Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 12:15:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153327.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_SRR1153327 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153327.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 12:15:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153327.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	60,998,036
Mapped reads	60,516,961 / 99.21%
Unmapped reads	481,075 / 0.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	323,866 / 0.53%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	42,633,512 / 69.89%
Duplication rate	61.81%
Clipped reads	7,741,794 / 12.69%

2.2. ACGT Content

Number/percentage of A's	1,557,247,350 / 26.44%
Number/percentage of C's	1,378,099,319 / 23.4%
Number/percentage of T's	1,602,032,410 / 27.2%
Number/percentage of G's	1,350,868,700 / 22.93%
Number/percentage of N's	1,982,835 / 0.03%
GC Percentage	46.33%

2.3. Coverage

Mean	1.903

Standard Deviation	21.9623

2.4. Mapping Quality

Mean Mapping Quality	50.53

2.5. Mismatches and indels

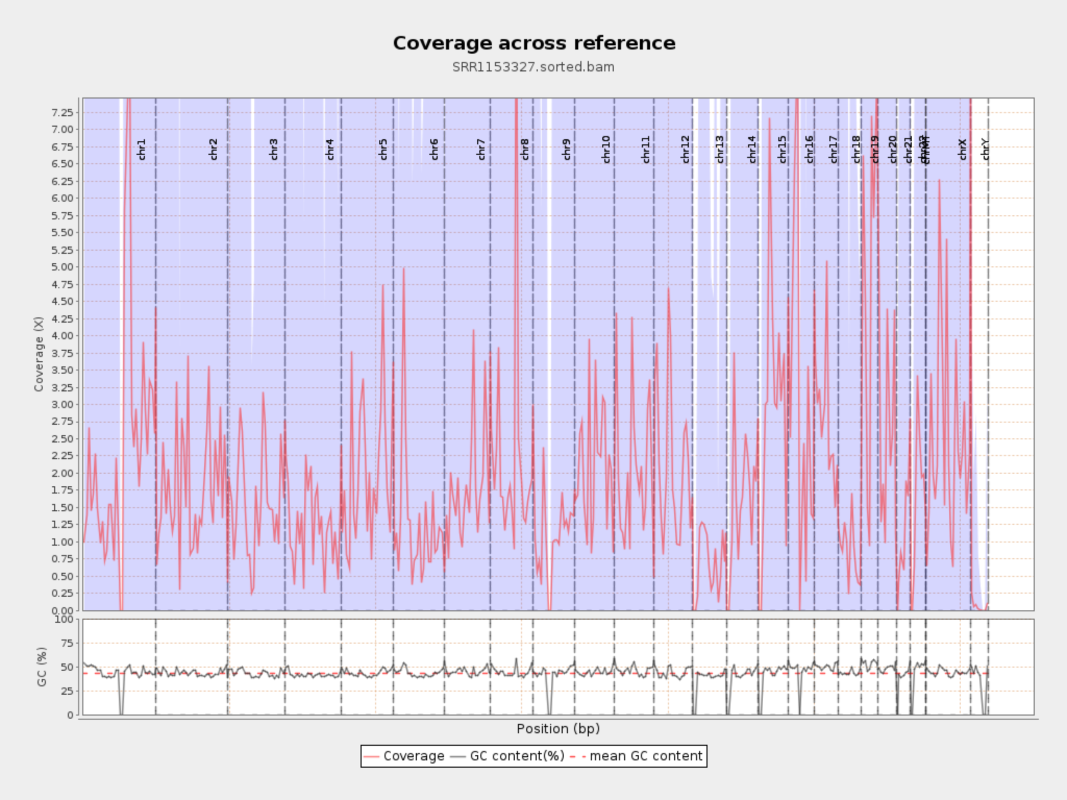
General error rate	0.28%
Mismatches	16,082,948
Insertions	420,173
Mapped reads with at least one insertion	0.69%
Deletions	371,368
Mapped reads with at least one deletion	0.61%
Homopolymer indels	49.81%

2.6. Chromosome stats

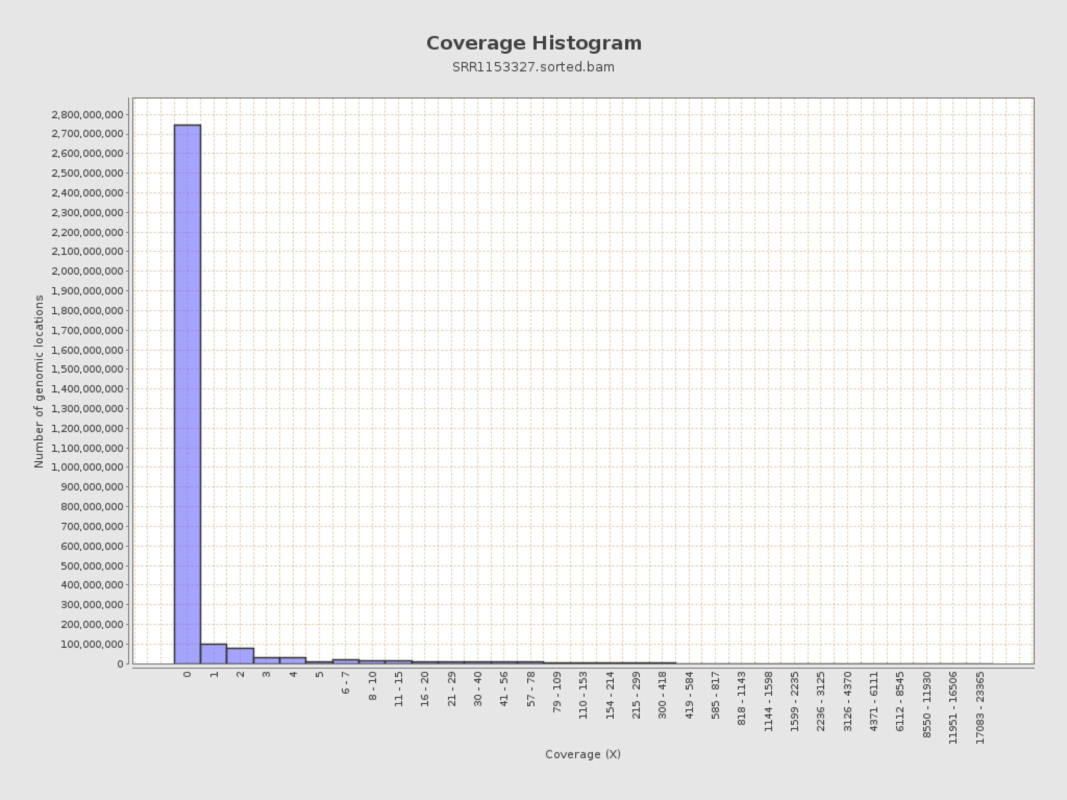
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	589172100	2.3638	21.97
chr2	243199373	438359865	1.8025	16.7424
chr3	198022430	308692541	1.5589	15.0487
chr4	191154276	235207398	1.2305	13.4286
chr5	180915260	370400928	2.0474	20.493
chr6	171115067	211432388	1.2356	15.0979
chr7	159138663	283363543	1.7806	18.7308

chr8	146364022	333266252	2.277	45.1442
chr9	141213431	148926831	1.0546	10.8608
chr10	135534747	289740756	2.1378	20.669
chr11	135006516	280455159	2.0773	18.7672
chr12	133851895	295675221	2.209	18.6598
chr13	115169878	77720408	0.6748	8.8068
chr14	107349540	171680884	1.5993	15.6595
chr15	102531392	291517676	2.8432	29.3585
chr16	90354753	273520397	3.0272	29.5287
chr17	81195210	228383603	2.8128	20.8354
chr18	78077248	68117758	0.8724	10.3043
chr19	59128983	283092829	4.7877	35.833
chr20	63025520	167460636	2.657	45.1539
chr21	48129895	55690333	1.1571	12.8206
chr22	51304566	84443516	1.6459	16.4492
chrMT	16571	16428	0.9914	2.7916
chrX	155270560	401298596	2.5845	27.0216
chrY	59373566	3344186	0.0563	2.0964

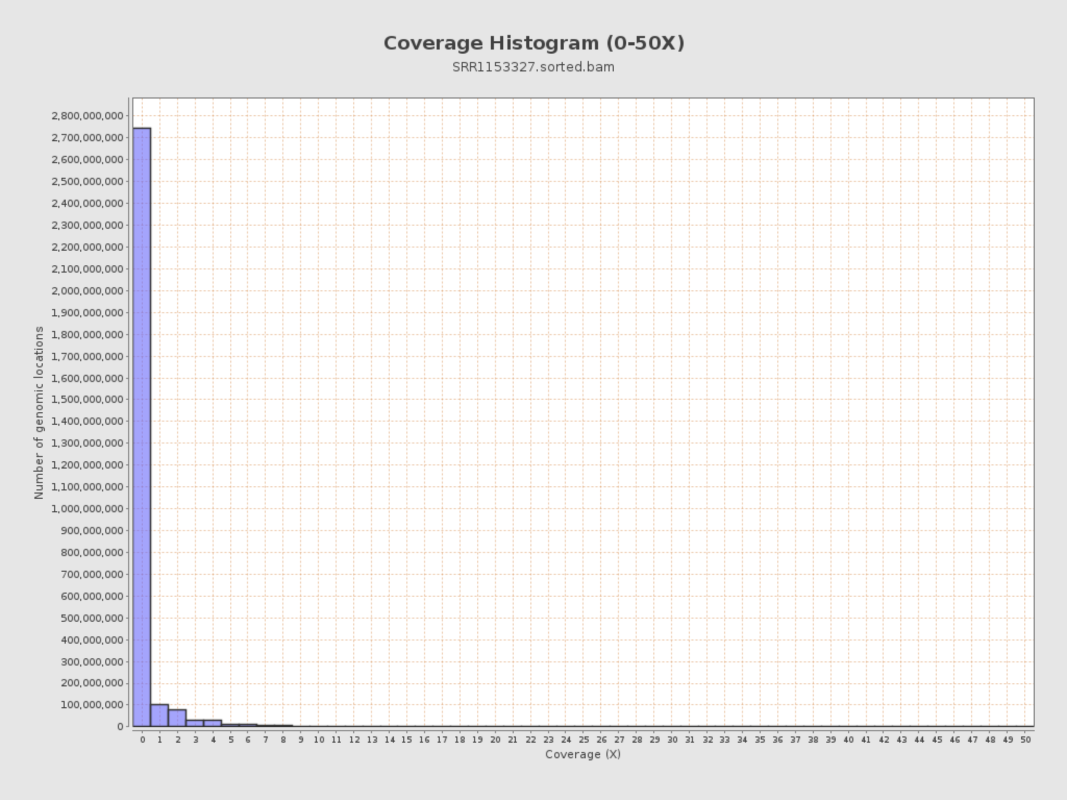
3. Results : Coverage across reference



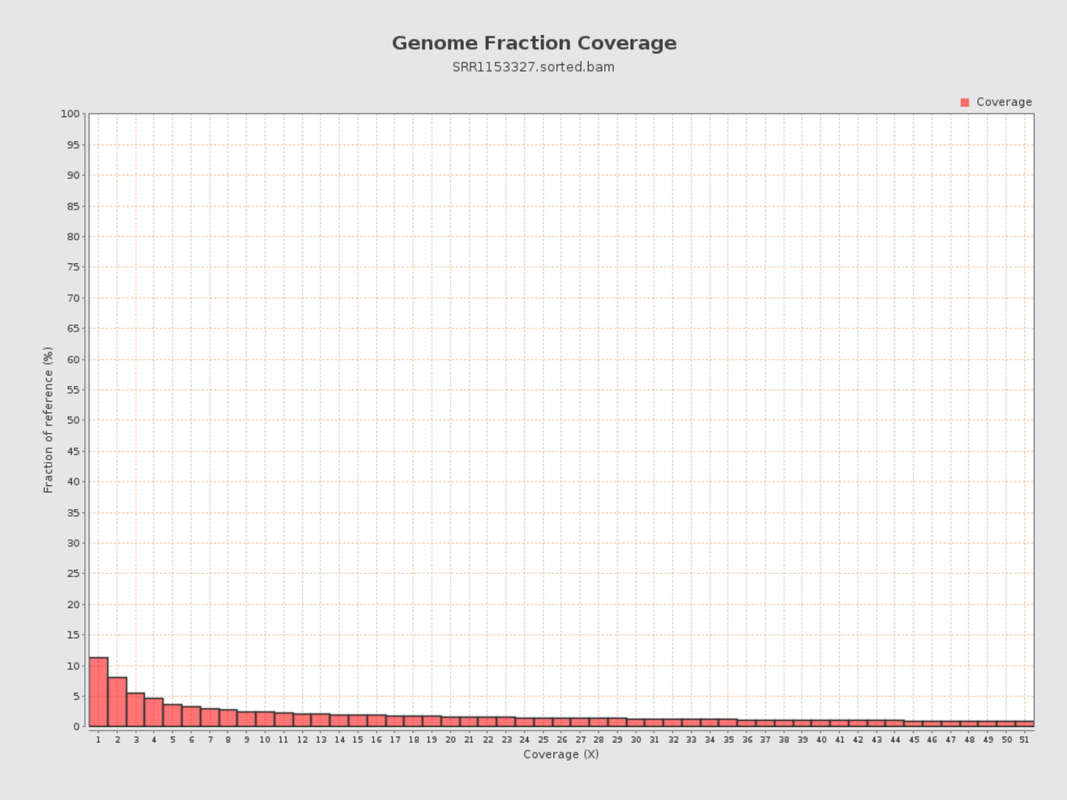
4. Results : Coverage Histogram



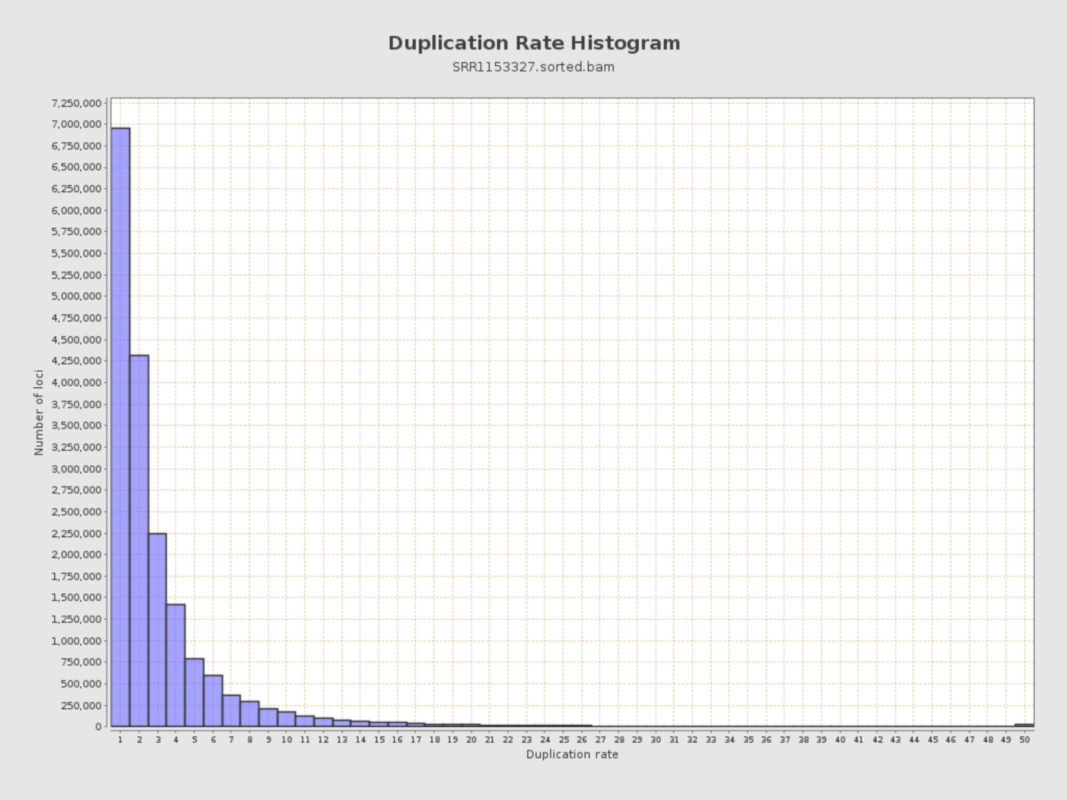
5. Results : Coverage Histogram (0-50X)



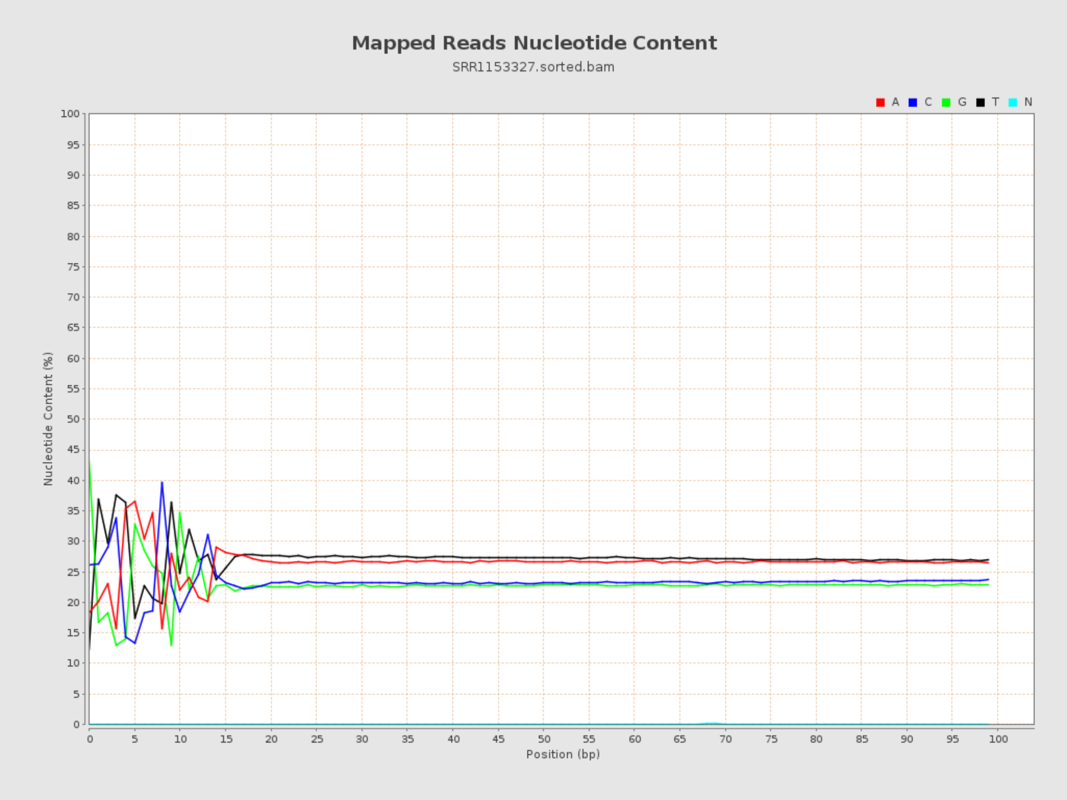
6. Results : Genome Fraction Coverage



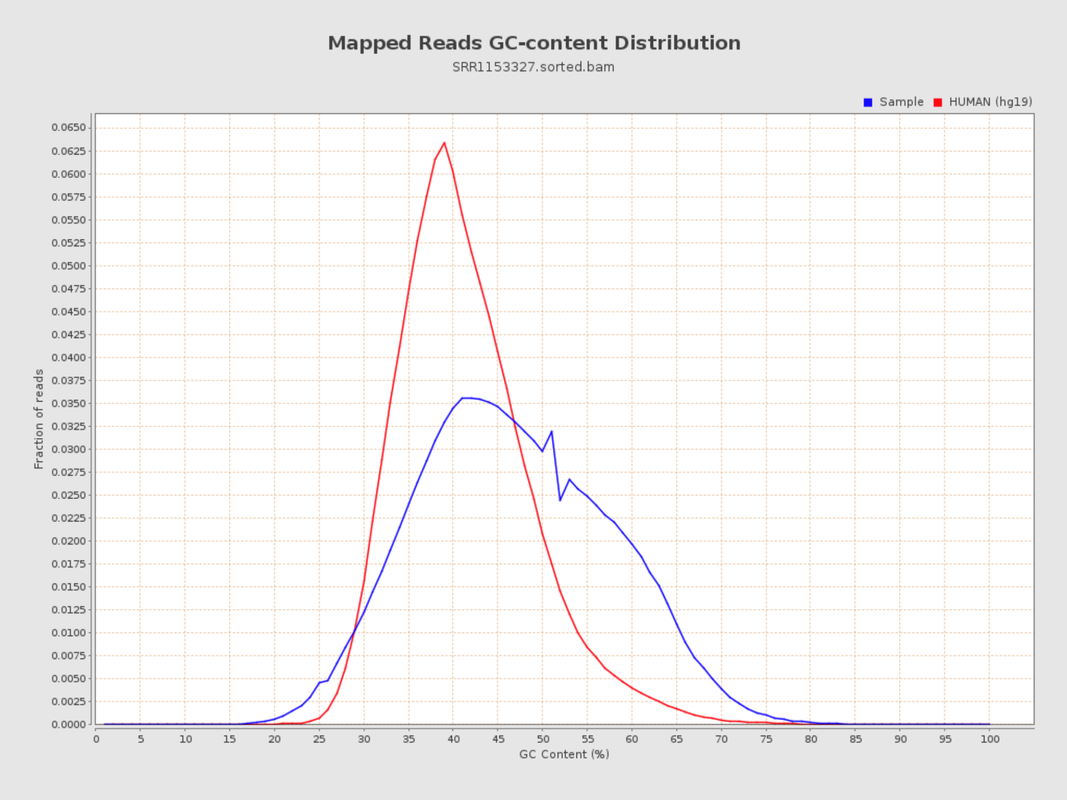
7. Results : Duplication Rate Histogram



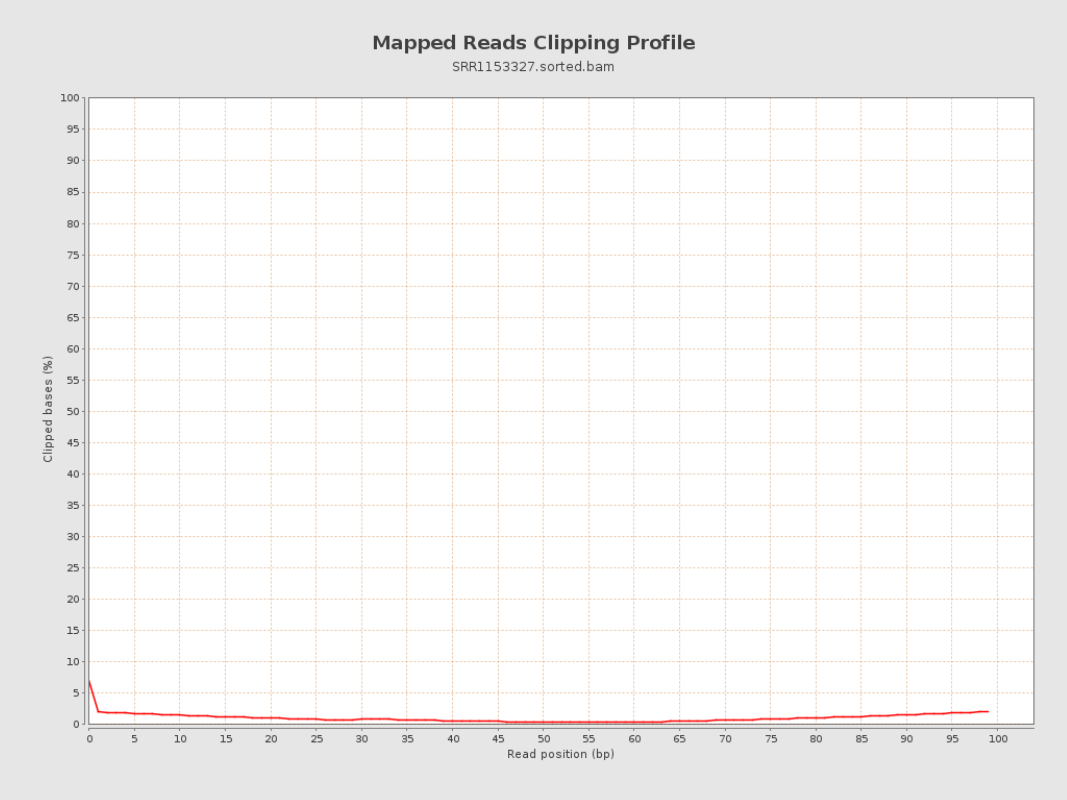
8. Results : Mapped Reads Nucleotide Content



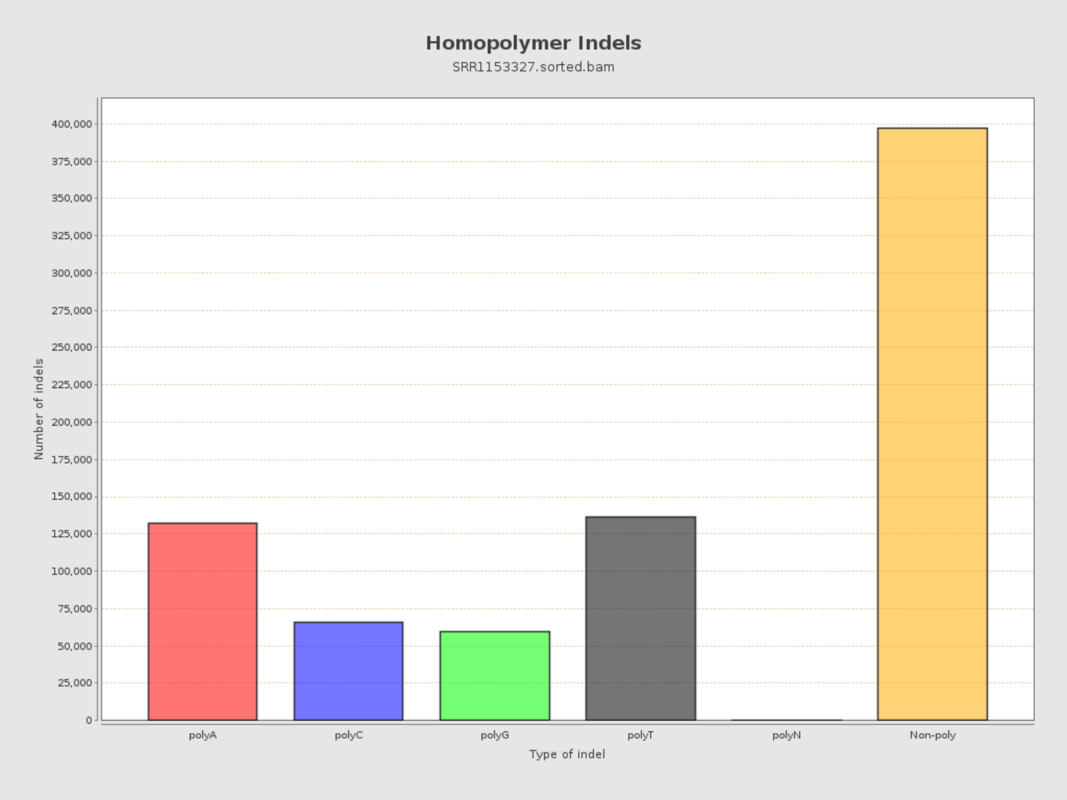
9. Results : Mapped Reads GC-content Distribution



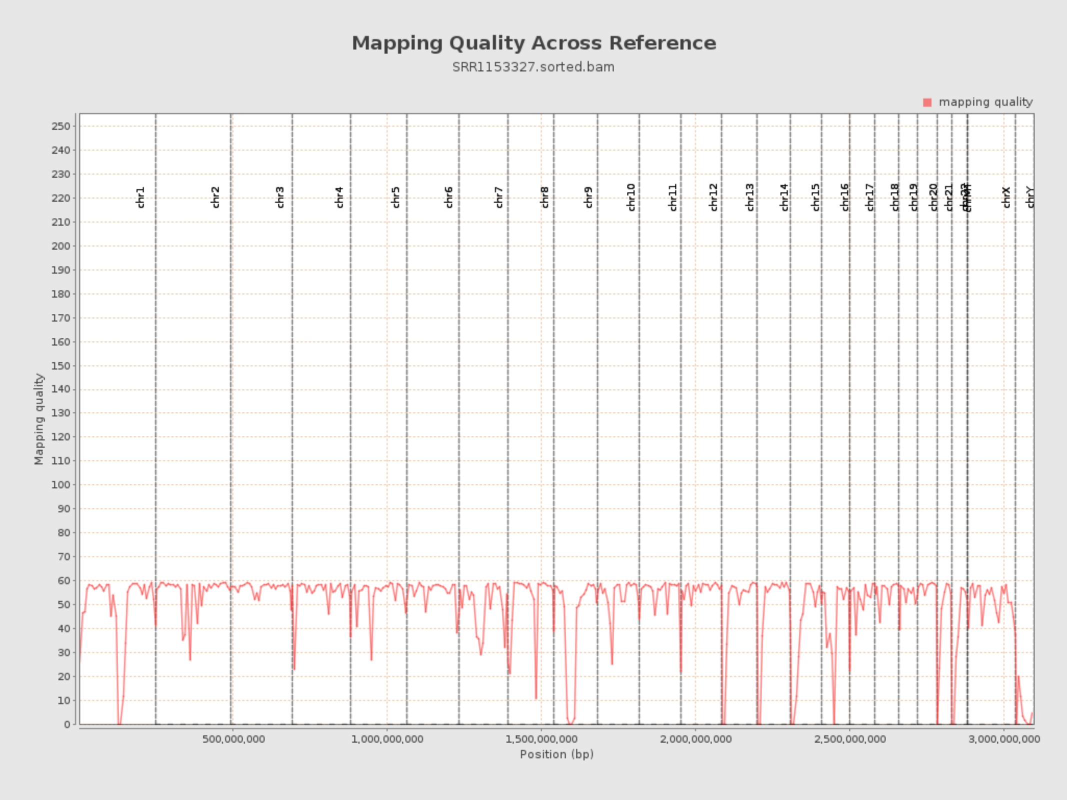
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram