Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/05 23:33:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1770535.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_SRR1770535 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1770535_1.fastq.gz SRR1770535_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Oct 05 23:33:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1770535.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	396,743,888
Mapped reads	380,371,909 / 95.87%
Unmapped reads	16,371,979 / 4.13%
Mapped paired reads	380,371,909 / 95.87%
Mapped reads, first in pair	191,859,218 / 48.36%
Mapped reads, second in pair	188,512,691 / 47.51%
Mapped reads, both in pair	375,137,522 / 94.55%
Mapped reads, singletons	5,234,387 / 1.32%
Secondary alignments	0
Supplementary alignments	396,716 / 0.1%
Read min/max/mean length	30 / 80 / 80.04
Duplicated reads (estimated)	42,583,557 / 10.73%
Duplication rate	7.21%
Clipped reads	15,827,923 / 3.99%

2.2. ACGT Content

Number/percentage of A's	8,822,100,500 / 29.26%
Number/percentage of C's	6,226,412,621 / 20.65%
Number/percentage of T's	8,849,440,413 / 29.35%
Number/percentage of G's	6,241,663,507 / 20.7%
Number/percentage of N's	7,612,626 / 0.03%

GC Percentage	41.36%

2.3. Coverage

Mean	9.7408
Standard Deviation	99.6027

2.4. Mapping Quality

Mean Mapping Quality	53.19

2.5. Insert size

Mean	26,514.06
Standard Deviation	1,541,103.72
P25/Median/P75	154 / 199 / 263

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	151,541,661
Insertions	2,552,299
Mapped reads with at least one insertion	0.66%
Deletions	3,336,082
Mapped reads with at least one deletion	0.86%
Homopolymer indels	43.18%

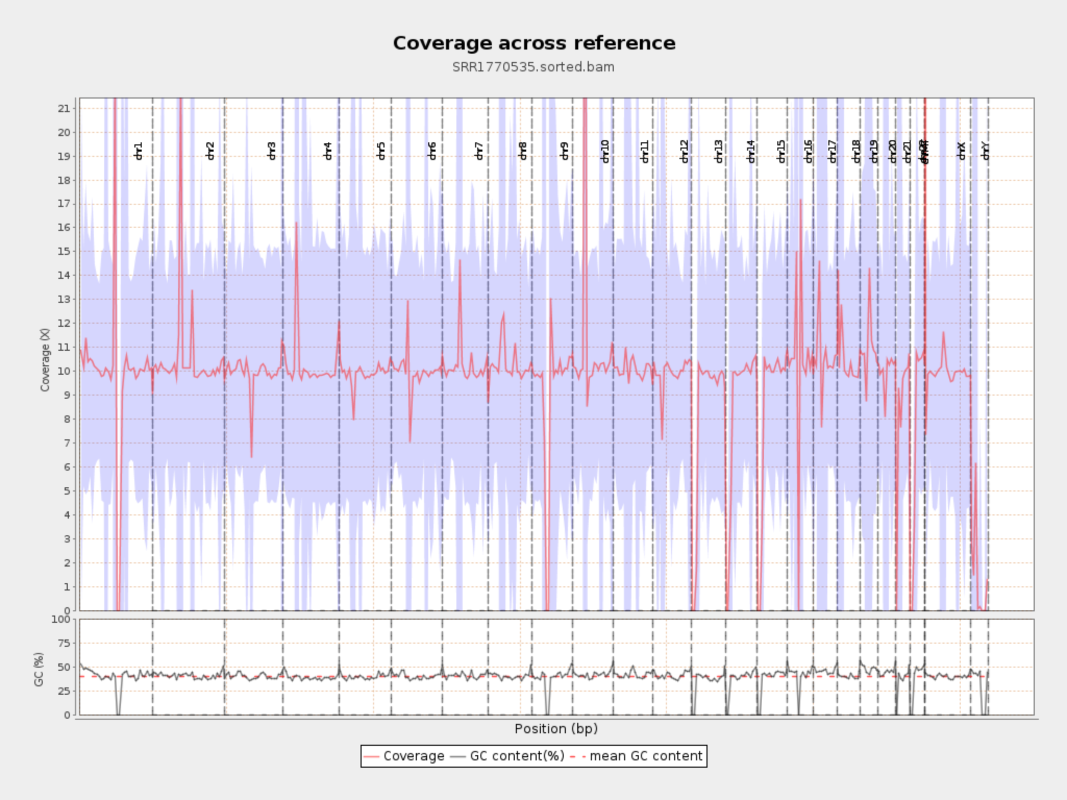
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

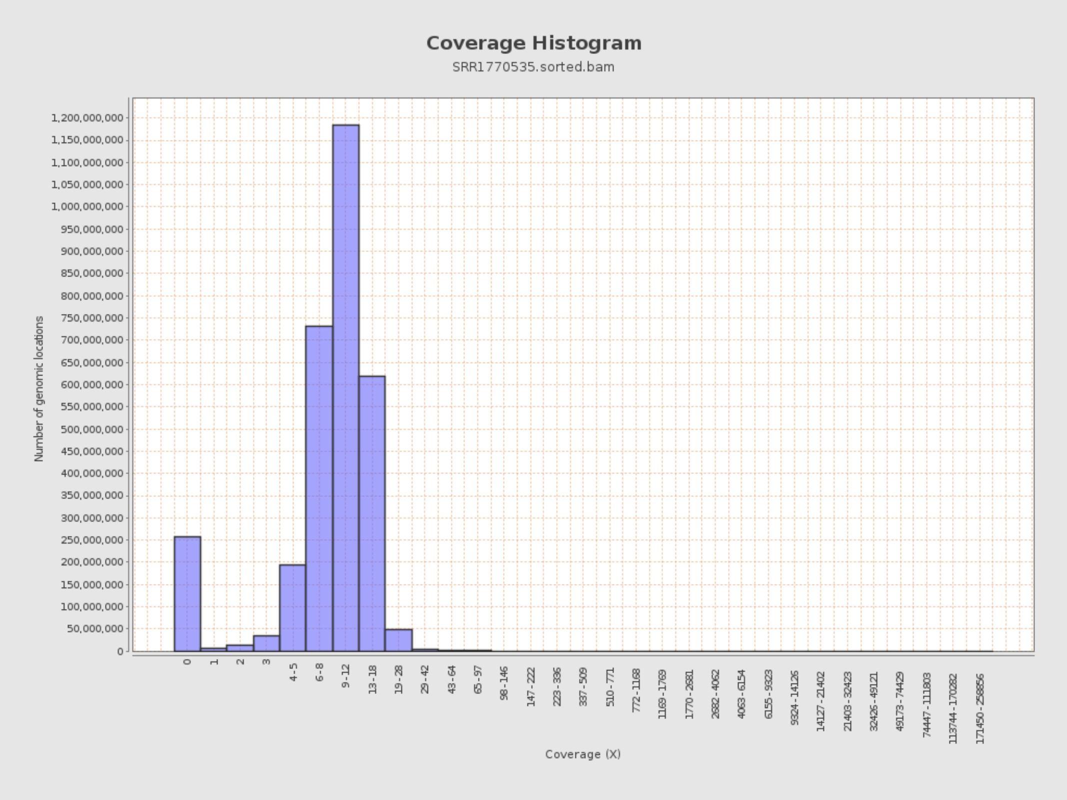
		bases	coverage	deviation
chr1	249250621	2470711494	9.9126	257.7079
chr2	243199373	2574847202	10.5874	72.532
chr3	198022430	1962878063	9.9124	9.9131
chr4	191154276	1956412636	10.2347	43.7682
chr5	180915260	1792799114	9.9096	8.2587
chr6	171115067	1710777197	9.9978	37.3151
chr7	159138663	1638419847	10.2955	86.7139
chr8	146364022	1510116391	10.3175	129.6339
chr9	141213431	1265442772	8.9612	92.3528
chr10	135534747	1541501595	11.3735	173.2941
chr11	135006516	1366192644	10.1195	38.9618
chr12	133851895	1326241911	9.9083	9.9122
chr13	115169878	950959732	8.257	6.0935
chr14	107349540	904344518	8.4243	12.471
chr15	102531392	847873005	8.2694	6.0741
chr16	90354753	949945329	10.5135	59.7358
chr17	81195210	857269544	10.5581	54.0785
chr18	78077248	814902779	10.4371	111.4216
chr19	59128983	652272117	11.0313	141.8616
chr20	63025520	630595729	10.0054	16.0279
chr21	48129895	415257172	8.6278	29.924
chr22	51304566	378022991	7.3682	7.5938
chrMT	16571	11558966	697.5419	75.2287
chrX	155270560	1539469116	9.9148	23.643

chrY	59373566	85628107	1.4422	55.9965

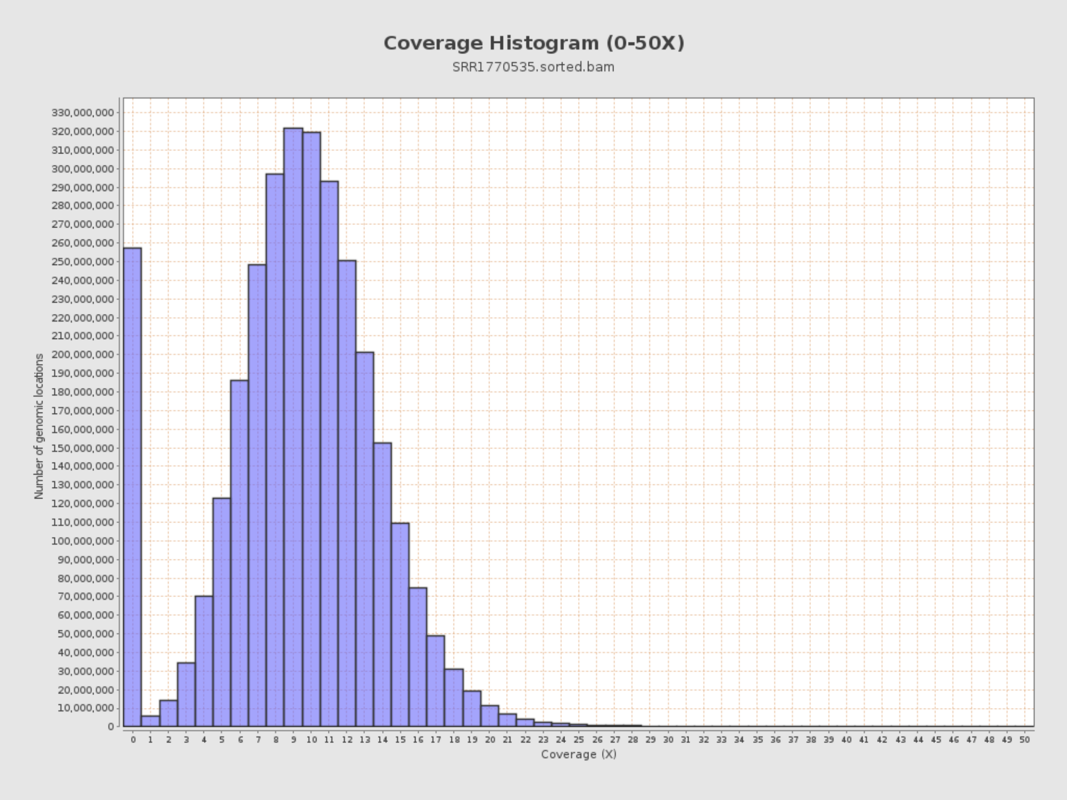
3. Results : Coverage across reference



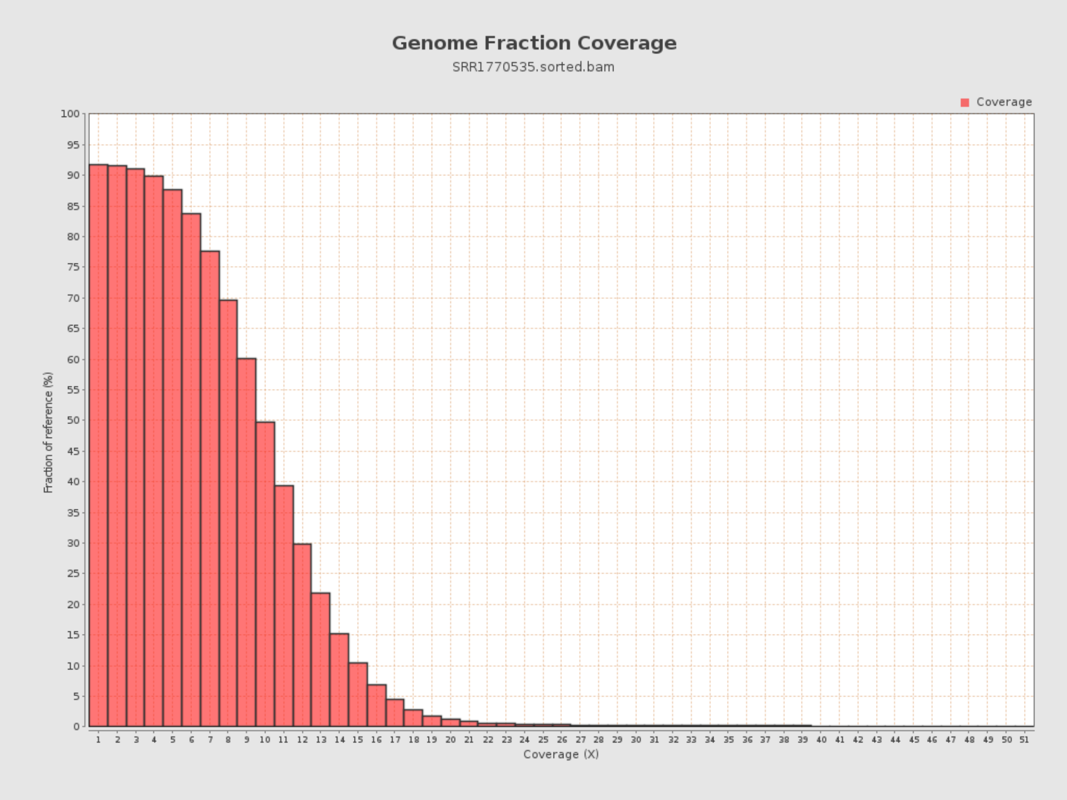
4. Results : Coverage Histogram



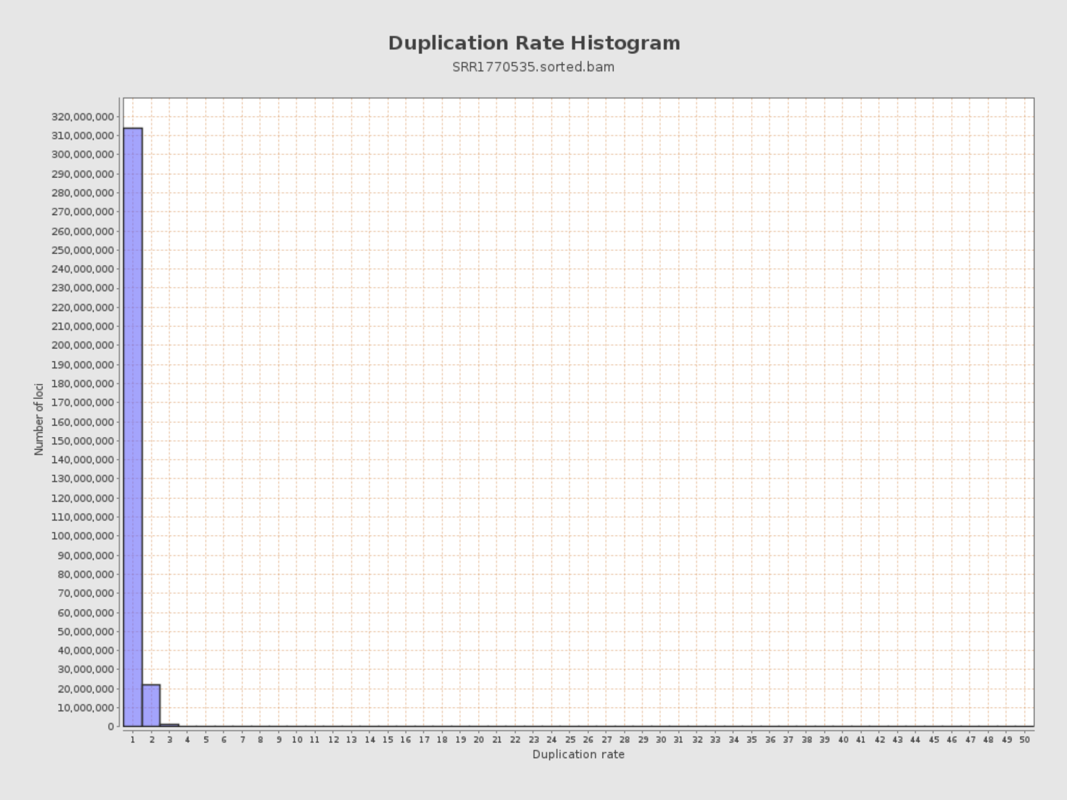
5. Results : Coverage Histogram (0-50X)



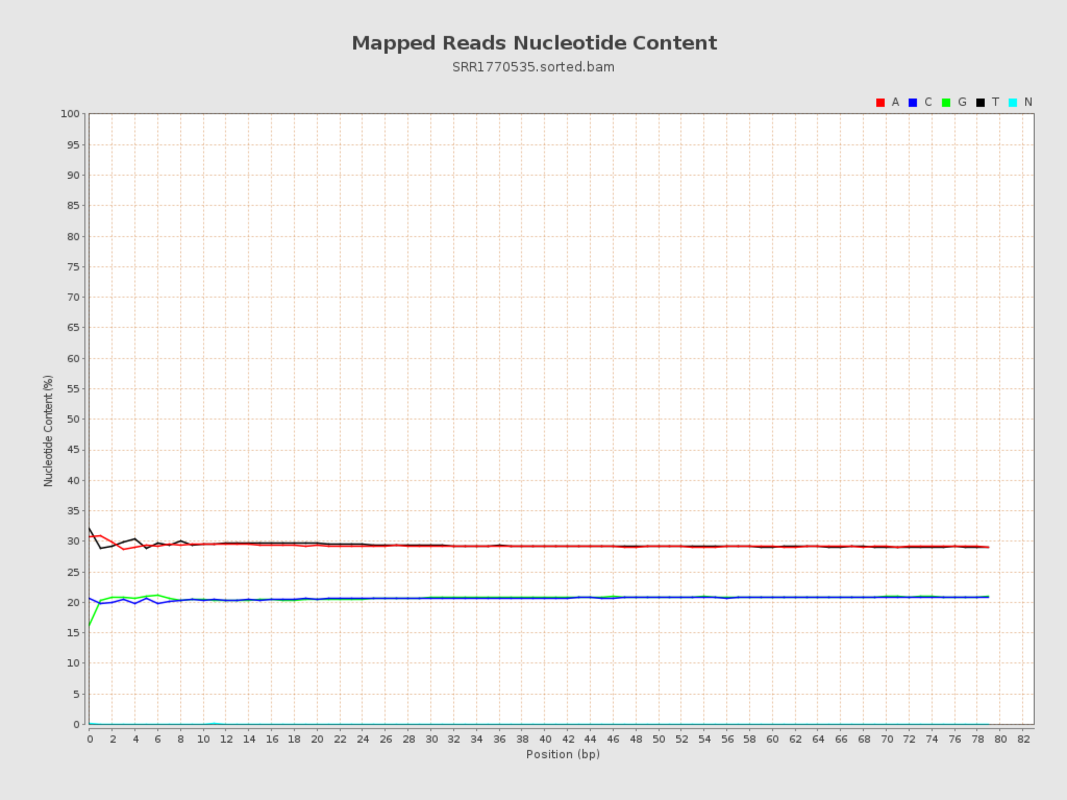
6. Results : Genome Fraction Coverage



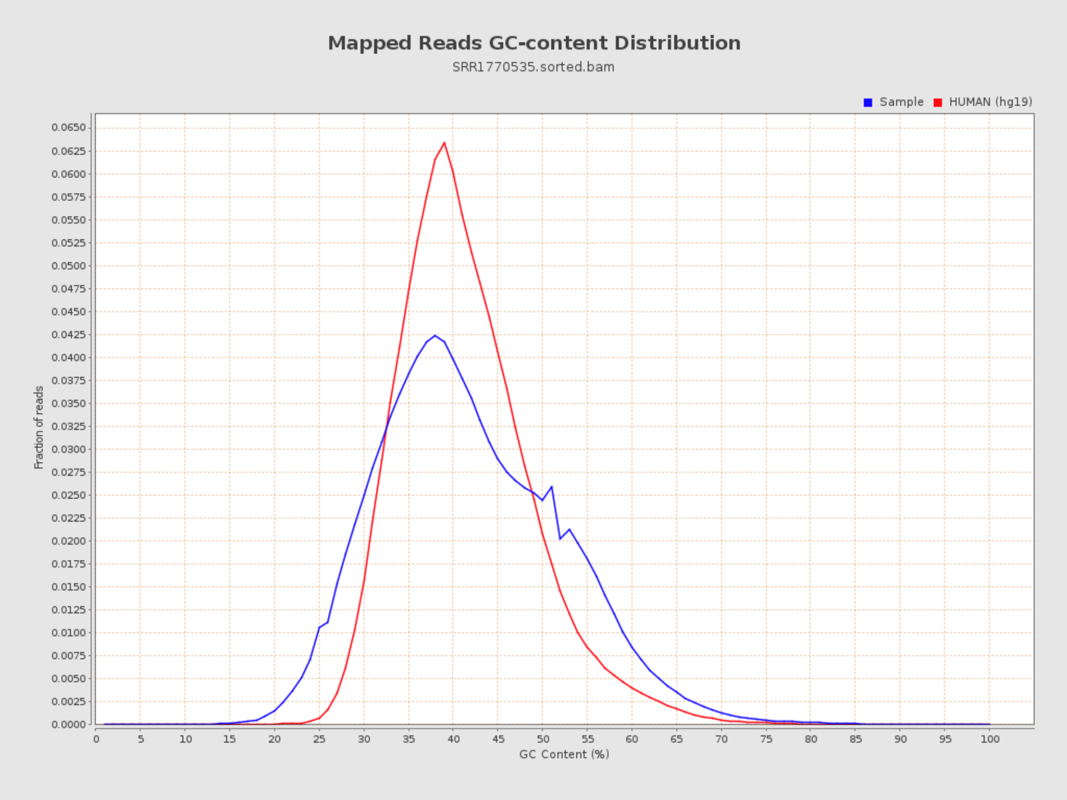
7. Results : Duplication Rate Histogram



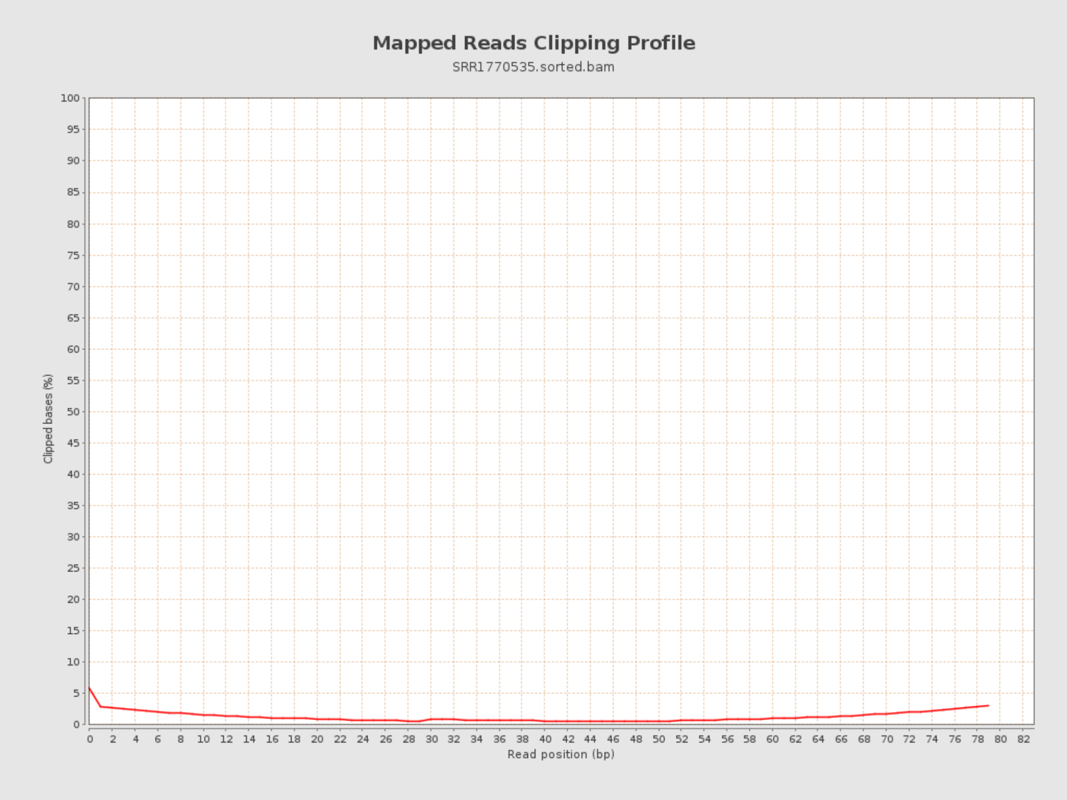
8. Results : Mapped Reads Nucleotide Content



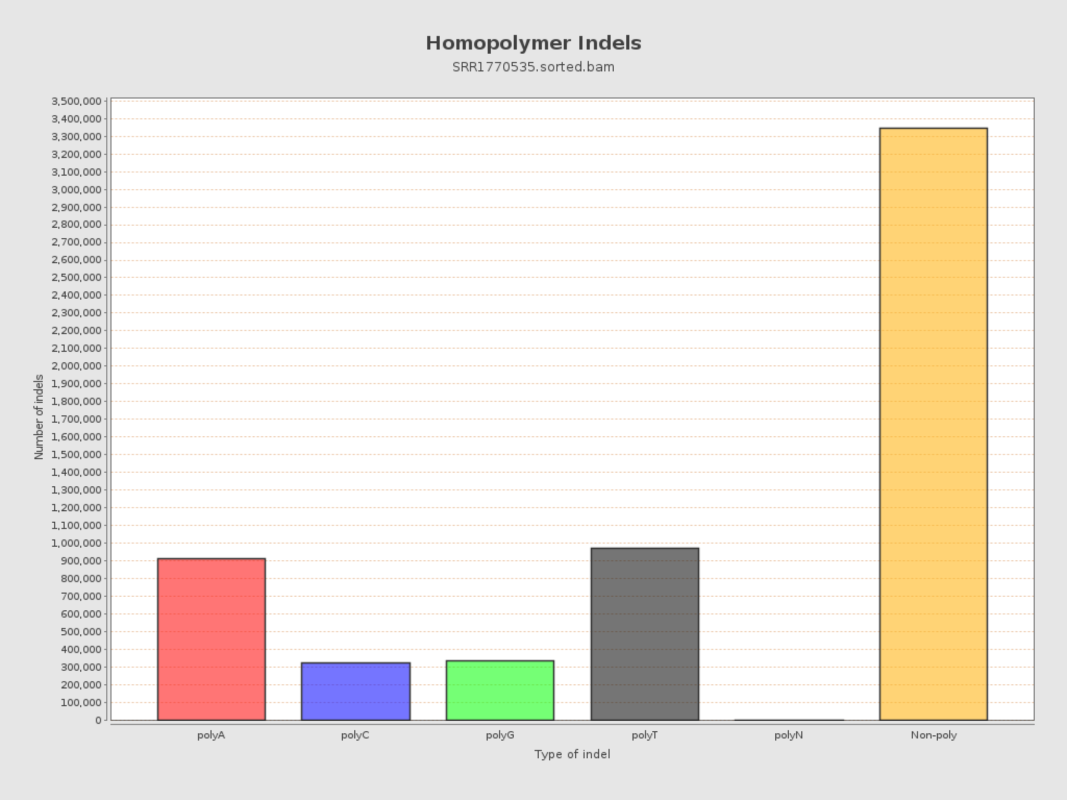
9. Results : Mapped Reads GC-content Distribution



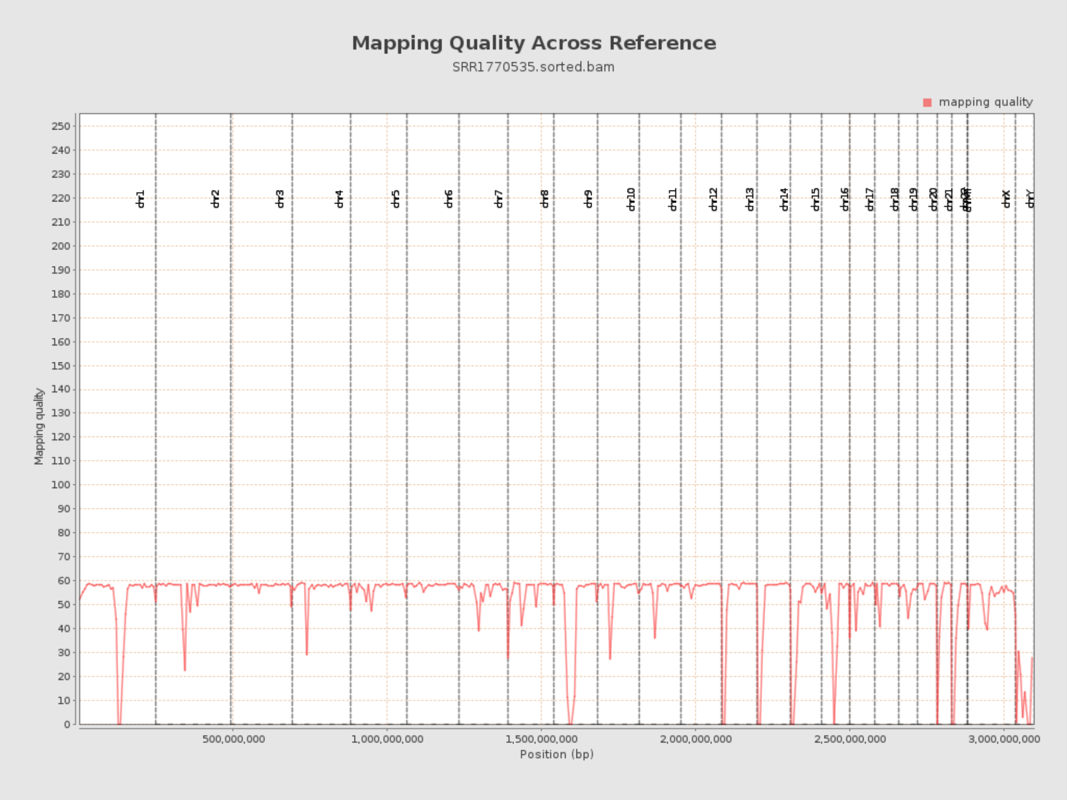
10. Results : Mapped Reads Clipping Profile



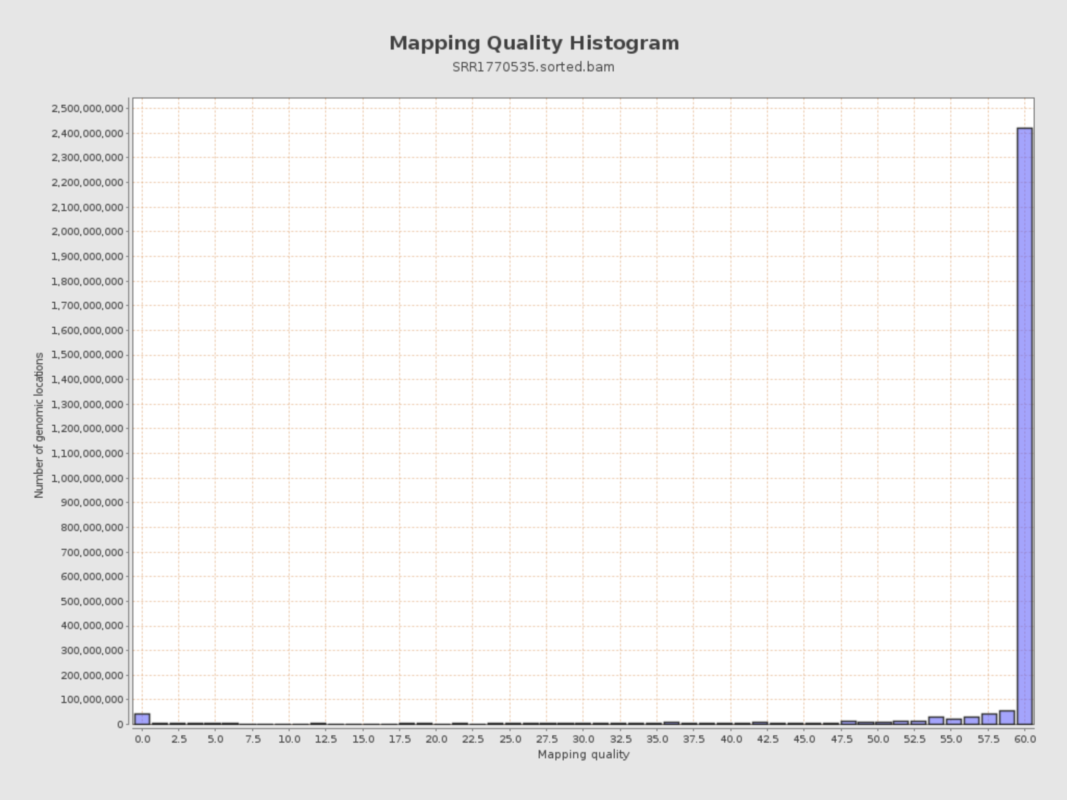
11. Results : Homopolymer Indels



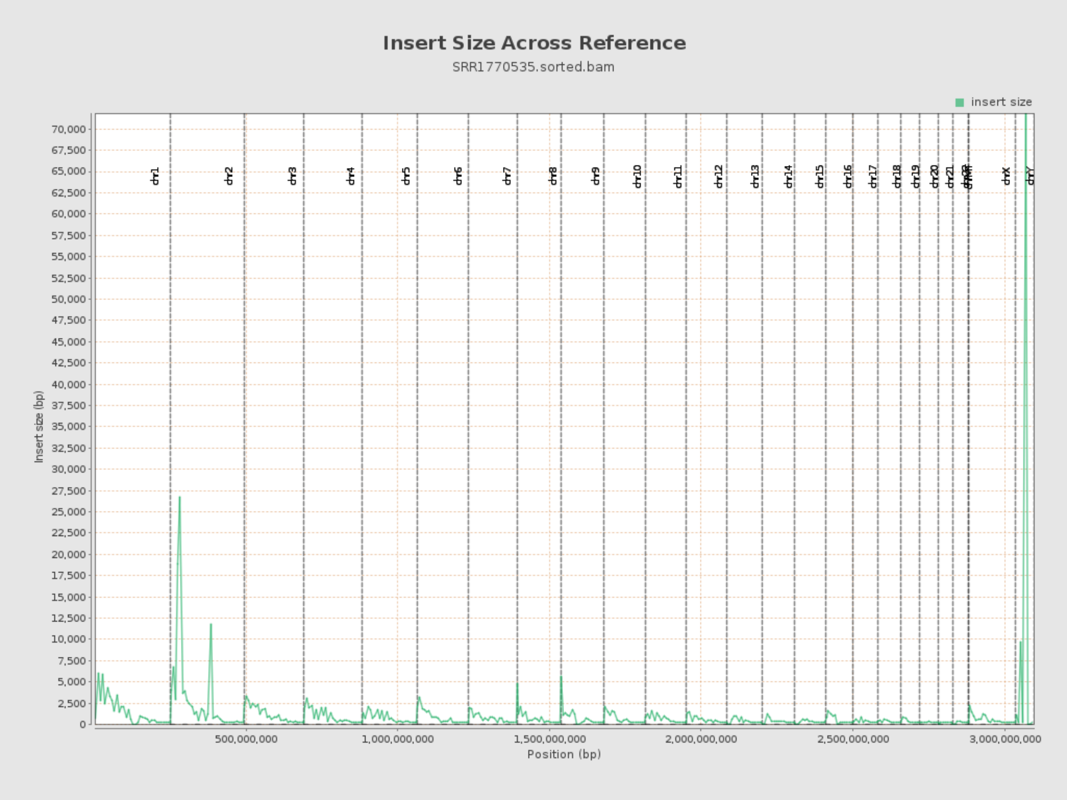
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram