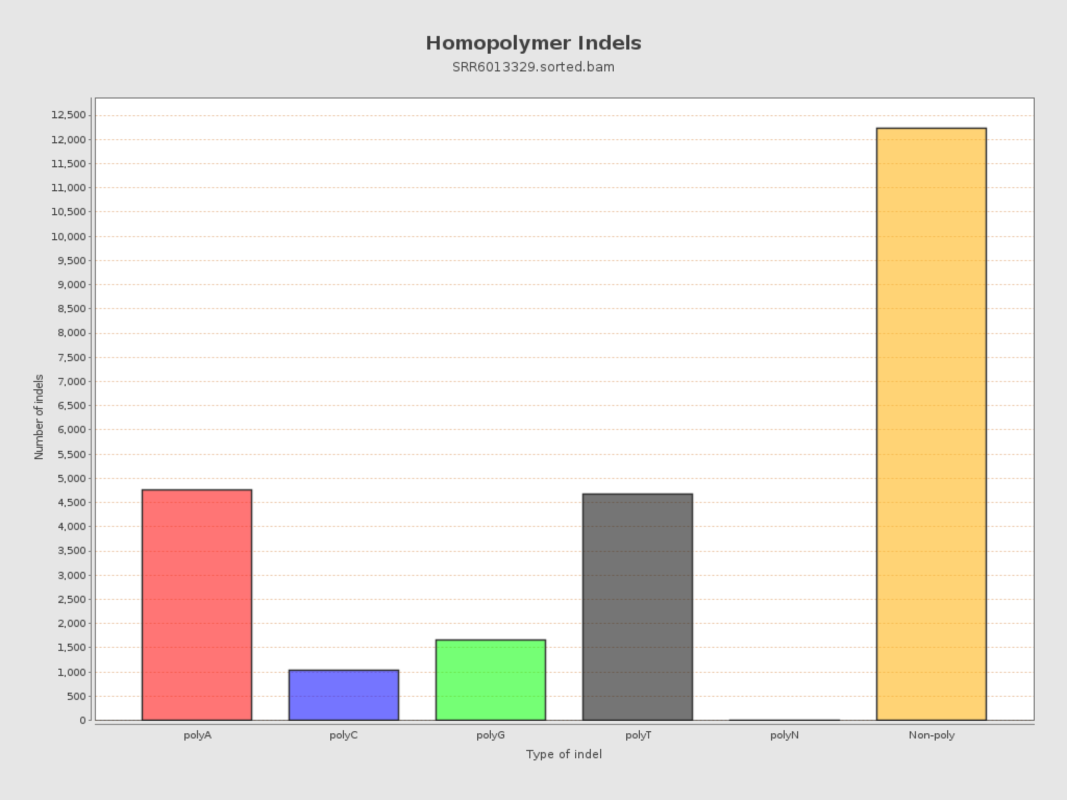
9. Results : Mapped Reads GC-content Distribution



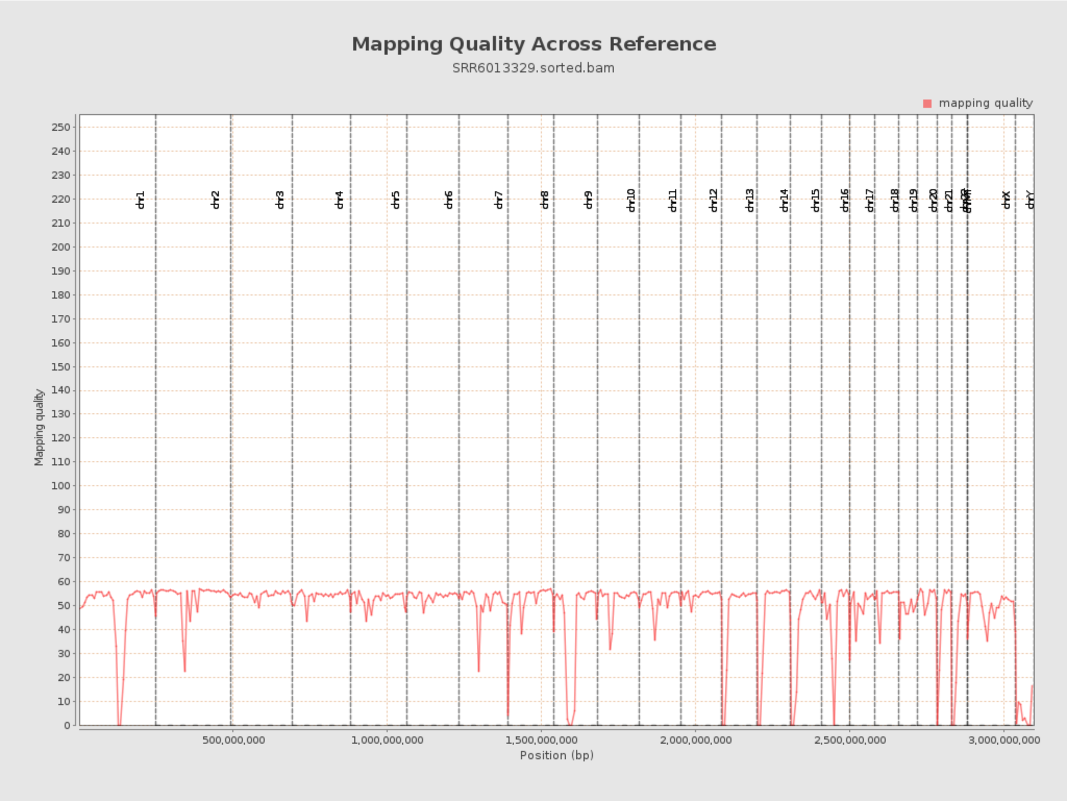
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram