Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 17:00:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153331.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_SRR1153331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153331.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 17:00:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153331.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	43,075,792
Mapped reads	42,790,107 / 99.34%
Unmapped reads	285,685 / 0.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	226,684 / 0.53%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	28,700,719 / 66.63%
Duplication rate	60%
Clipped reads	6,422,293 / 14.91%

2.2. ACGT Content

Number/percentage of A's	1,093,404,919 / 26.4%
Number/percentage of C's	971,007,131 / 23.45%
Number/percentage of T's	1,125,611,813 / 27.18%
Number/percentage of G's	949,963,360 / 22.94%
Number/percentage of N's	1,331,934 / 0.03%
GC Percentage	46.39%

2.3. Coverage

Mean	1.3379

Standard Deviation	14.3429

2.4. Mapping Quality

Mean Mapping Quality	50.68

2.5. Mismatches and indels

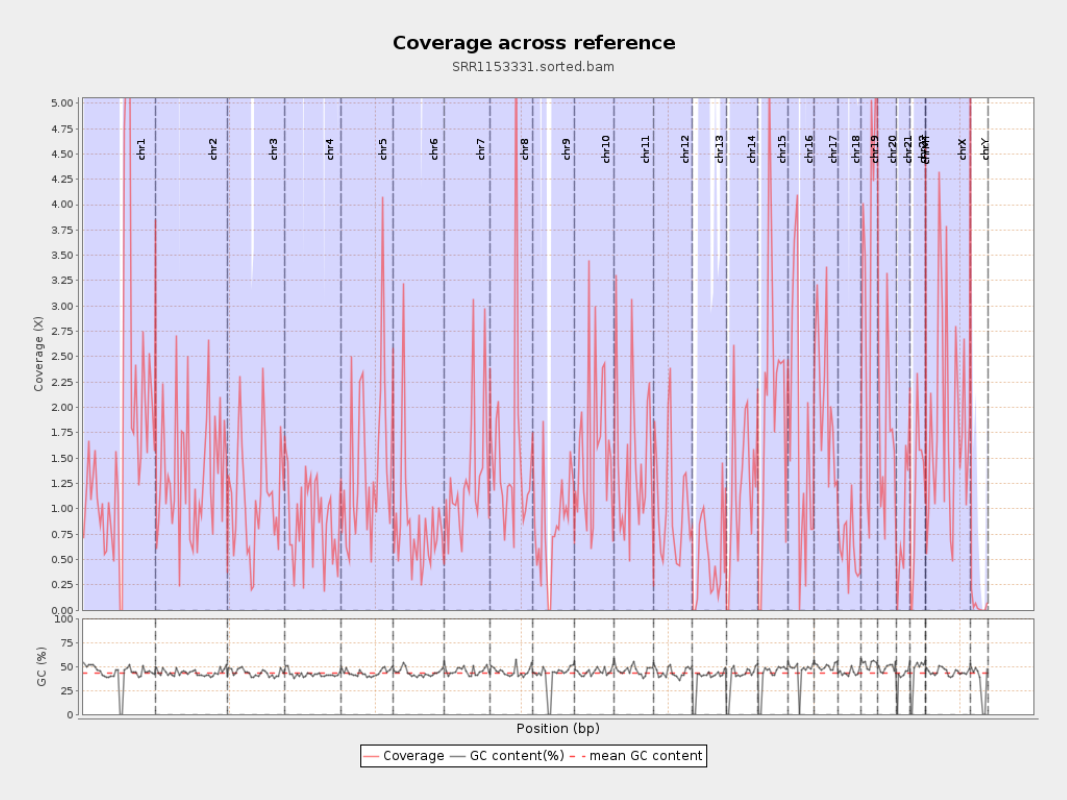
General error rate	0.27%
Mismatches	10,827,144
Insertions	295,828
Mapped reads with at least one insertion	0.69%
Deletions	255,218
Mapped reads with at least one deletion	0.59%
Homopolymer indels	49.57%

2.6. Chromosome stats

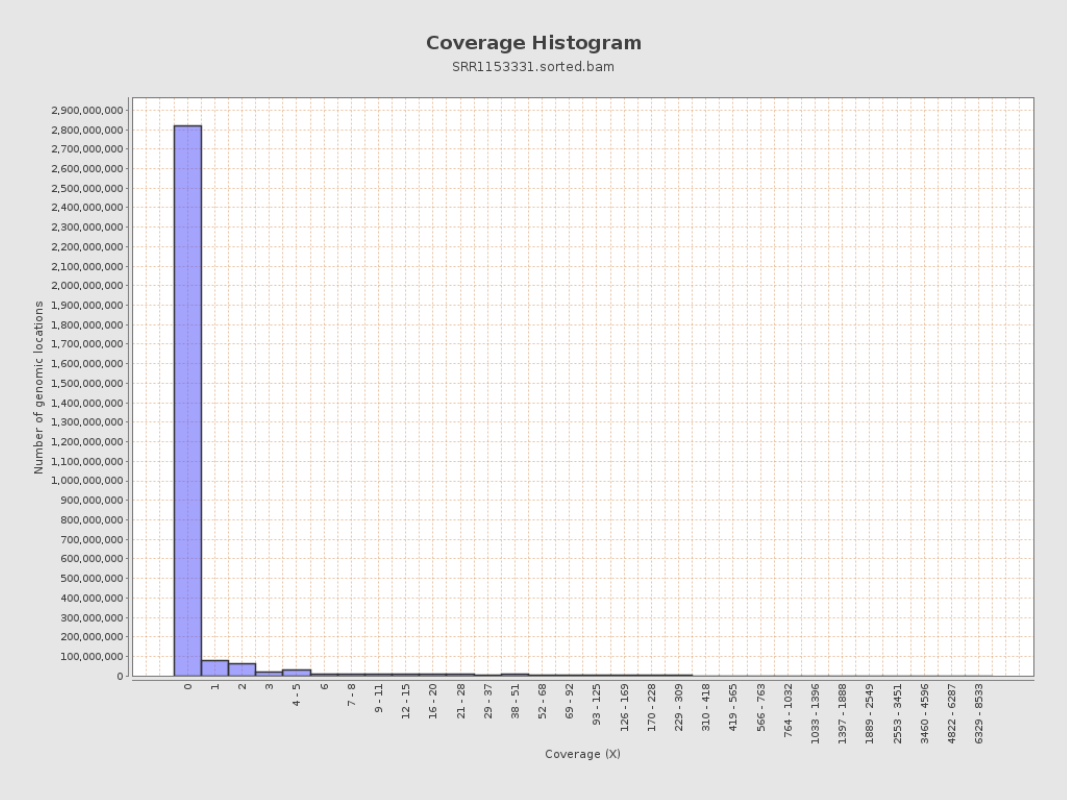
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	429090985	1.7215	16.1679
chr2	243199373	328321375	1.35	13.0353
chr3	198022430	220100083	1.1115	10.8973
chr4	191154276	170549656	0.8922	9.9872
chr5	180915260	267123541	1.4765	16.0085
chr6	171115067	141234285	0.8254	8.9696
chr7	159138663	206290064	1.2963	14.0348

chr8	146364022	225611319	1.5414	24.9367
chr9	141213431	116126473	0.8223	8.9276
chr10	135534747	219147427	1.6169	15.5082
chr11	135006516	198506407	1.4703	13.1173
chr12	133851895	142428230	1.0641	9.8674
chr13	115169878	57628342	0.5004	8.0877
chr14	107349540	131078656	1.221	12.2111
chr15	102531392	206700898	2.016	18.2249
chr16	90354753	151630930	1.6782	15.8956
chr17	81195210	173432392	2.136	16.0325
chr18	78077248	47983183	0.6146	7.4222
chr19	59128983	200327348	3.388	22.8054
chr20	63025520	106210785	1.6852	15.6447
chr21	48129895	44220963	0.9188	10.2074
chr22	51304566	60113295	1.1717	11.611
chrMT	16571	76118	4.5934	13.4003
chrX	155270560	295328910	1.902	19.7347
chrY	59373566	2571873	0.0433	1.5909

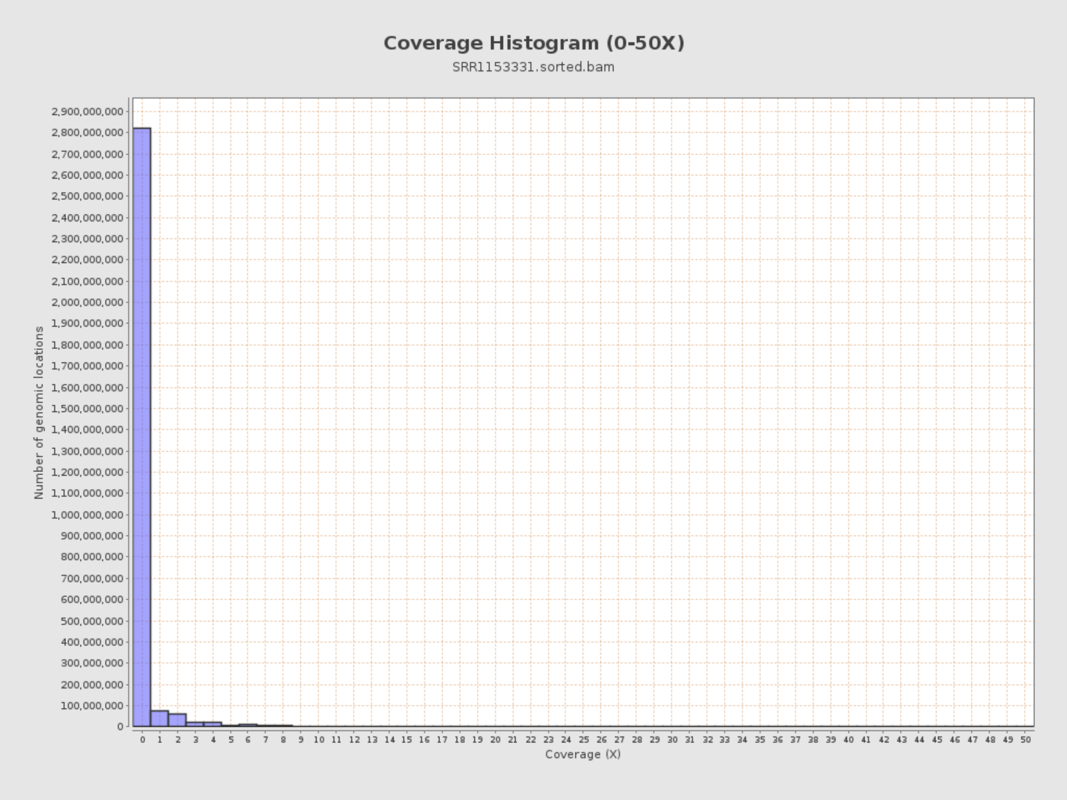
3. Results : Coverage across reference



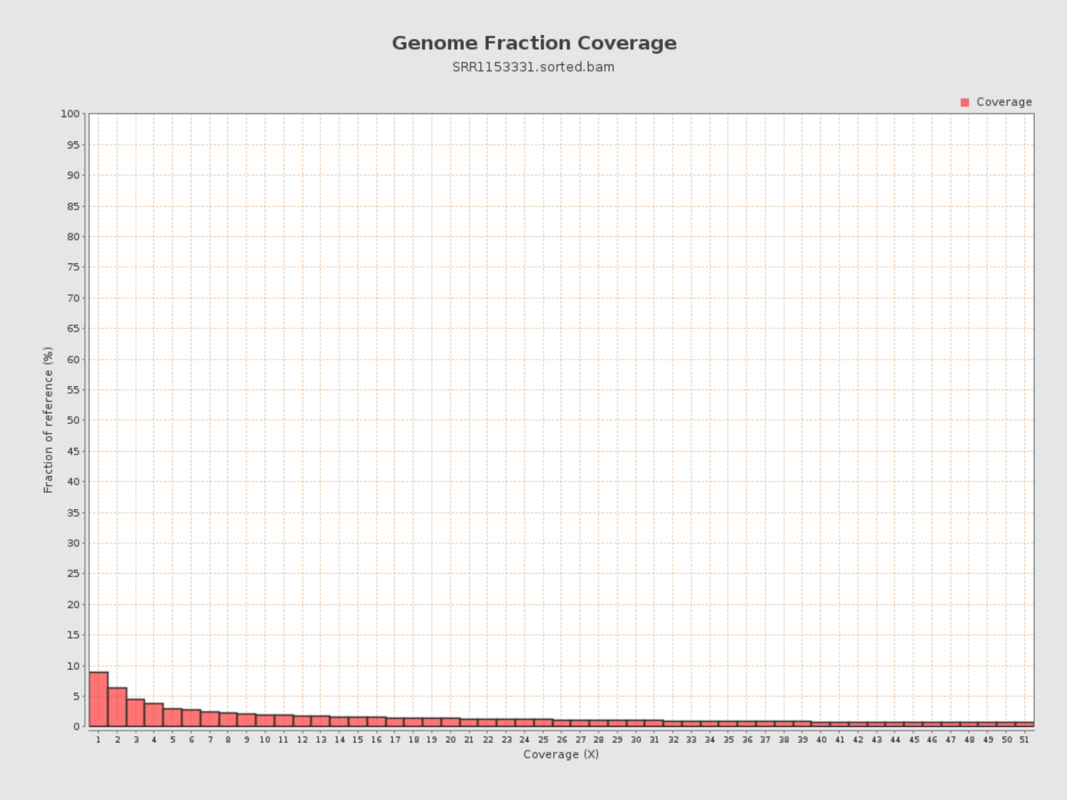
4. Results : Coverage Histogram



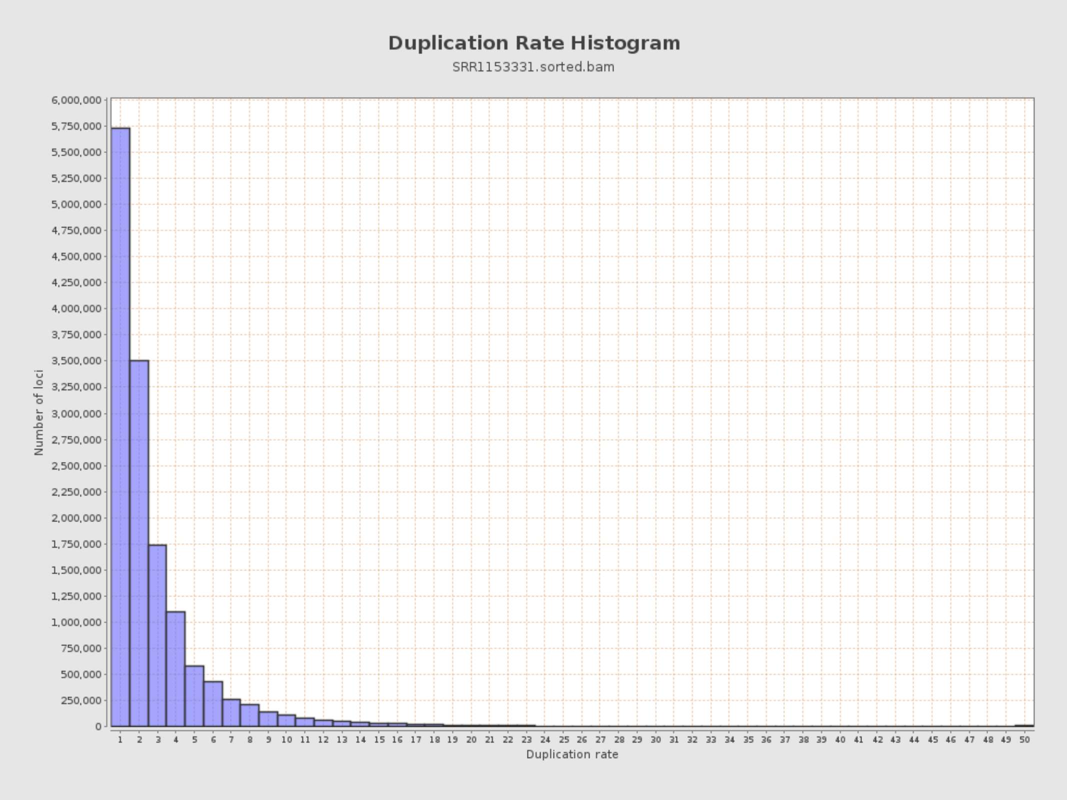
5. Results : Coverage Histogram (0-50X)



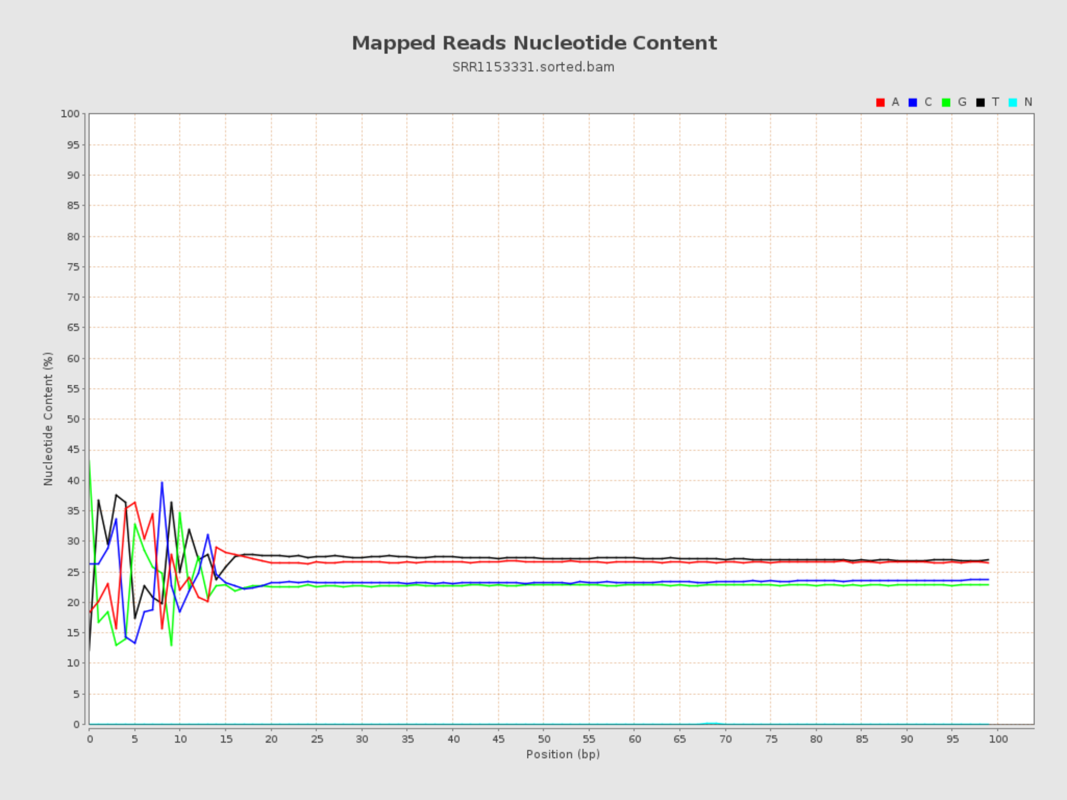
6. Results : Genome Fraction Coverage



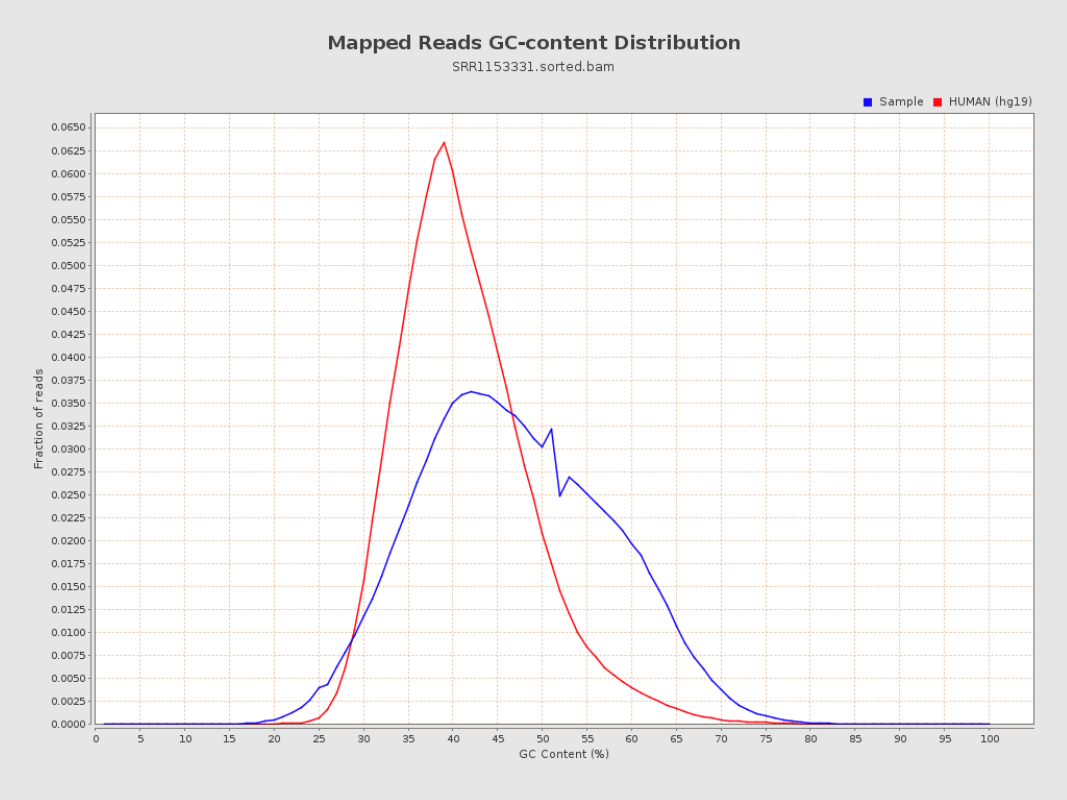
7. Results : Duplication Rate Histogram



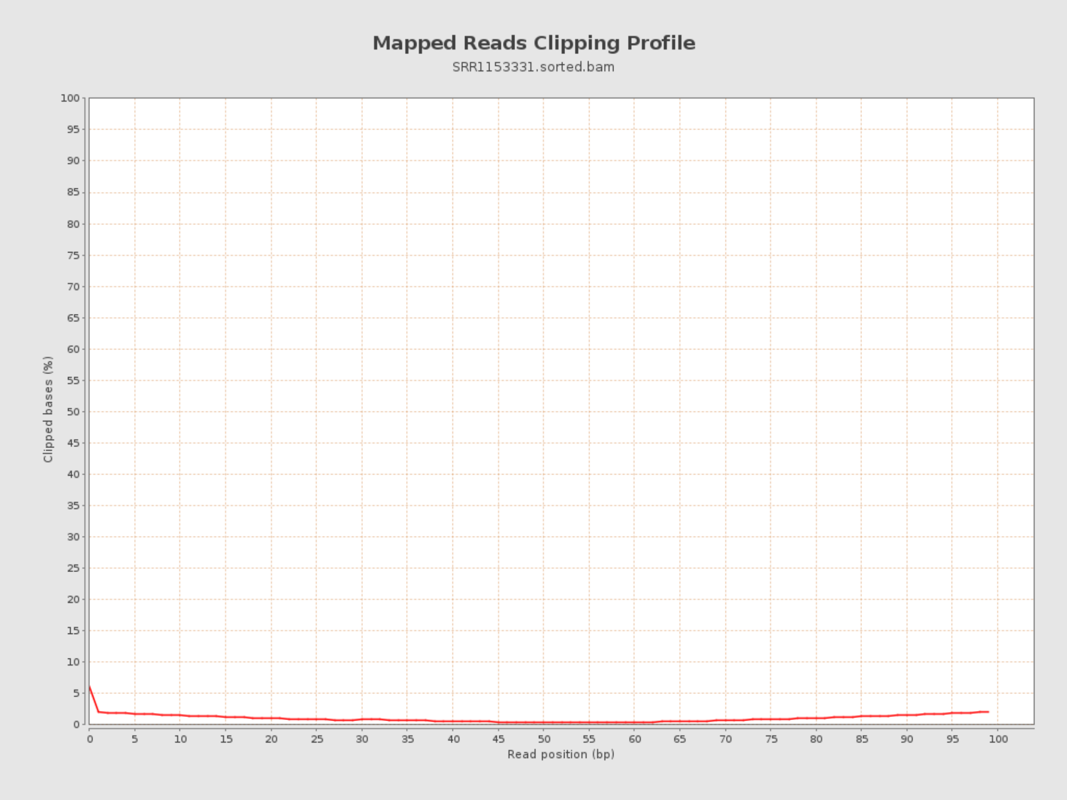
8. Results : Mapped Reads Nucleotide Content



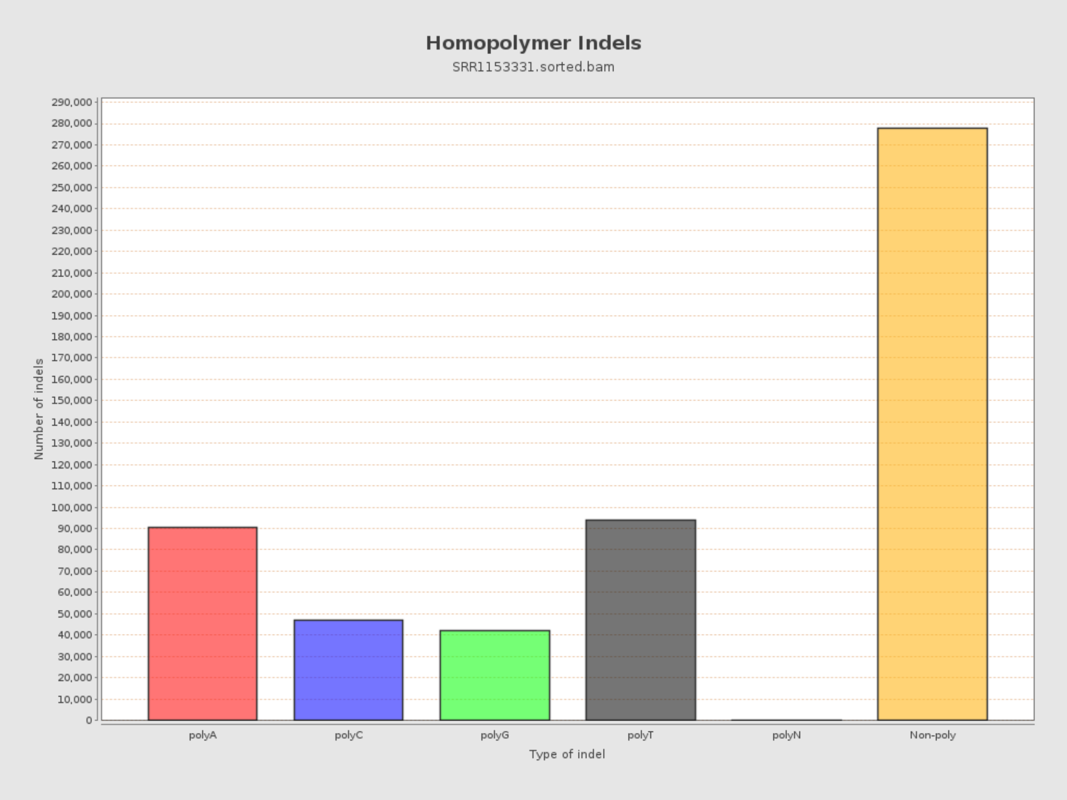
9. Results : Mapped Reads GC-content Distribution



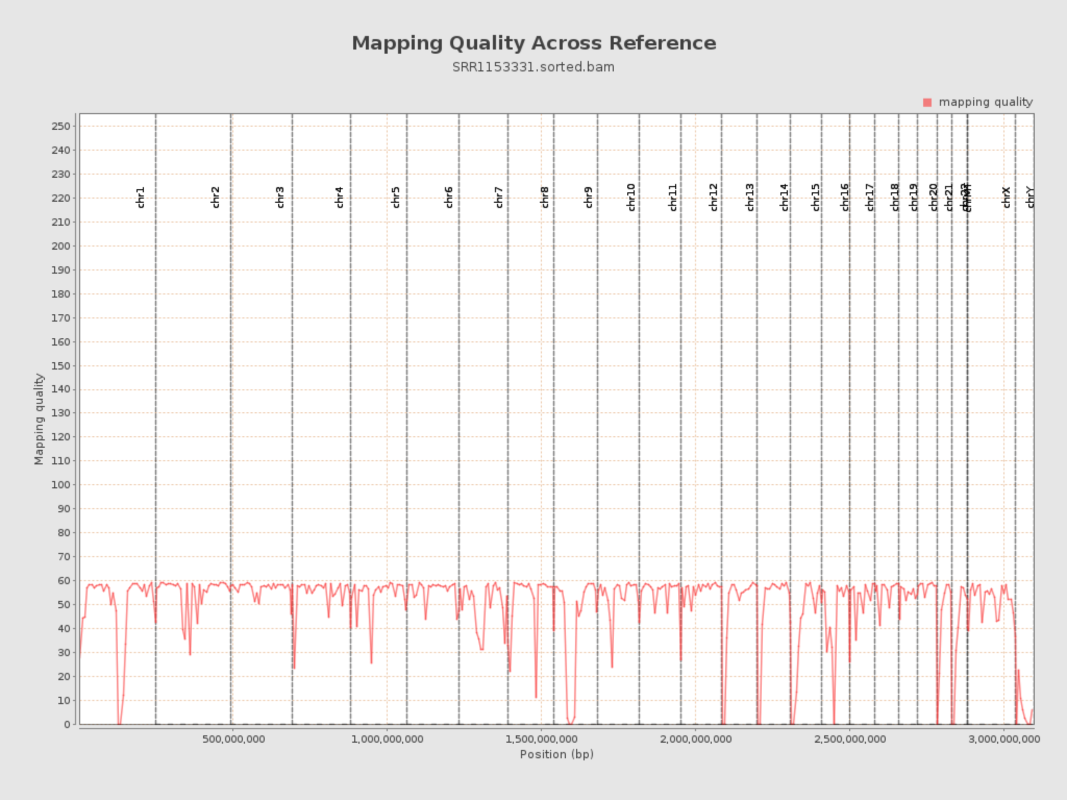
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram