Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 00:37:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153340.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_SRR1153340 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153340.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 00:37:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153340.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	74,608,466
Mapped reads	73,662,077 / 98.73%
Unmapped reads	946,389 / 1.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	526,032 / 0.71%
Read min/max/mean length	30 / 100 / 100.29
Duplicated reads (estimated)	32,319,681 / 43.32%
Duplication rate	35.19%
Clipped reads	3,373,774 / 4.52%

2.2. ACGT Content

Number/percentage of A's	1,893,794,433 / 25.84%
Number/percentage of C's	1,767,026,233 / 24.11%
Number/percentage of T's	1,892,820,227 / 25.83%
Number/percentage of G's	1,773,793,314 / 24.21%
Number/percentage of N's	330,962 / 0%
GC Percentage	48.32%

2.3. Coverage

Mean	2.3674

Standard Deviation	24.099

2.4. Mapping Quality

Mean Mapping Quality	48.85

2.5. Mismatches and indels

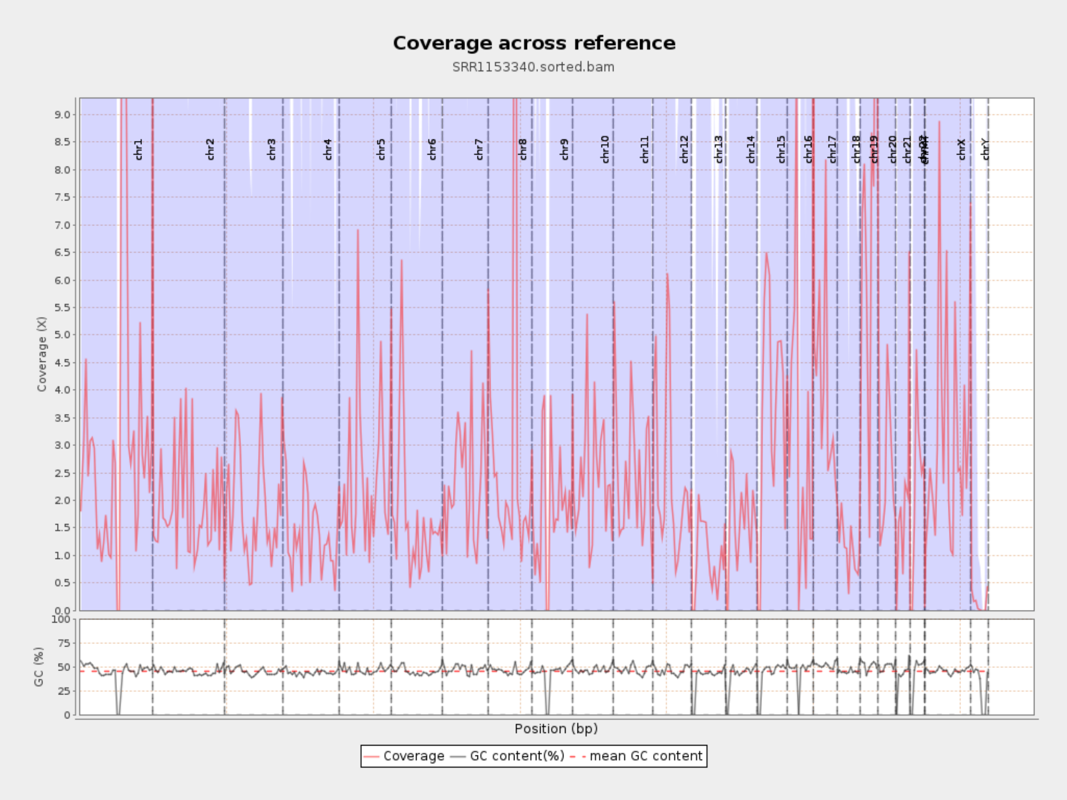
General error rate	0.32%
Mismatches	22,519,858
Insertions	610,486
Mapped reads with at least one insertion	0.82%
Deletions	428,303
Mapped reads with at least one deletion	0.57%
Homopolymer indels	47.47%

2.6. Chromosome stats

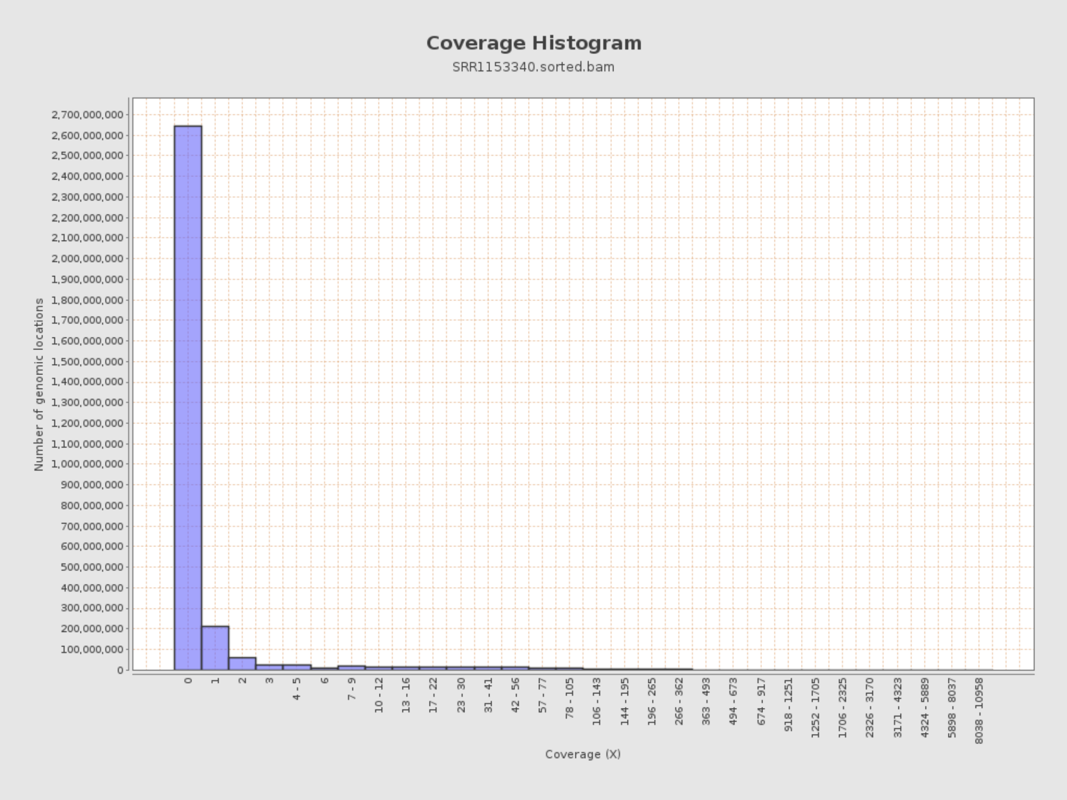
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	812797417	3.261	27.1618
chr2	243199373	471349802	1.9381	15.3199
chr3	198022430	365458930	1.8455	15.4209
chr4	191154276	269828354	1.4116	14.5217
chr5	180915260	441558891	2.4407	31.8495
chr6	171115067	282973613	1.6537	14.0247
chr7	159138663	371138805	2.3322	21.1779

chr8	146364022	412559495	2.8187	52.5358
chr9	141213431	255149132	1.8068	16.4461
chr10	135534747	332757964	2.4551	19.1698
chr11	135006516	344231768	2.5497	18.6676
chr12	133851895	325396979	2.431	19.095
chr13	115169878	107553271	0.9339	9.7488
chr14	107349540	166921443	1.5549	13.6776
chr15	102531392	368368101	3.5927	30.4499
chr16	90354753	282243505	3.1237	23.6706
chr17	81195210	323526713	3.9846	27.6026
chr18	78077248	86637049	1.1096	10.5857
chr19	59128983	433916701	7.3385	40.9268
chr20	63025520	170687630	2.7082	20.7666
chr21	48129895	97911175	2.0343	43.5037
chr22	51304566	117613744	2.2925	17.3412
chrMT	16571	972	0.0587	0.2479
chrX	155270560	479682266	3.0893	26.2897
chrY	59373566	8482843	0.1429	6.3513

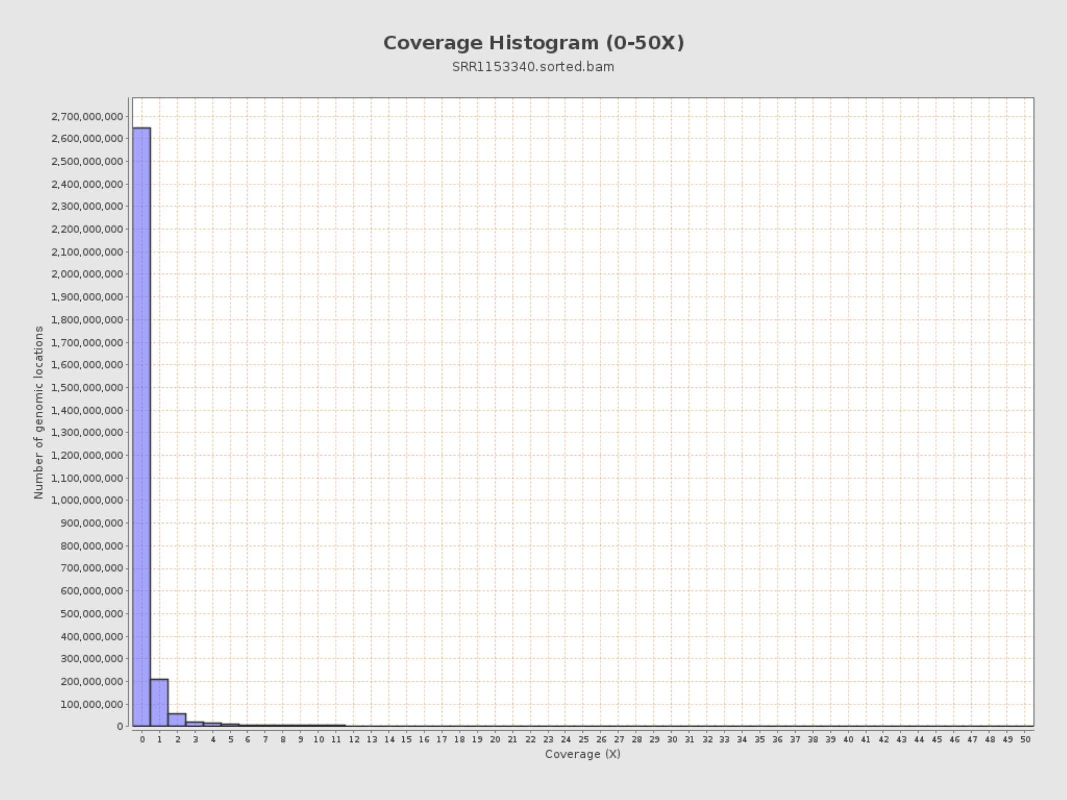
3. Results : Coverage across reference



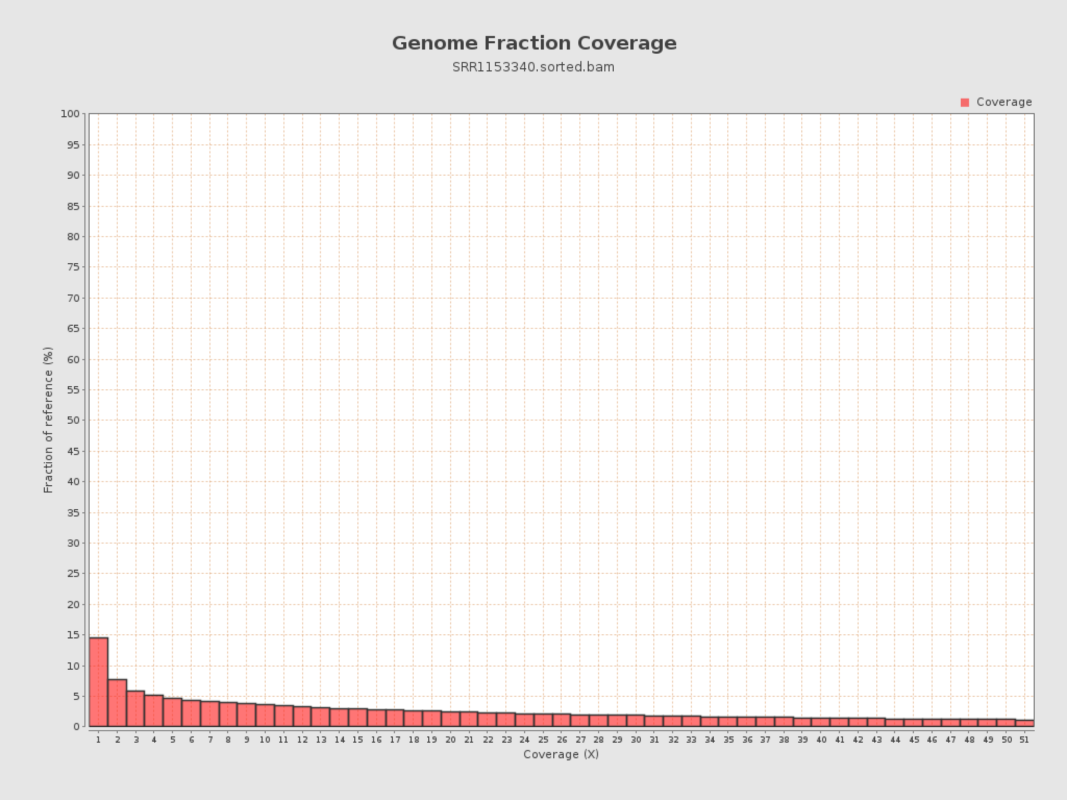
4. Results : Coverage Histogram



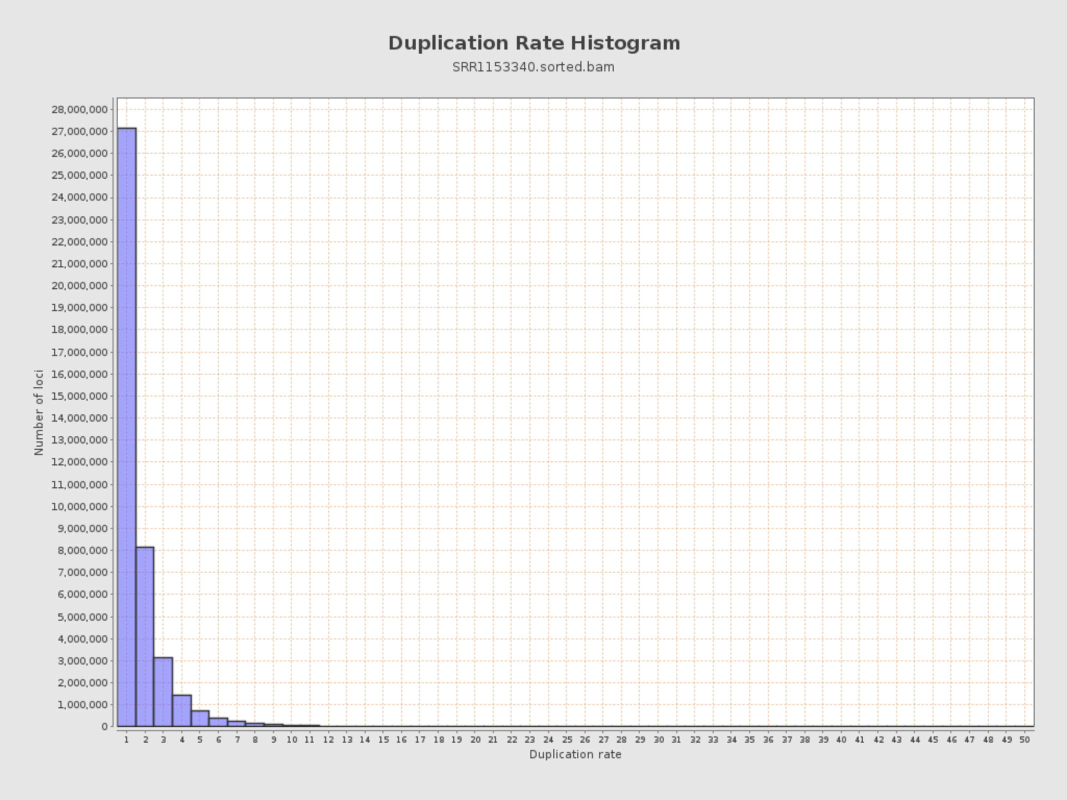
5. Results : Coverage Histogram (0-50X)



6. Results : Genome Fraction Coverage

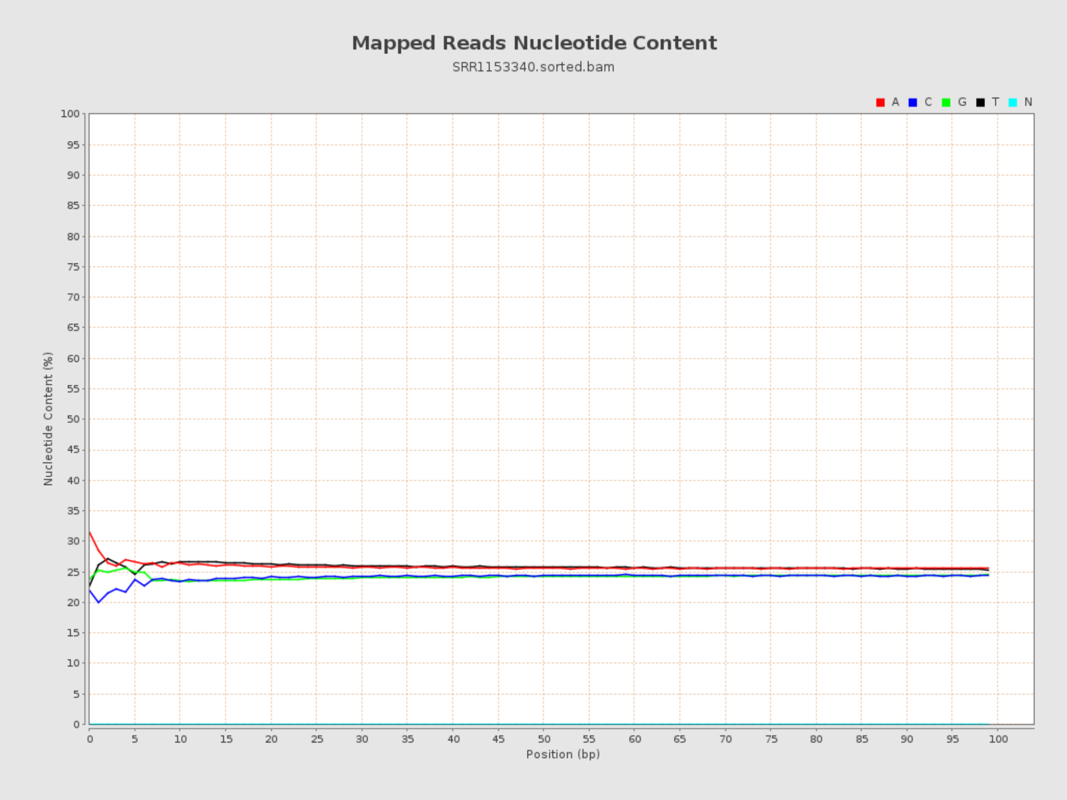


7. Results : Duplication Rate Histogram

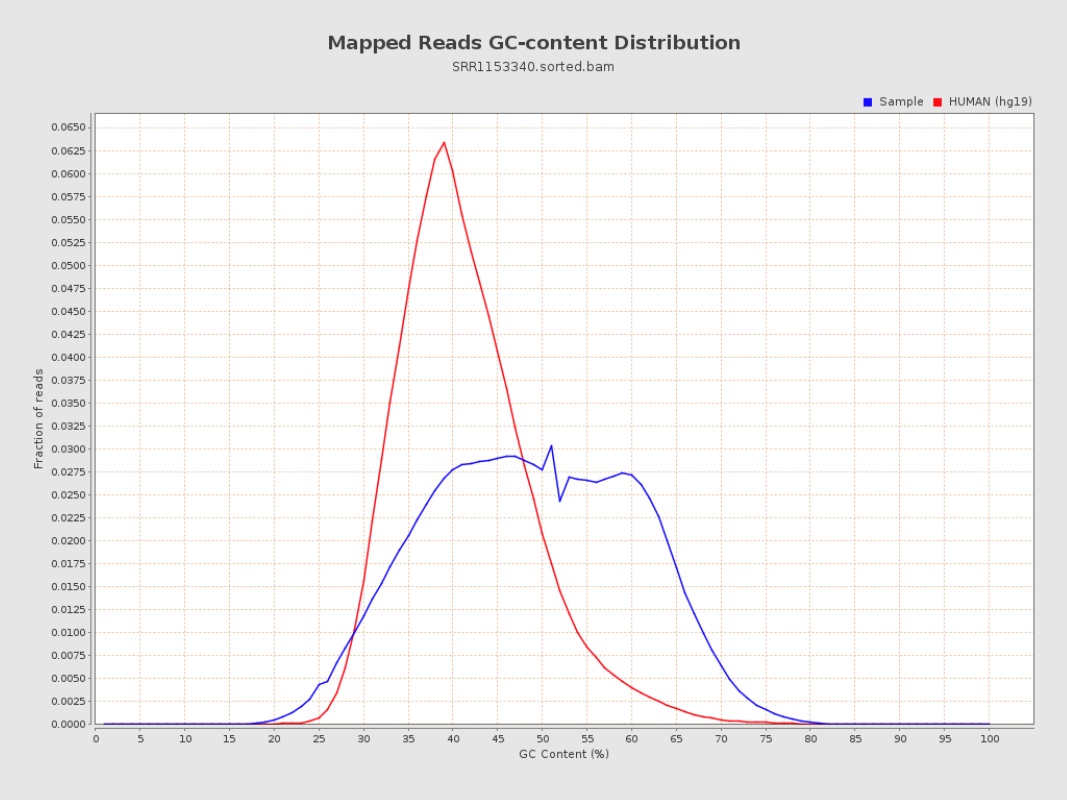

Duplication Rate Histogram

SRR1153340.sorted.bam

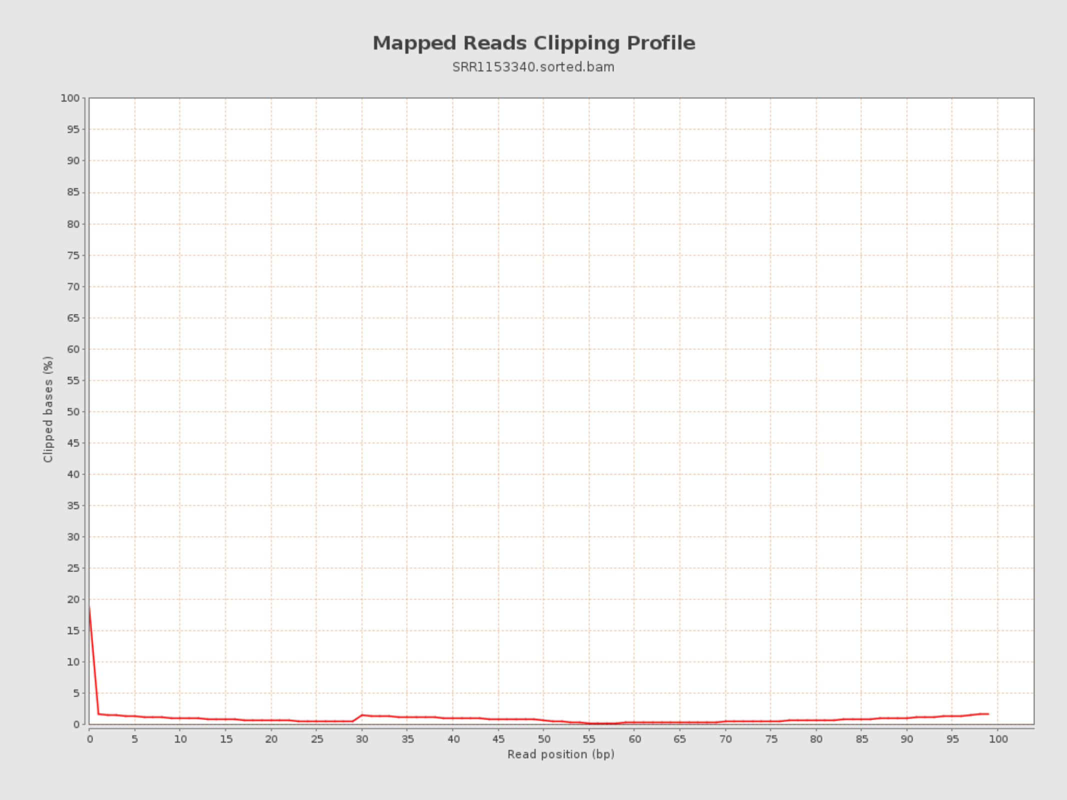
8. Results : Mapped Reads Nucleotide Content



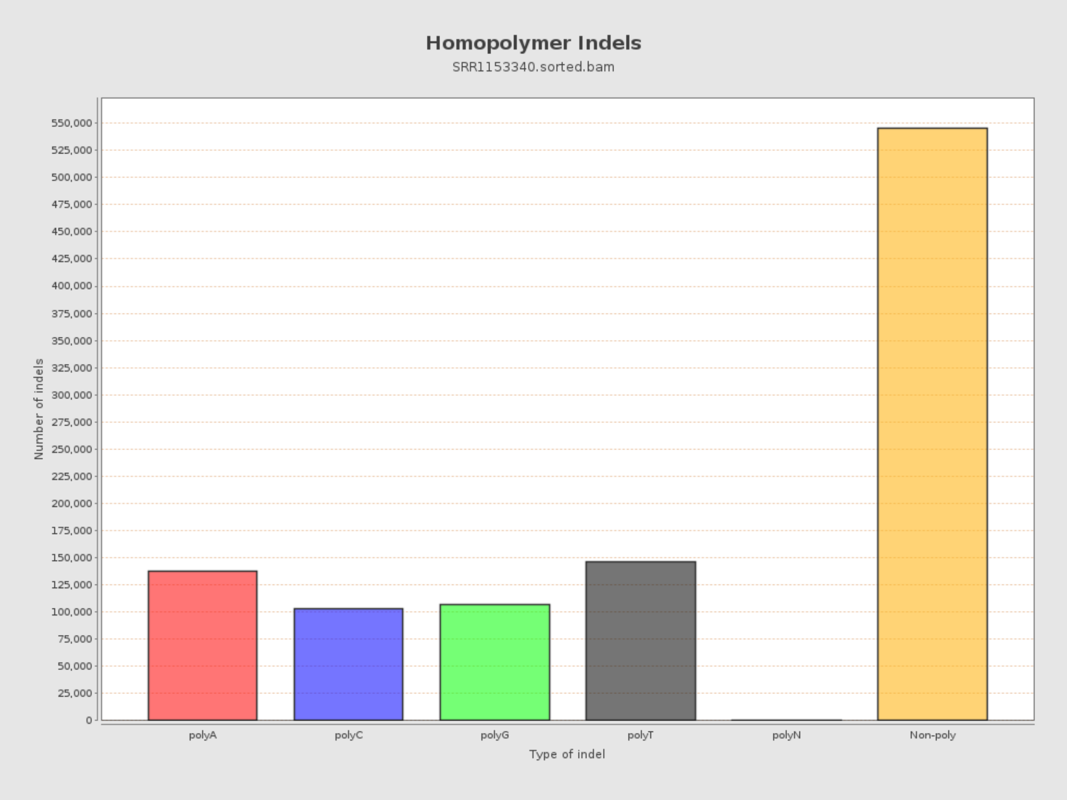
9. Results : Mapped Reads GC-content Distribution



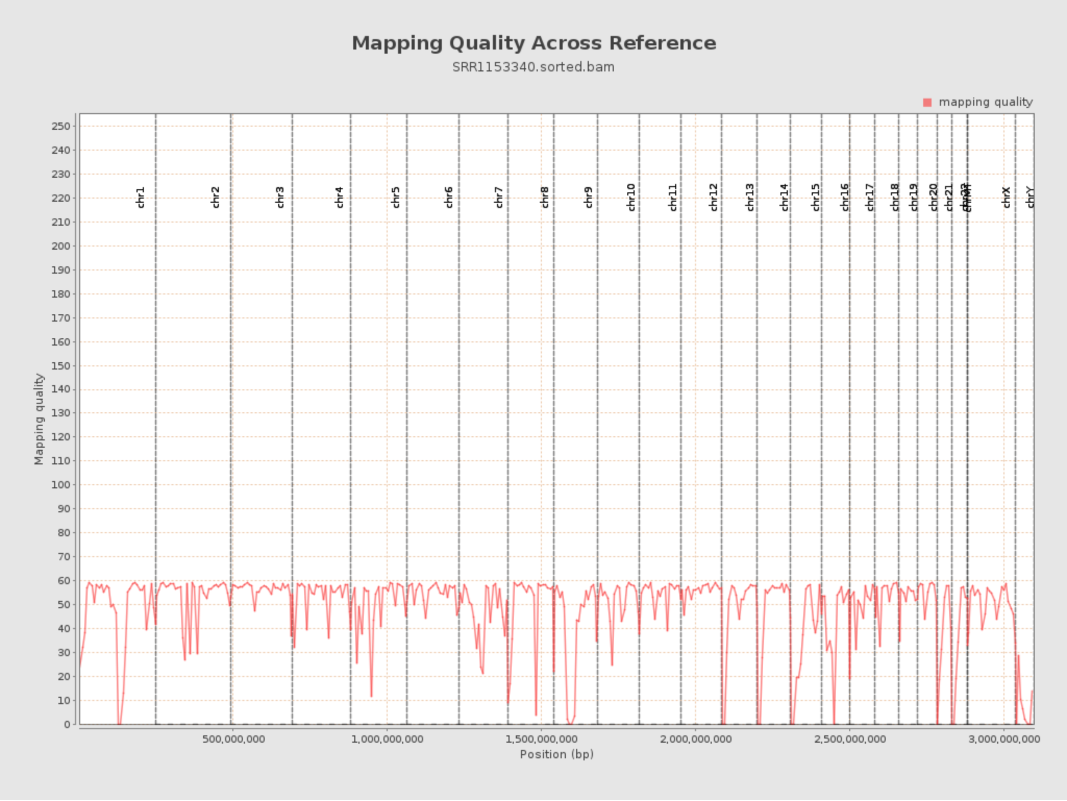
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram