Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:03:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013335.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_SRR6013335 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013335.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:03:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013335.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,882,101
Mapped reads	2,499,035 / 86.71%
Unmapped reads	383,066 / 13.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,402 / 1.26%
Read min/max/mean length	30 / 76 / 76.44
Duplicated reads (estimated)	316,128 / 10.97%
Duplication rate	9.31%
Clipped reads	1,213,865 / 42.12%

2.2. ACGT Content

Number/percentage of A's	45,478,253 / 27.59%
Number/percentage of C's	31,373,806 / 19.03%
Number/percentage of T's	51,245,748 / 31.09%
Number/percentage of G's	36,740,185 / 22.29%
Number/percentage of N's	18,719 / 0.01%
GC Percentage	41.32%

2.3. Coverage

Mean	0.0533

Standard Deviation	0.5118

2.4. Mapping Quality

Mean Mapping Quality	37.88

2.5. Mismatches and indels

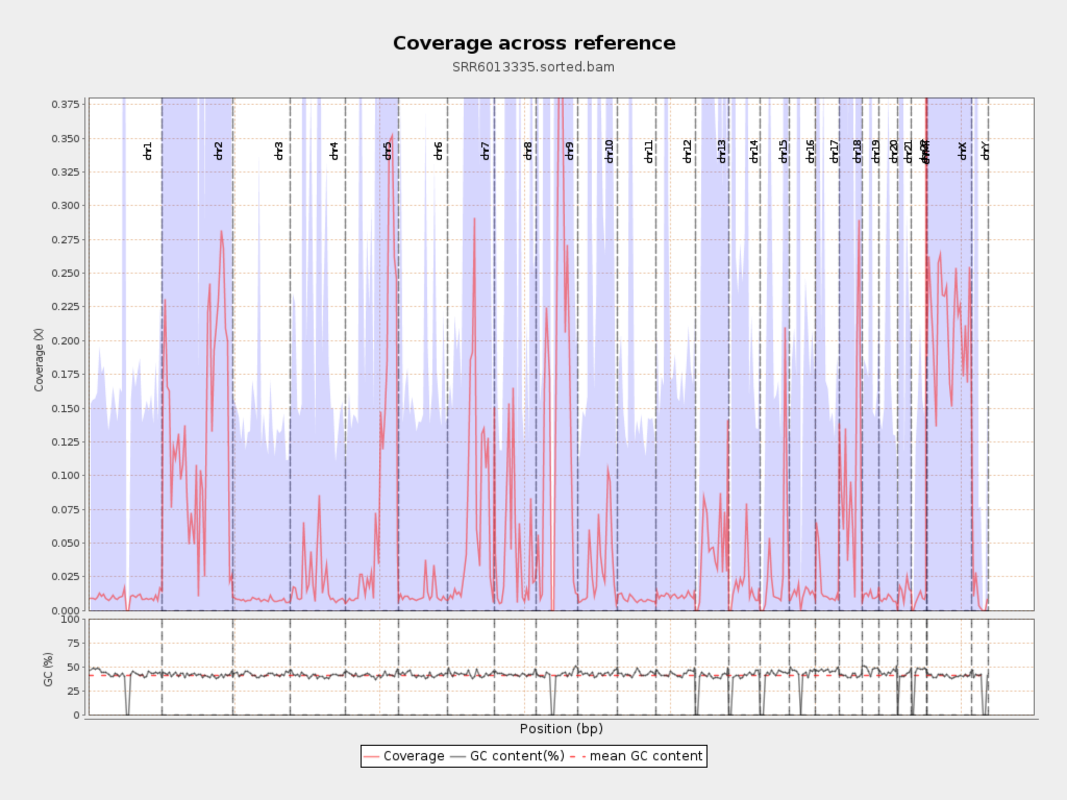
General error rate	0.73%
Mismatches	1,169,835
Insertions	11,248
Mapped reads with at least one insertion	0.45%
Deletions	36,273
Mapped reads with at least one deletion	1.44%
Homopolymer indels	45.15%

2.6. Chromosome stats

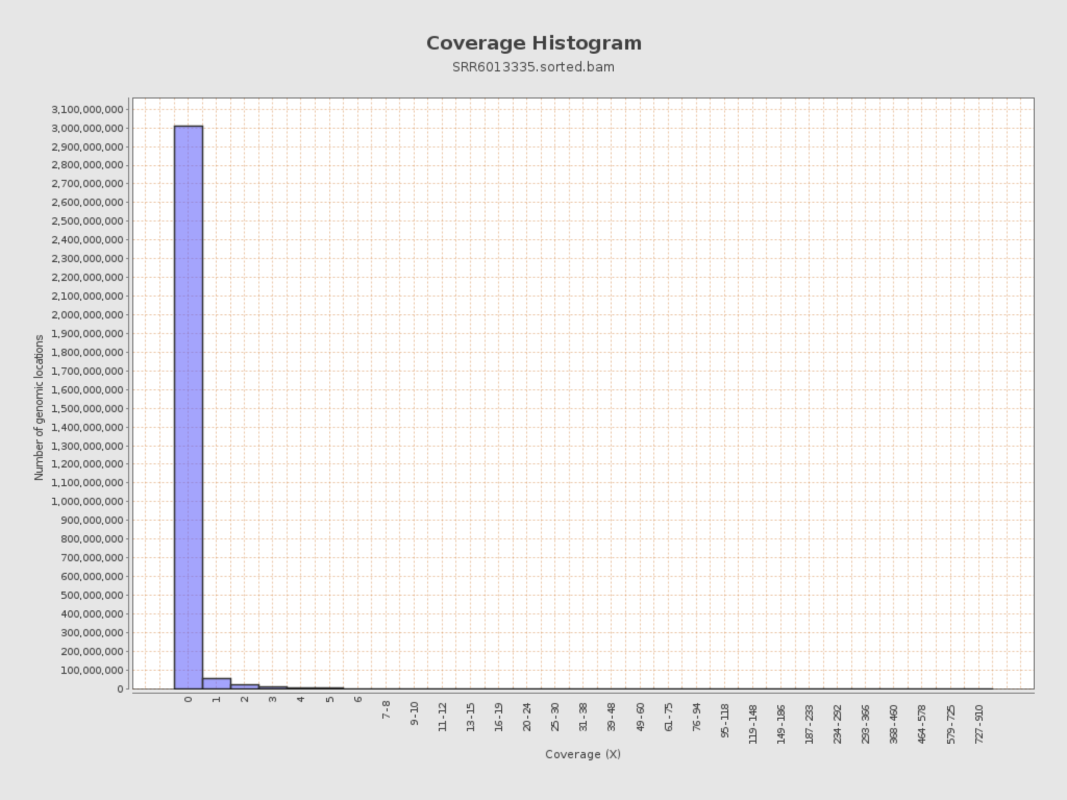
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2390282	0.0096	0.2265
chr2	243199373	33238954	0.1367	0.8272
chr3	198022430	1581227	0.008	0.1426
chr4	191154276	3922853	0.0205	0.4023
chr5	180915260	16380320	0.0905	0.5236
chr6	171115067	1998966	0.0117	0.1839
chr7	159138663	11943279	0.075	0.4656

chr8	146364022	6522606	0.0446	0.374
chr9	141213431	21641018	0.1533	0.9084
chr10	135534747	4483645	0.0331	0.639
chr11	135006516	1131021	0.0084	0.2159
chr12	133851895	1497083	0.0112	0.2963
chr13	115169878	5158542	0.0448	0.3559
chr14	107349540	1927662	0.018	0.4805
chr15	102531392	3543673	0.0346	0.317
chr16	90354753	1110008	0.0123	0.3678
chr17	81195210	1554041	0.0191	0.2519
chr18	78077248	8425274	0.1079	1.0508
chr19	59128983	670458	0.0113	0.2866
chr20	63025520	538663	0.0085	0.2007
chr21	48129895	693645	0.0144	0.4222
chr22	51304566	381797	0.0074	0.1355
chrMT	16571	66117	3.9899	3.6763
chrX	155270560	33379474	0.215	0.8293
chrY	59373566	740698	0.0125	0.3748

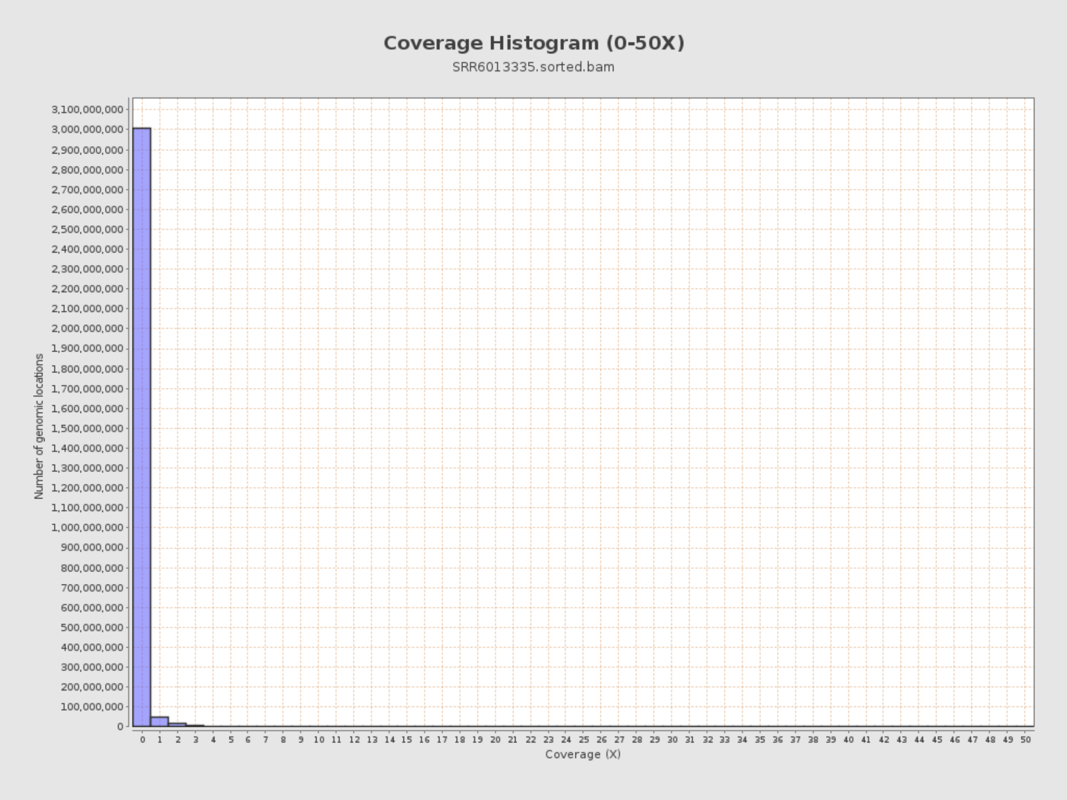
3. Results : Coverage across reference



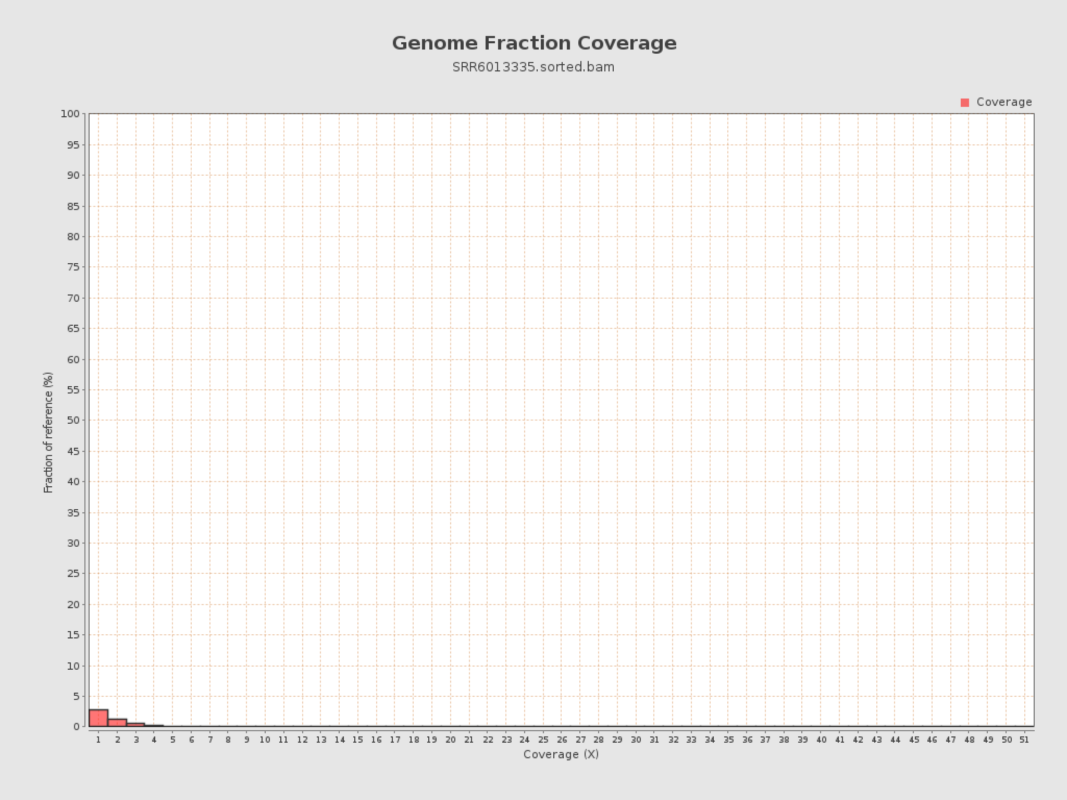
4. Results : Coverage Histogram



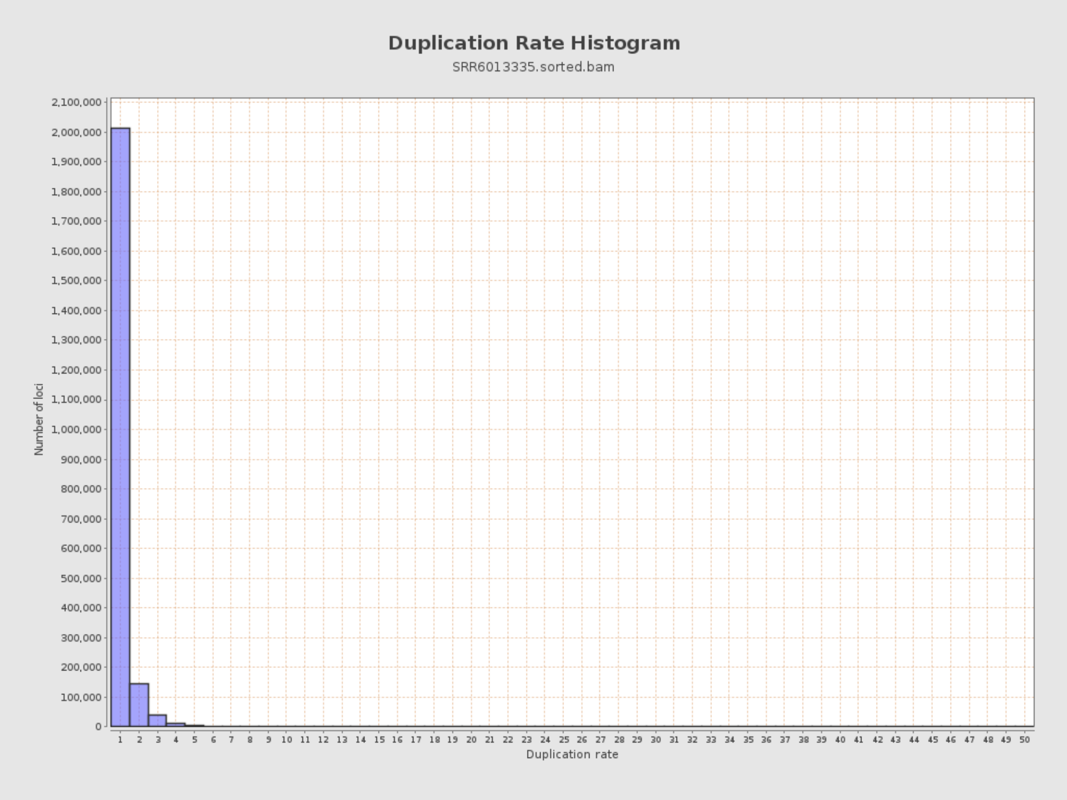
5. Results : Coverage Histogram (0-50X)



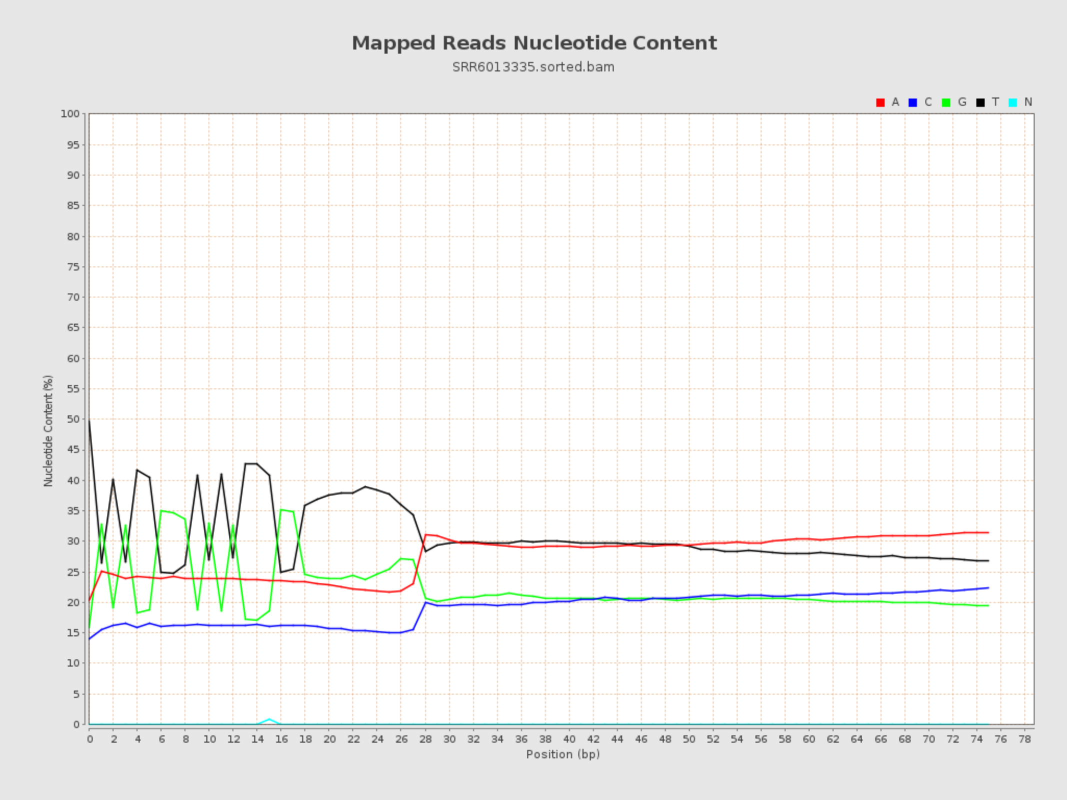
6. Results : Genome Fraction Coverage



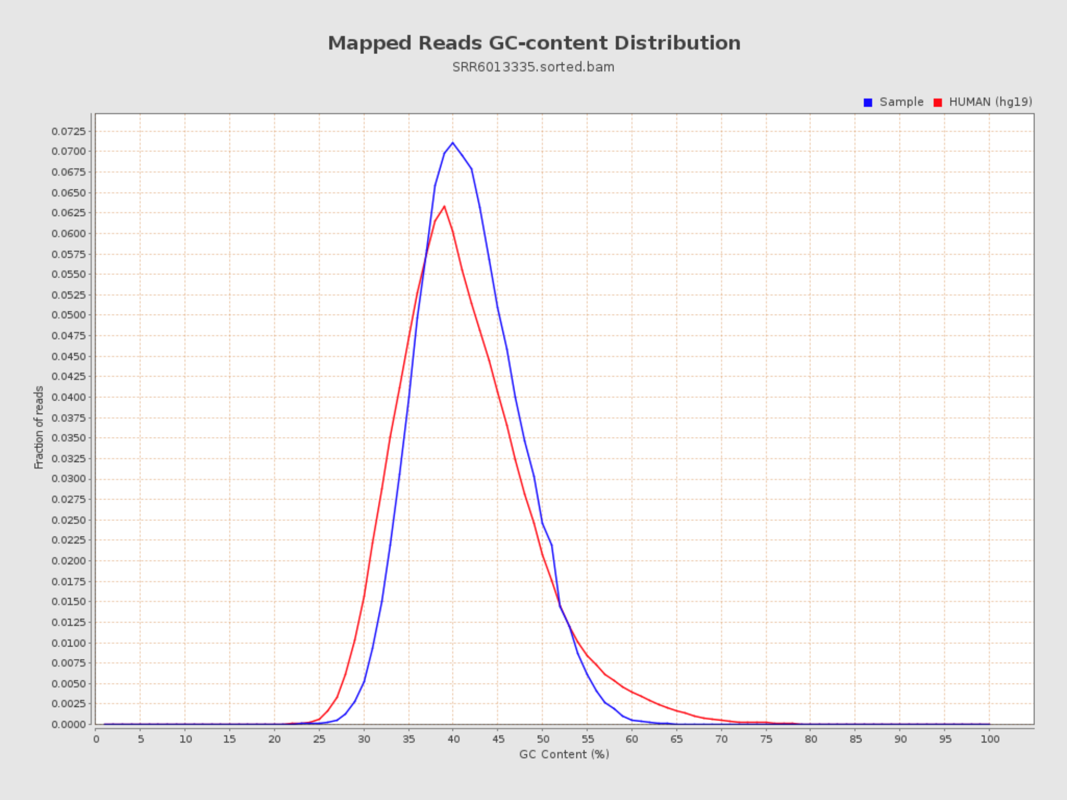
7. Results : Duplication Rate Histogram



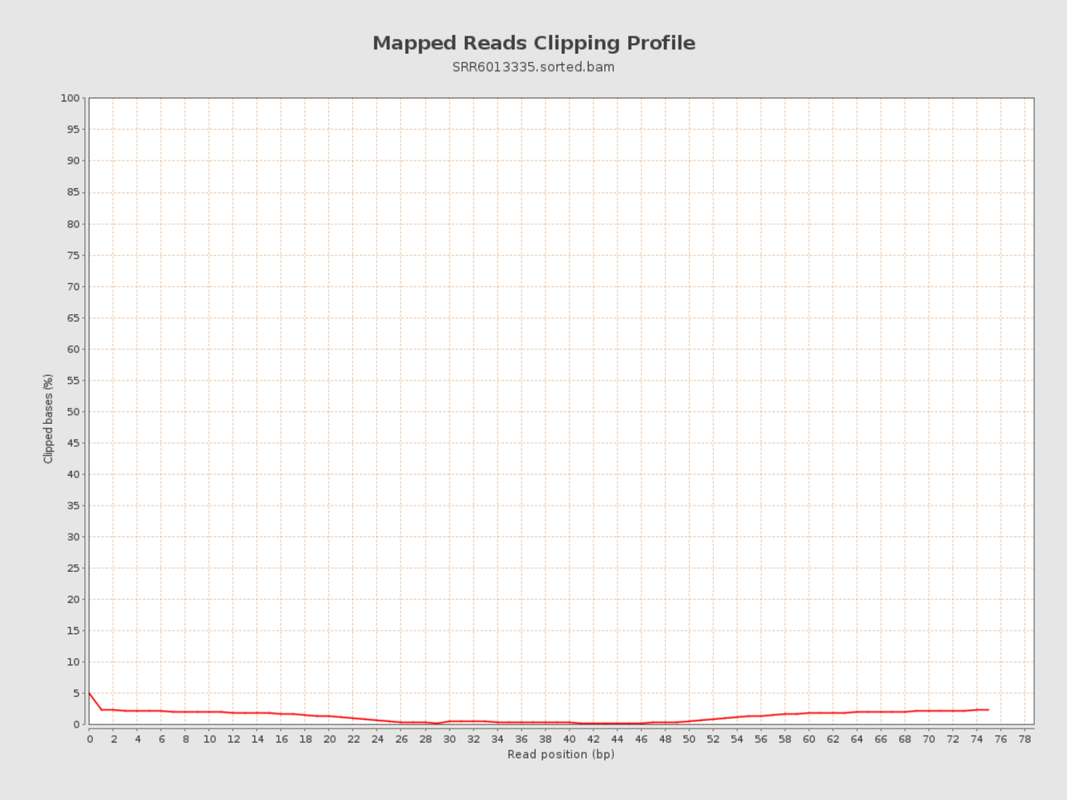
8. Results : Mapped Reads Nucleotide Content



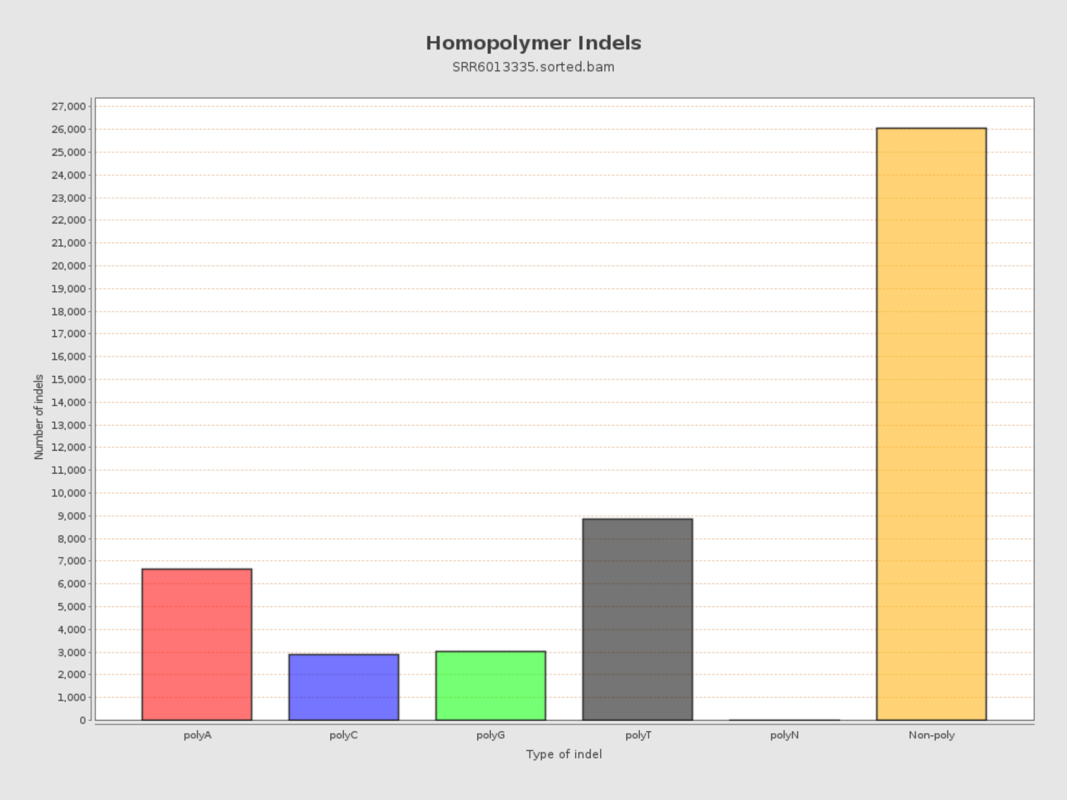
9. Results : Mapped Reads GC-content Distribution



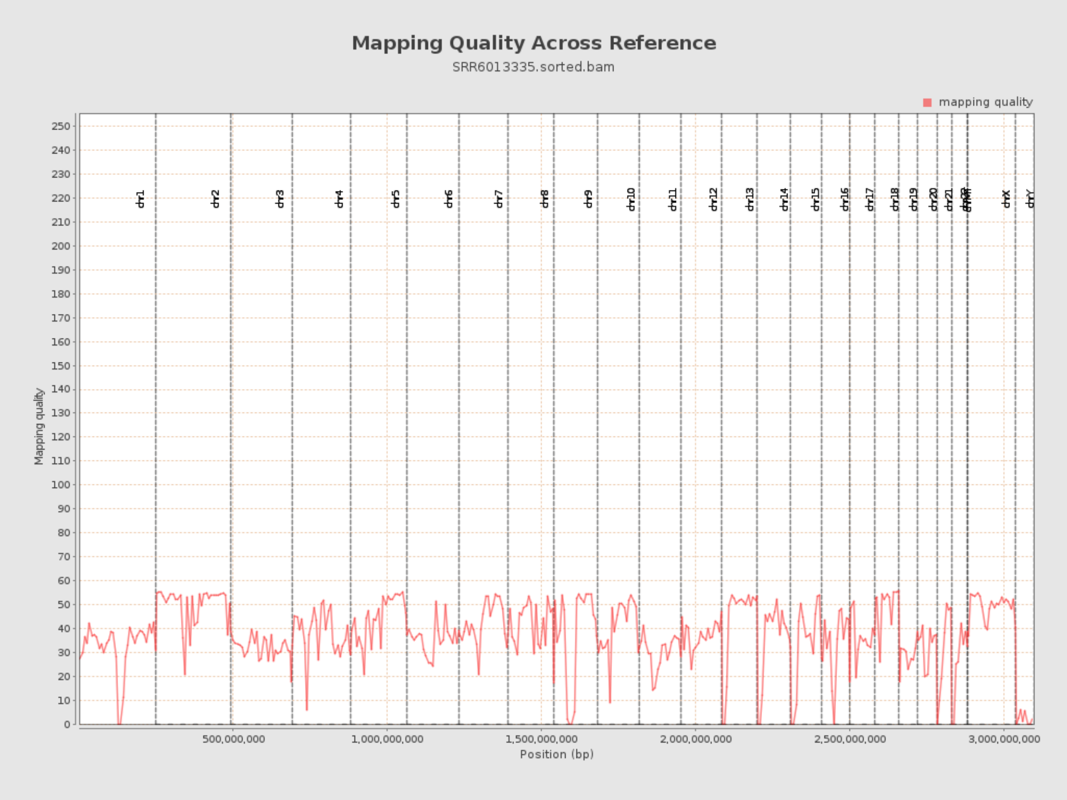
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram