Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/06 10:31:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1778448.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_SRR1778448 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1778448_1.fastq.gz SRR1778448_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Oct 06 10:31:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1778448.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	341,794,014
Mapped reads	329,845,406 / 96.5%
Unmapped reads	11,948,608 / 3.5%
Mapped paired reads	329,845,406 / 96.5%
Mapped reads, first in pair	166,085,396 / 48.59%
Mapped reads, second in pair	163,760,010 / 47.91%
Mapped reads, both in pair	325,633,970 / 95.27%
Mapped reads, singletons	4,211,436 / 1.23%
Secondary alignments	0
Supplementary alignments	843,792 / 0.25%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	45,943,985 / 13.44%
Duplication rate	8.82%
Clipped reads	18,587,413 / 5.44%

2.2. ACGT Content

Number/percentage of A's	7,769,336,999 / 29.79%
Number/percentage of C's	5,284,137,309 / 20.26%
Number/percentage of T's	7,698,889,919 / 29.52%
Number/percentage of G's	5,322,511,251 / 20.41%
Number/percentage of N's	7,309,188 / 0.03%

GC Percentage	40.67%

2.3. Coverage

Mean	8.4276
Standard Deviation	95.9098

2.4. Mapping Quality

Mean Mapping Quality	53

2.5. Insert size

Mean	68,317.67
Standard Deviation	2,485,439.99
P25/Median/P75	146 / 192 / 252

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	130,112,848
Insertions	2,451,411
Mapped reads with at least one insertion	0.73%
Deletions	3,172,582
Mapped reads with at least one deletion	0.94%
Homopolymer indels	43%

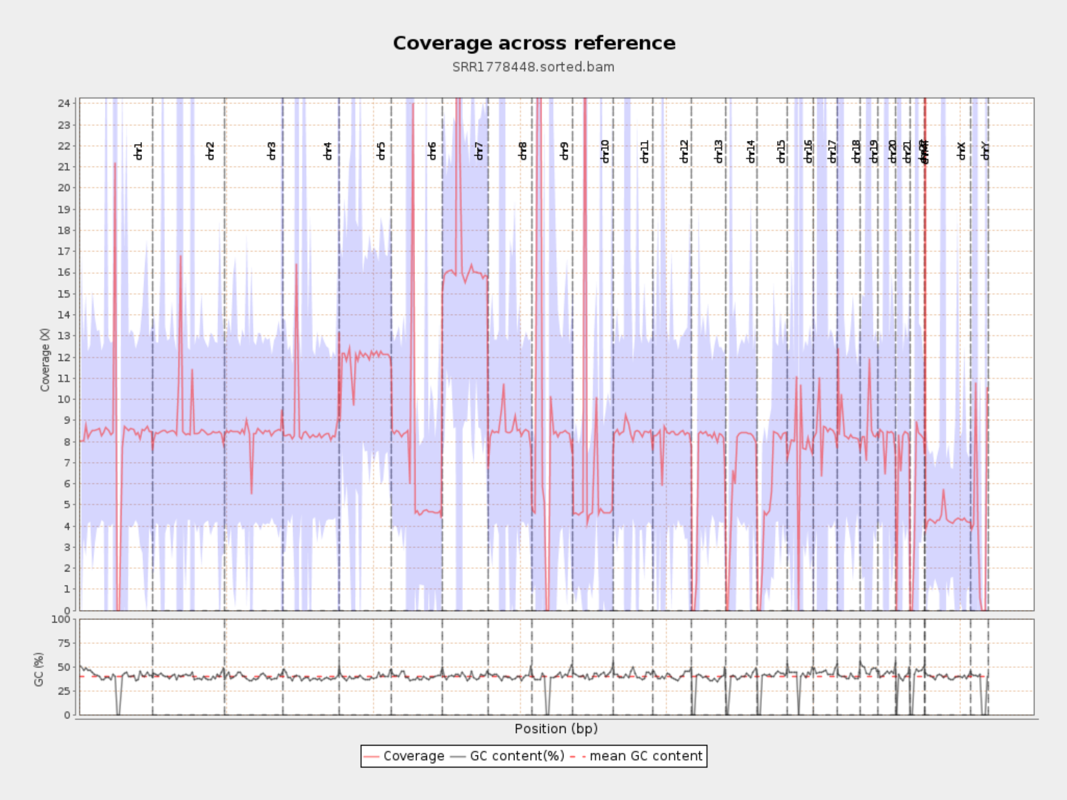
2.7. Chromosome stats

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

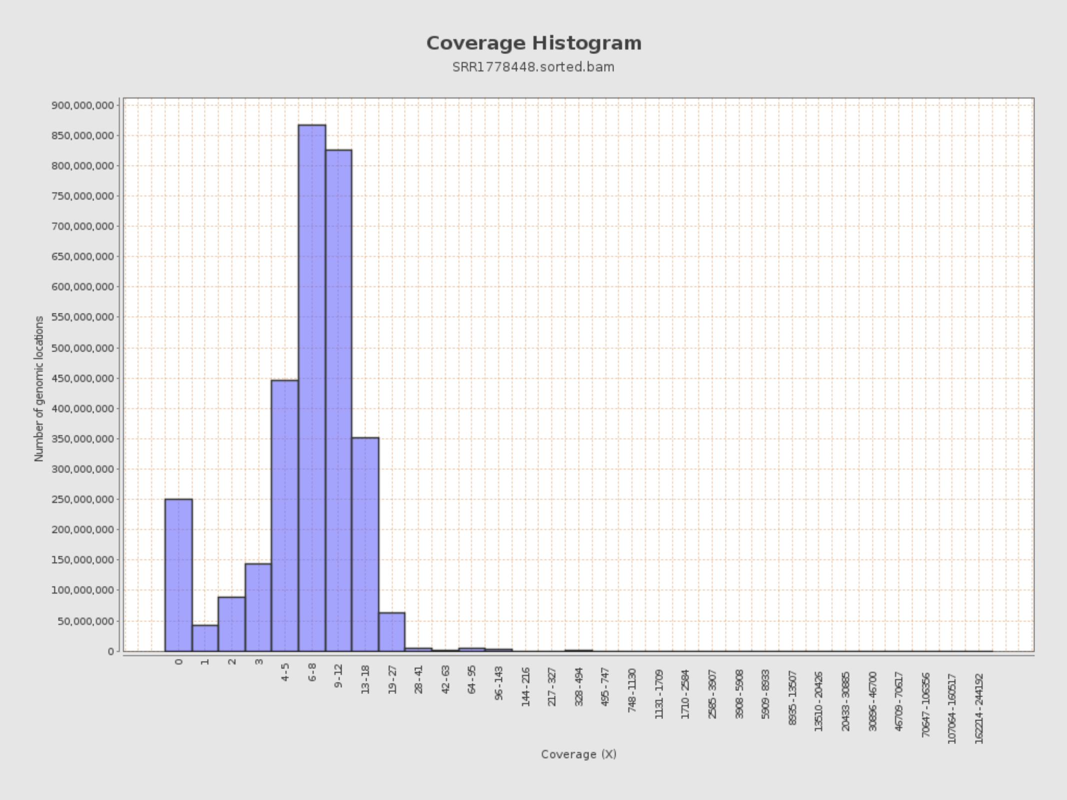
		bases	coverage	deviation
chr1	249250621	2070766909	8.308	245.7505
chr2	243199373	2151804489	8.8479	56.5741
chr3	198022430	1657997540	8.3728	11.8564
chr4	191154276	1651450891	8.6394	51.7053
chr5	180915260	2140095824	11.8293	9.0991
chr6	171115067	1180773890	6.9005	28.3171
chr7	159138663	2800015272	17.5948	135.5205
chr8	146364022	1264717805	8.6409	91.7279
chr9	141213431	1285406999	9.1026	70.0516
chr10	135534747	883852641	6.5212	179.1422
chr11	135006516	1142213387	8.4604	43.0053
chr12	133851895	1105455403	8.2588	8.4946
chr13	115169878	796220240	6.9134	5.3551
chr14	107349540	713336191	6.645	9.8393
chr15	102531392	577860631	5.6359	5.0353
chr16	90354753	689395453	7.6299	36.2828
chr17	81195210	689877972	8.4965	37.4225
chr18	78077248	671063984	8.5949	97.0712
chr19	59128983	507386125	8.581	130.9245
chr20	63025520	512730067	8.1353	14.6124
chr21	48129895	349309828	7.2576	34.6912
chr22	51304566	300132530	5.85	22.2821
chrMT	16571	20733866	1,251.2139	119.4376
chrX	155270560	672228055	4.3294	17.5591

chrY	59373566	254343447	4.2838	71.902

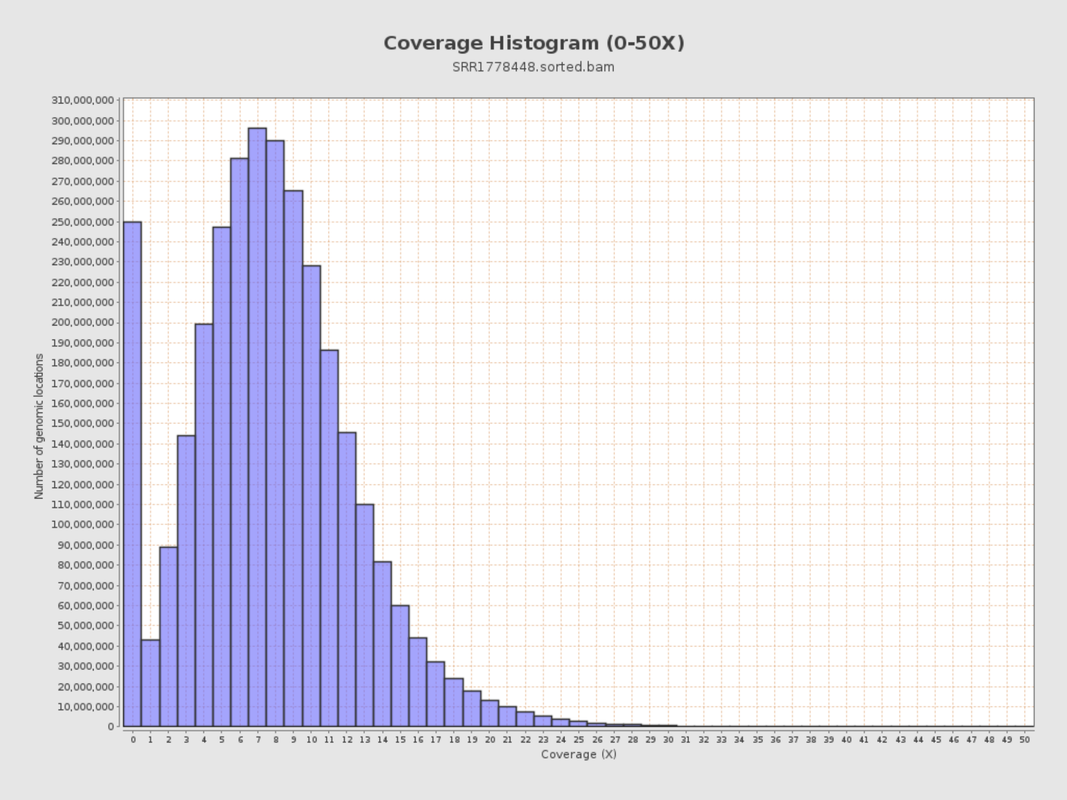
3. Results : Coverage across reference



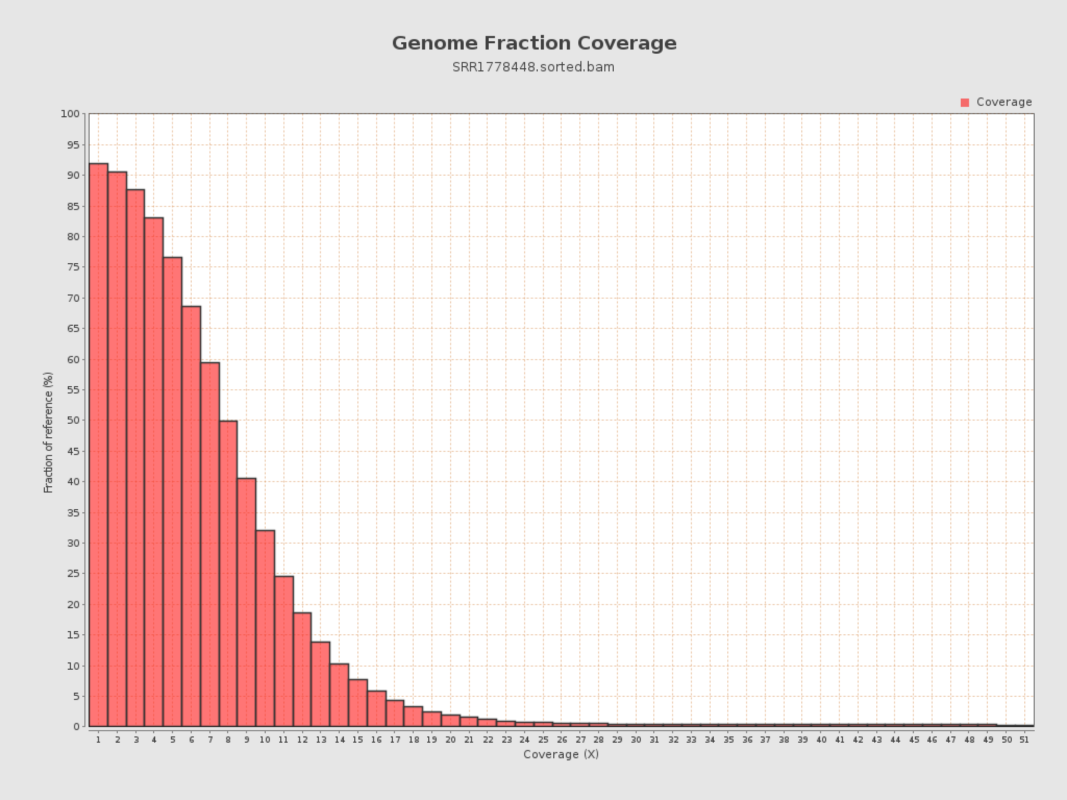
4. Results : Coverage Histogram



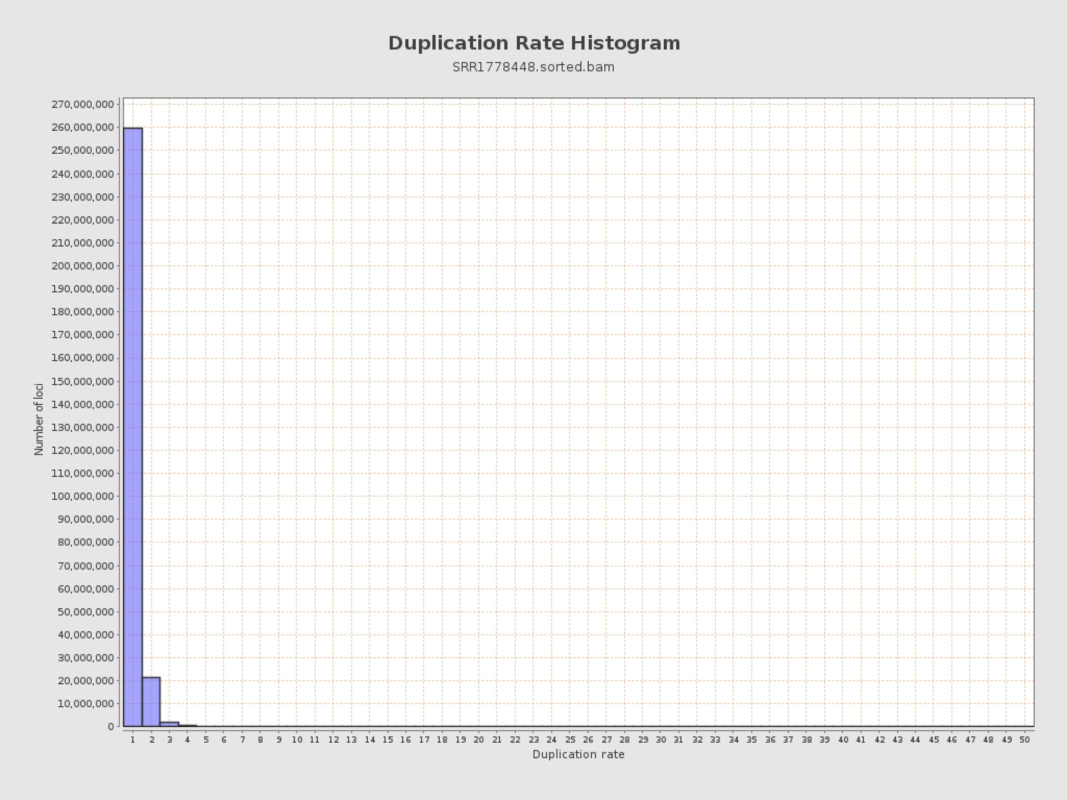
5. Results : Coverage Histogram (0-50X)



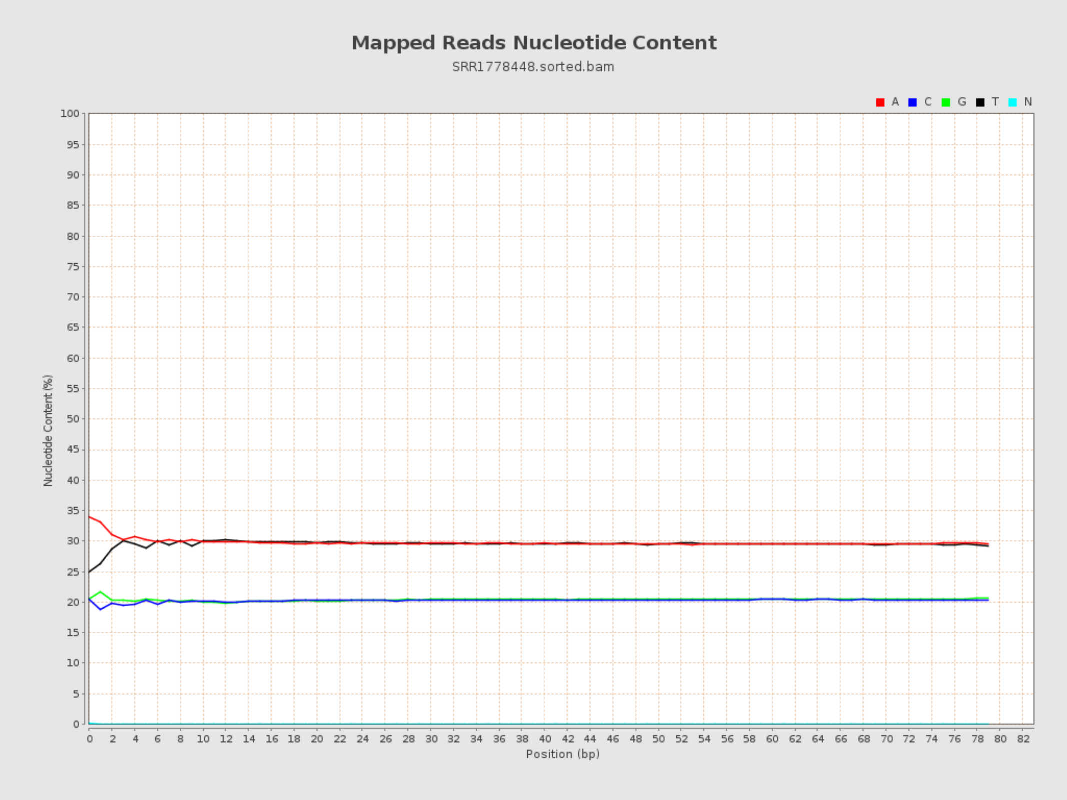
6. Results : Genome Fraction Coverage



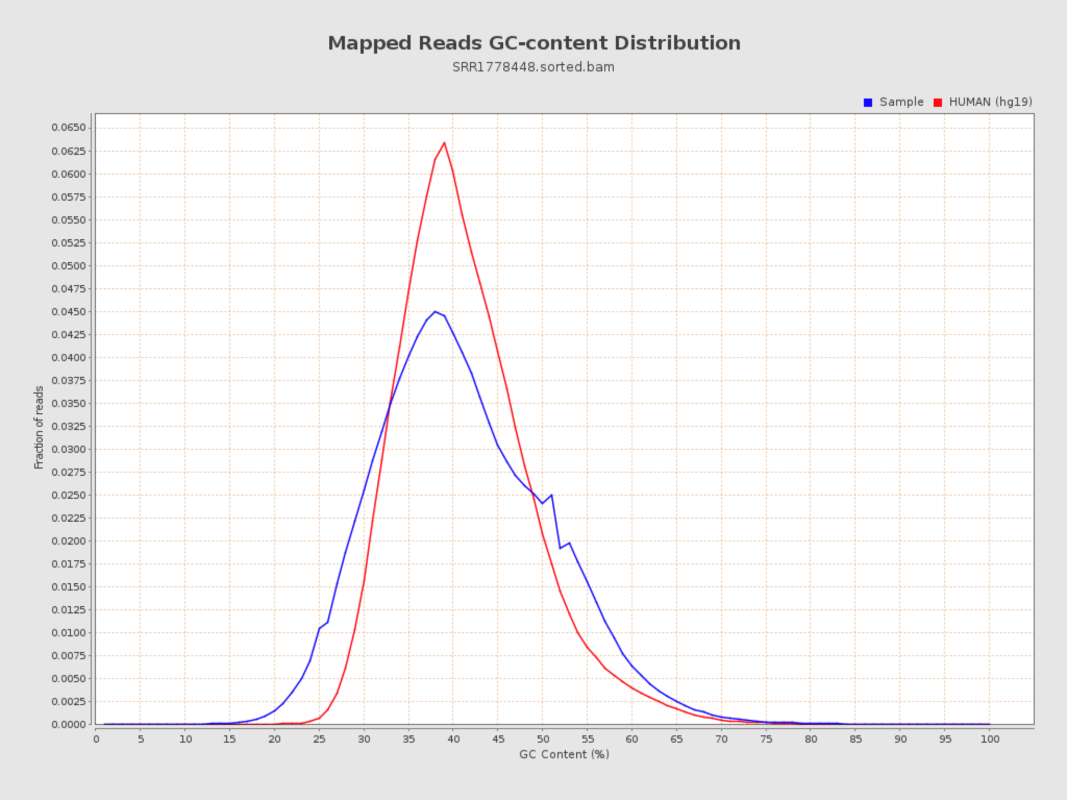
7. Results : Duplication Rate Histogram



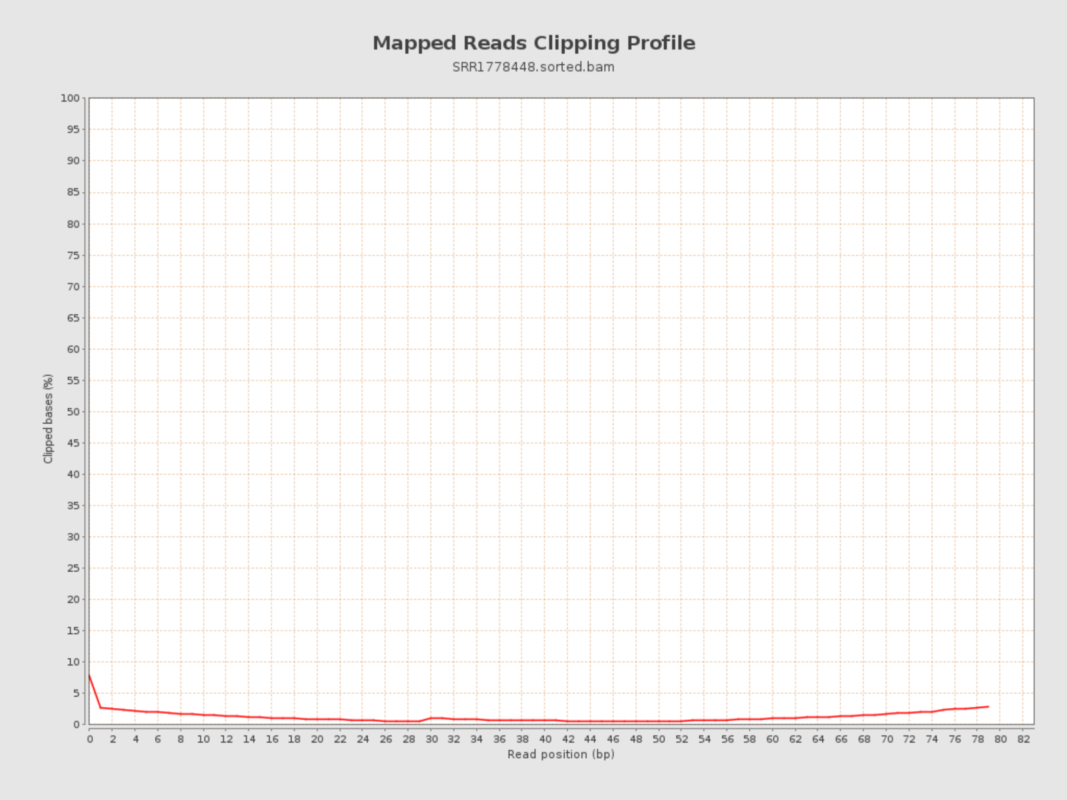
8. Results : Mapped Reads Nucleotide Content



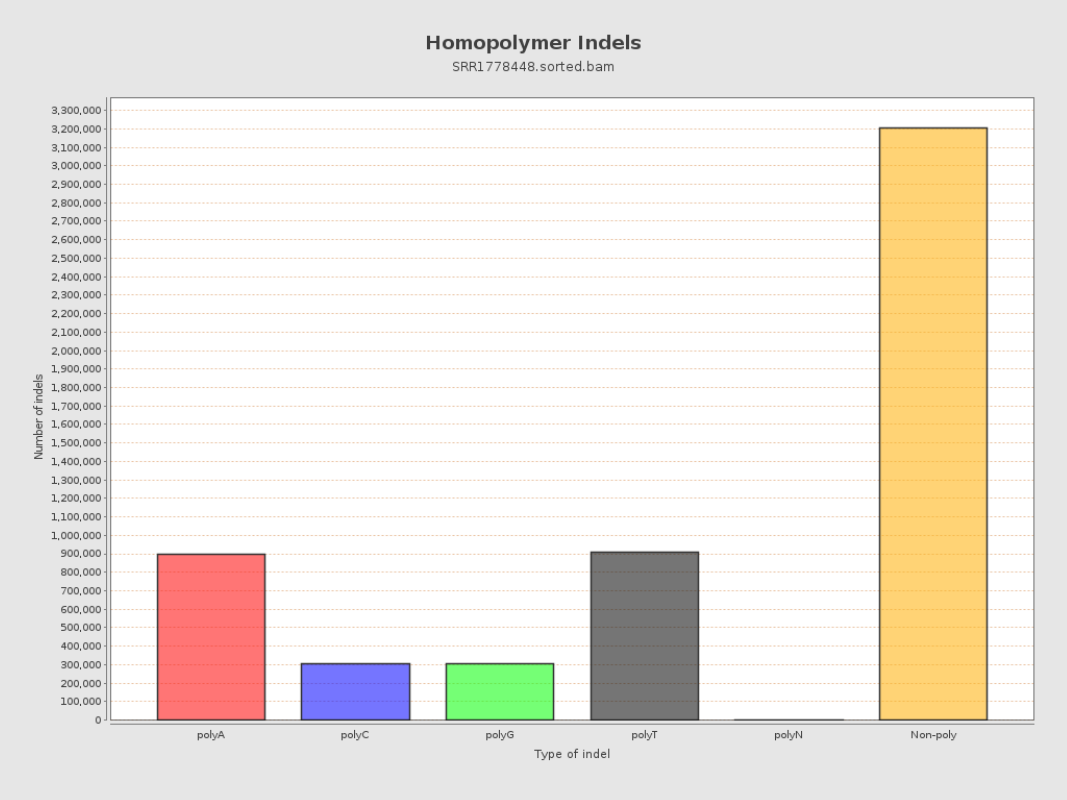
9. Results : Mapped Reads GC-content Distribution



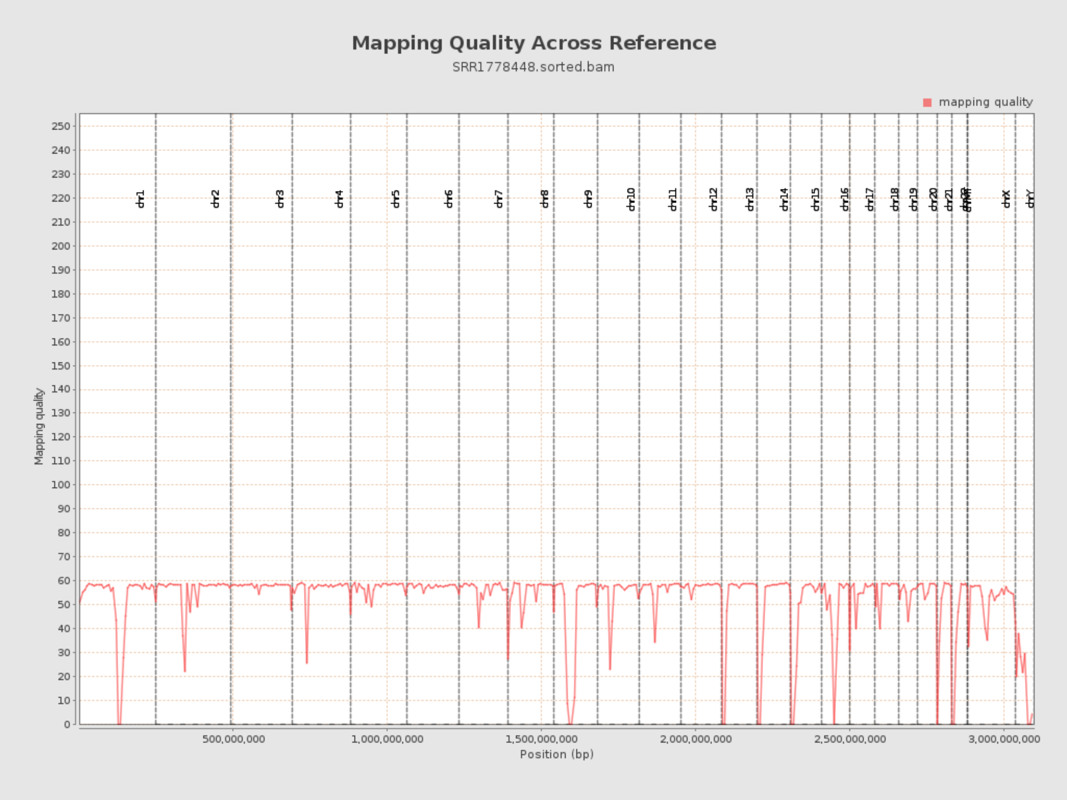
10. Results : Mapped Reads Clipping Profile



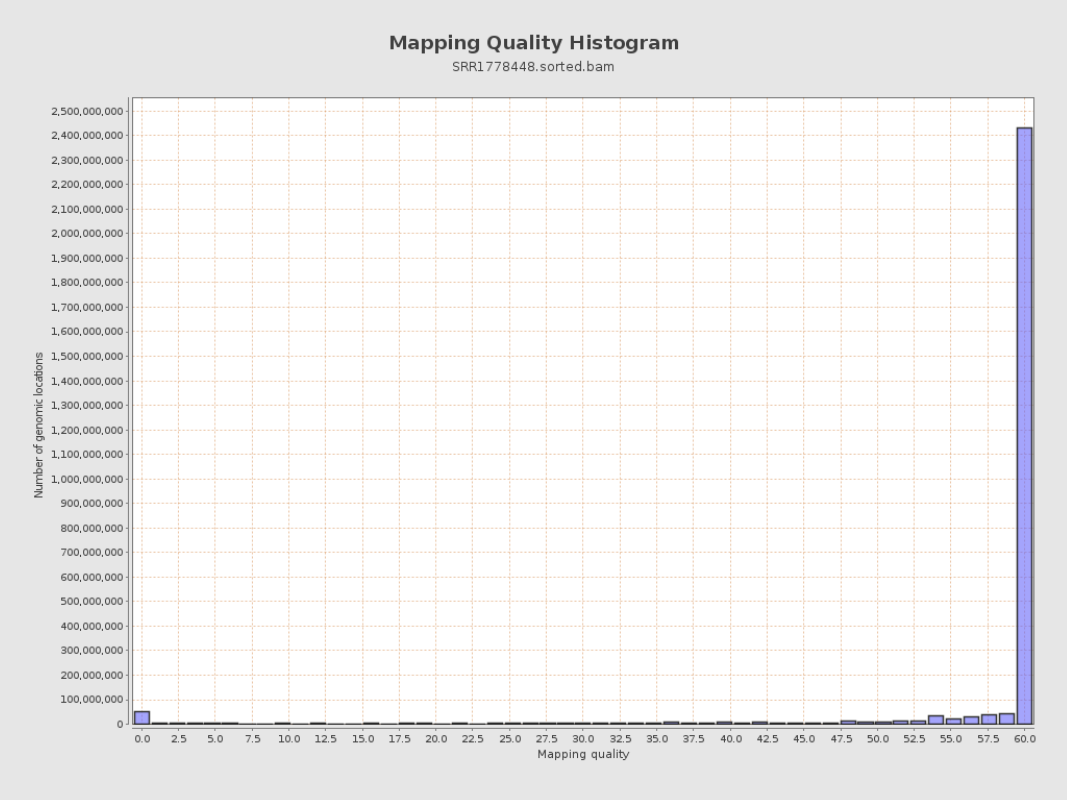
11. Results : Homopolymer Indels



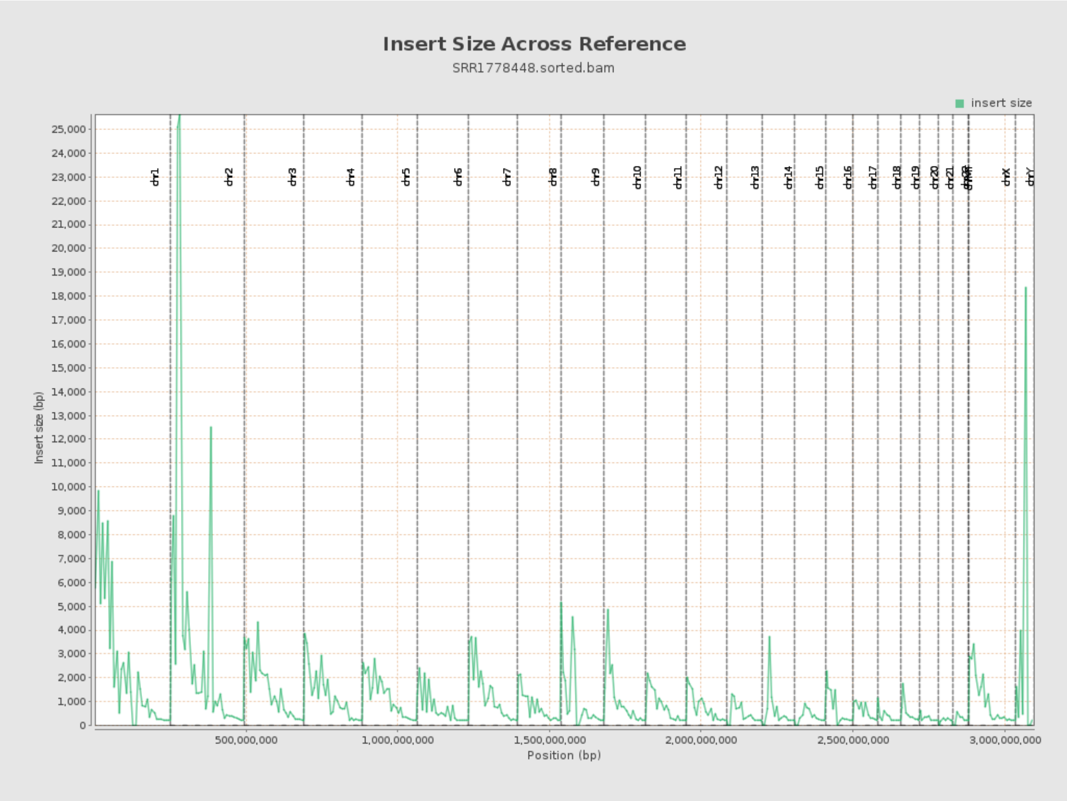
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram