Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 20:58:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779347.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_SRR1779347 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779347_1.fastq.gz SRR1779347_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 20:58:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779347.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	332,989,276
Mapped reads	316,363,832 / 95.01%
Unmapped reads	16,625,444 / 4.99%
Mapped paired reads	316,363,832 / 95.01%
Mapped reads, first in pair	159,612,870 / 47.93%
Mapped reads, second in pair	156,750,962 / 47.07%
Mapped reads, both in pair	310,501,004 / 93.25%
Mapped reads, singletons	5,862,828 / 1.76%
Secondary alignments	0
Supplementary alignments	2,107,669 / 0.63%
Read min/max/mean length	30 / 101 / 101.26
Duplicated reads (estimated)	39,876,887 / 11.98%
Duplication rate	10.61%
Clipped reads	16,787,745 / 5.04%

2.2. ACGT Content

Number/percentage of A's	9,423,831,479 / 29.73%
Number/percentage of C's	6,389,563,323 / 20.16%
Number/percentage of T's	9,382,987,383 / 29.6%
Number/percentage of G's	6,496,979,896 / 20.5%
Number/percentage of N's	6,700,398 / 0.02%

GC Percentage	40.65%

2.3. Coverage

Mean	10.2428
Standard Deviation	33.6365

2.4. Mapping Quality

Mean Mapping Quality	54.03

2.5. Insert size

Mean	67,364.8
Standard Deviation	2,515,676.43
P25/Median/P75	224 / 296 / 376

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	126,154,238
Insertions	3,153,215
Mapped reads with at least one insertion	0.98%
Deletions	3,848,165
Mapped reads with at least one deletion	1.19%
Homopolymer indels	47.97%

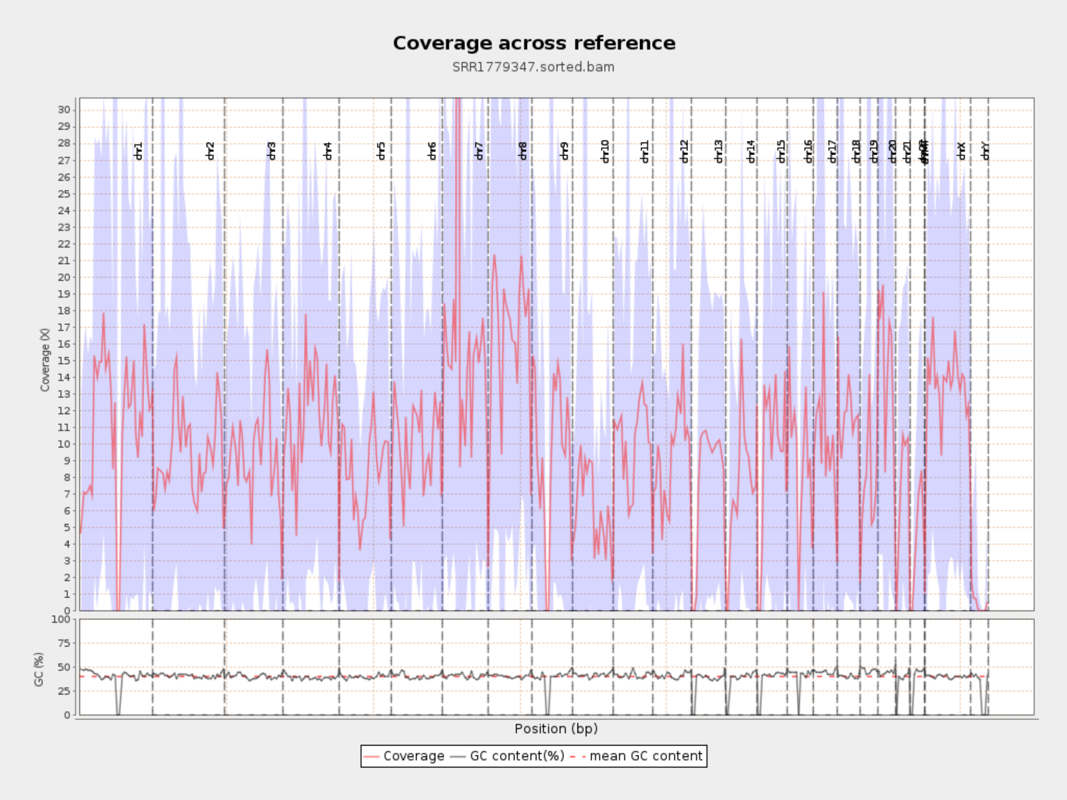
2.7. Chromosome stats

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

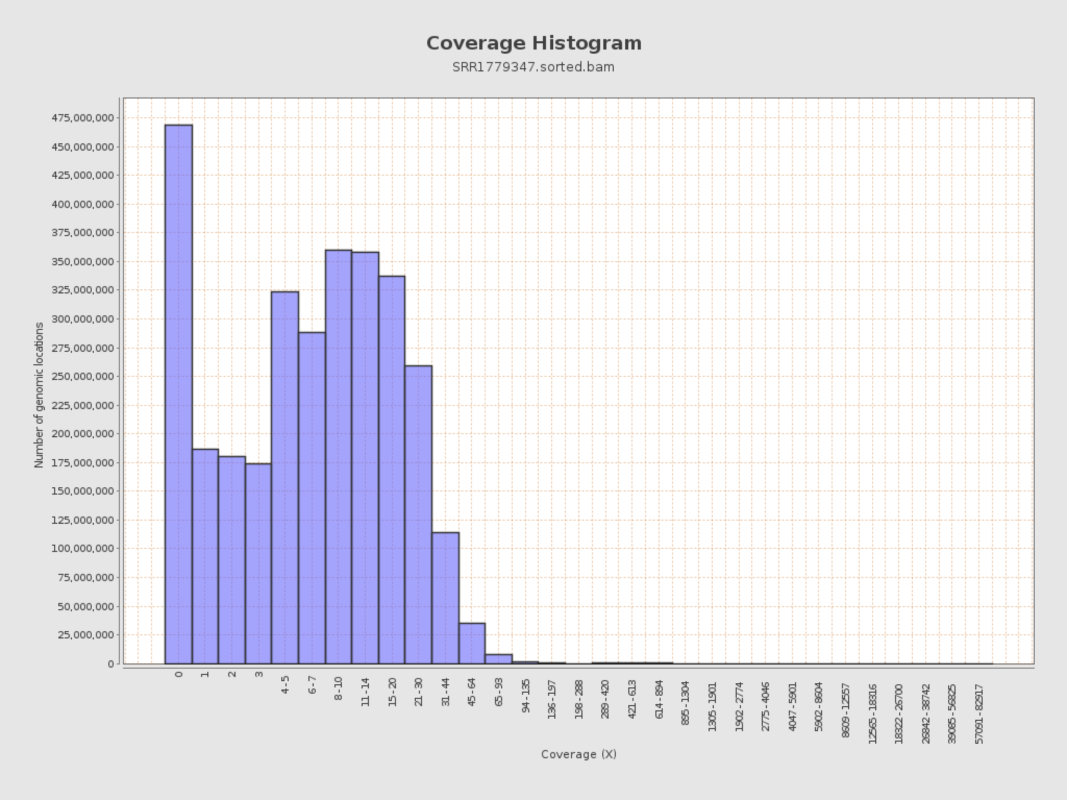
		bases	coverage	deviation
chr1	249250621	2787303431	11.1827	87.1453
chr2	243199373	2317490565	9.5292	18.9073
chr3	198022430	1859300391	9.3893	9.6448
chr4	191154276	2257503385	11.8099	11.6198
chr5	180915260	1491158063	8.2423	8.6557
chr6	171115067	1751440437	10.2355	17.2314
chr7	159138663	2783609365	17.4917	54.2485
chr8	146364022	2474522999	16.9066	15.2028
chr9	141213431	1329618151	9.4157	23.8919
chr10	135534747	828164554	6.1103	45.8269
chr11	135006516	1356971209	10.0512	12.7026
chr12	133851895	1241808096	9.2775	20.535
chr13	115169878	919588008	7.9846	9.1653
chr14	107349540	791959980	7.3774	9.5143
chr15	102531392	959010615	9.3533	11.9698
chr16	90354753	786948107	8.7095	11.1471
chr17	81195210	830446498	10.2278	31.593
chr18	78077248	912643194	11.689	26.581
chr19	59128983	430823229	7.2862	58.9826
chr20	63025520	918575787	14.5747	14.5104
chr21	48129895	353491667	7.3445	9.6515
chr22	51304566	214447506	4.1799	7.1594
chrMT	16571	17322	1.0453	2.1981
chrX	155270560	2087862277	13.4466	13.2625

chrY	59373566	23924155	0.4029	4.5302

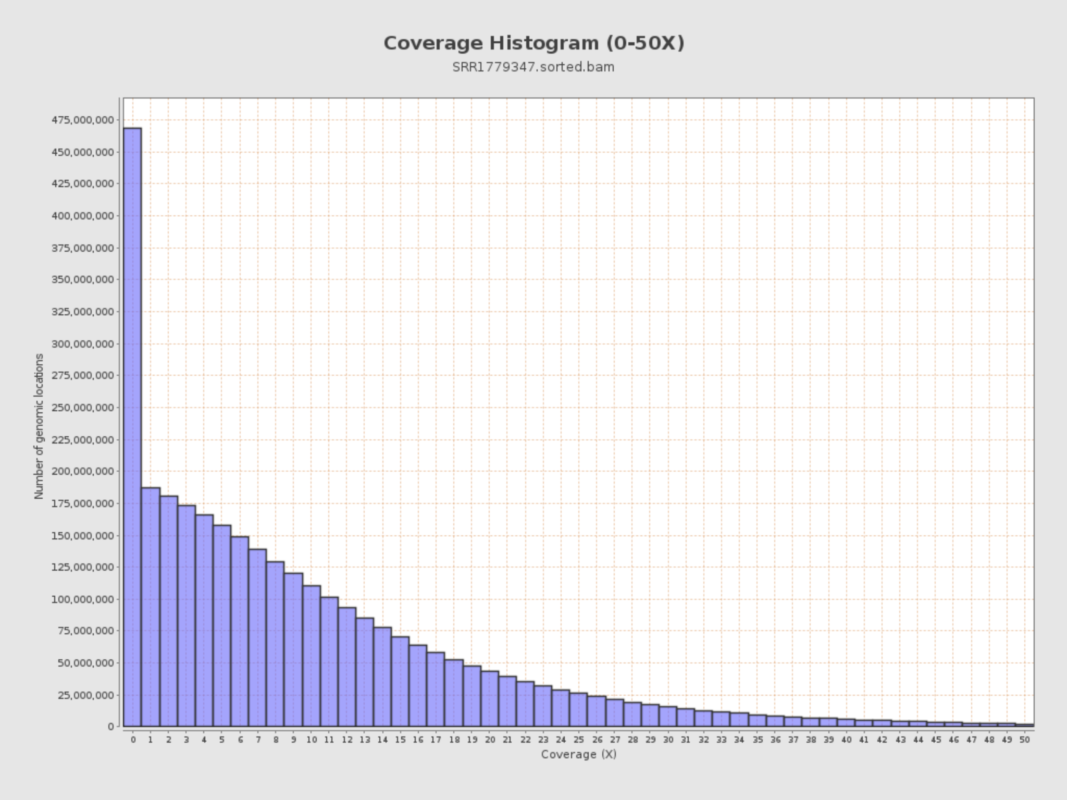
3. Results : Coverage across reference



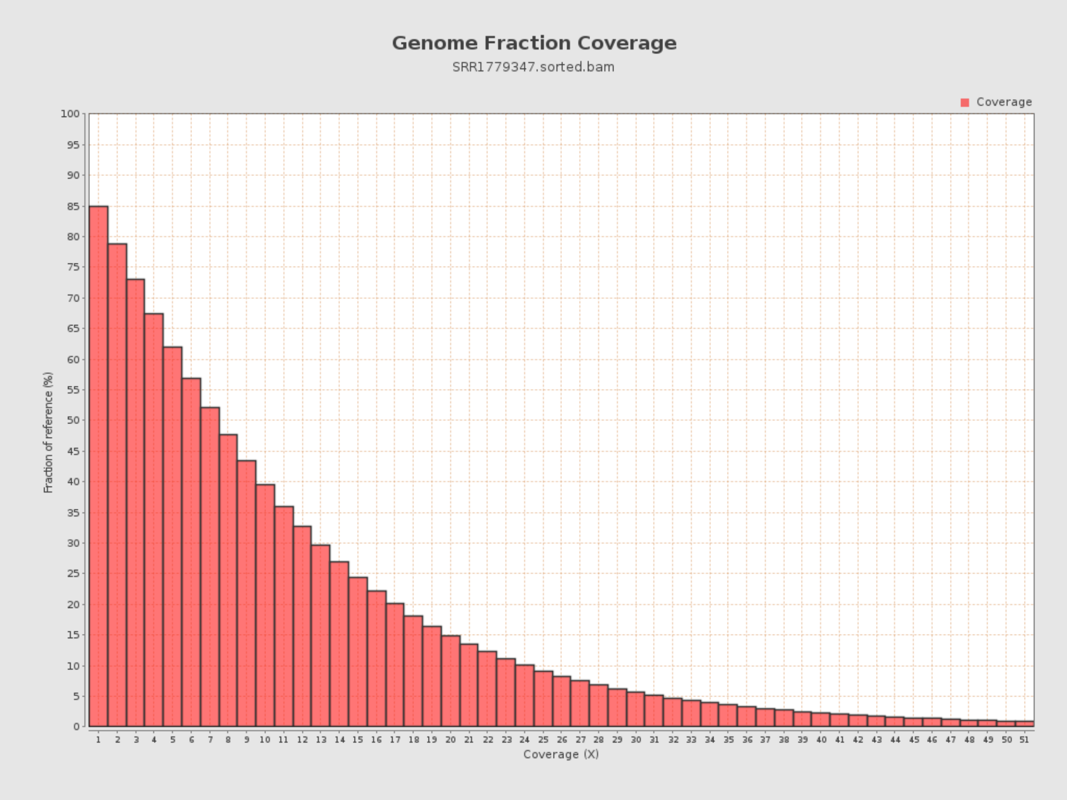
4. Results : Coverage Histogram



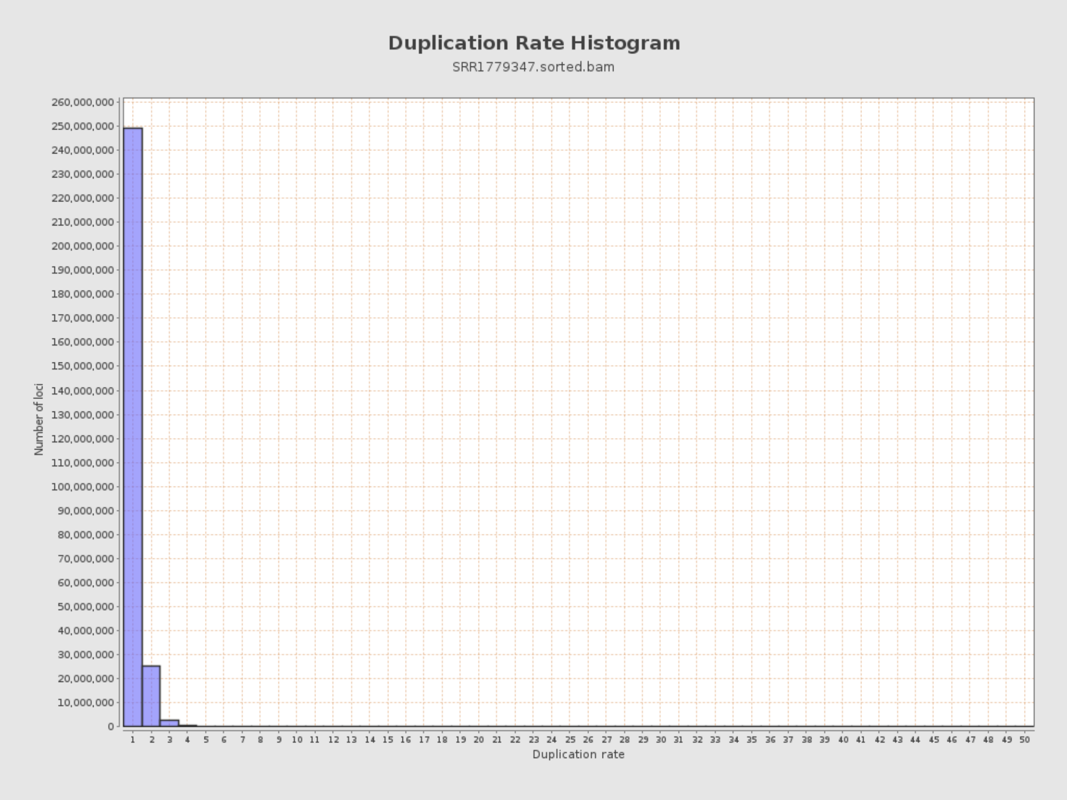
5. Results : Coverage Histogram (0-50X)



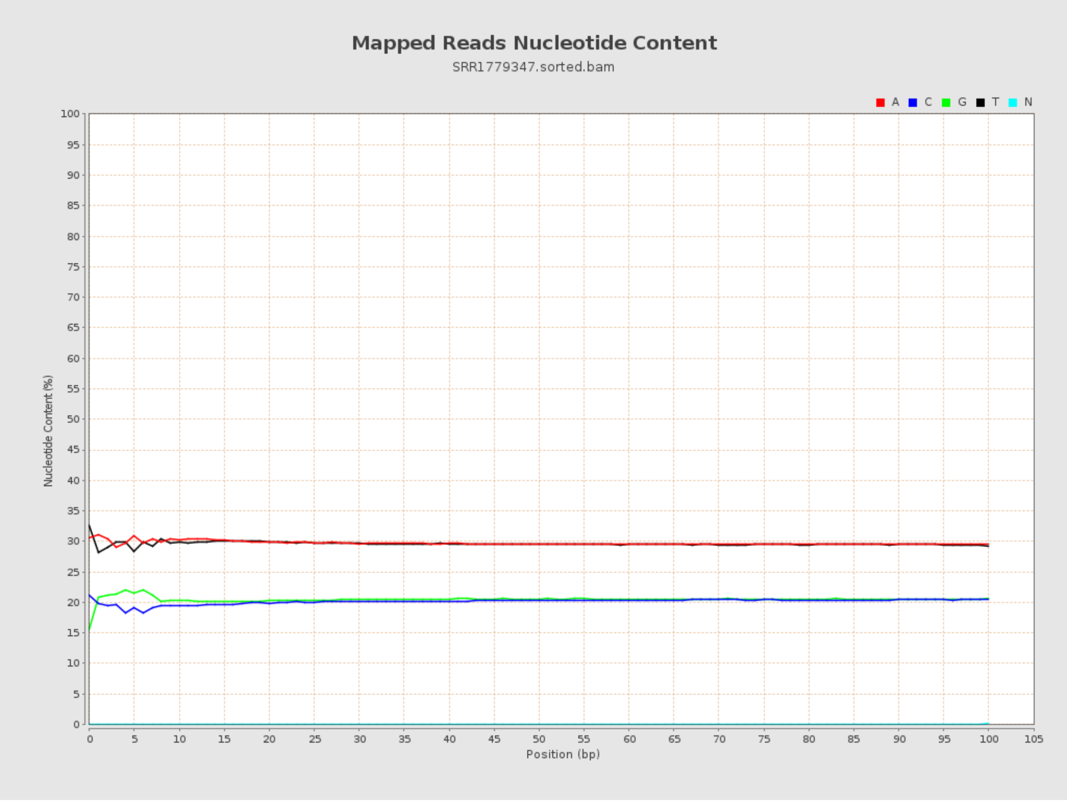
6. Results : Genome Fraction Coverage



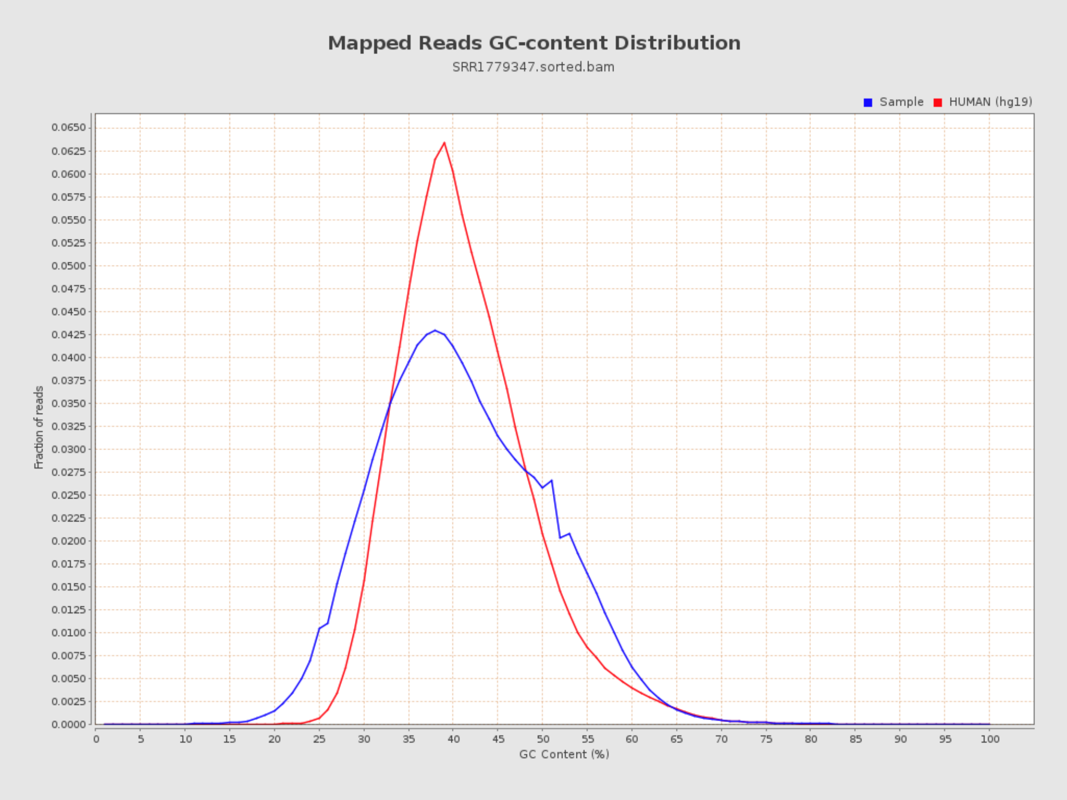
7. Results : Duplication Rate Histogram



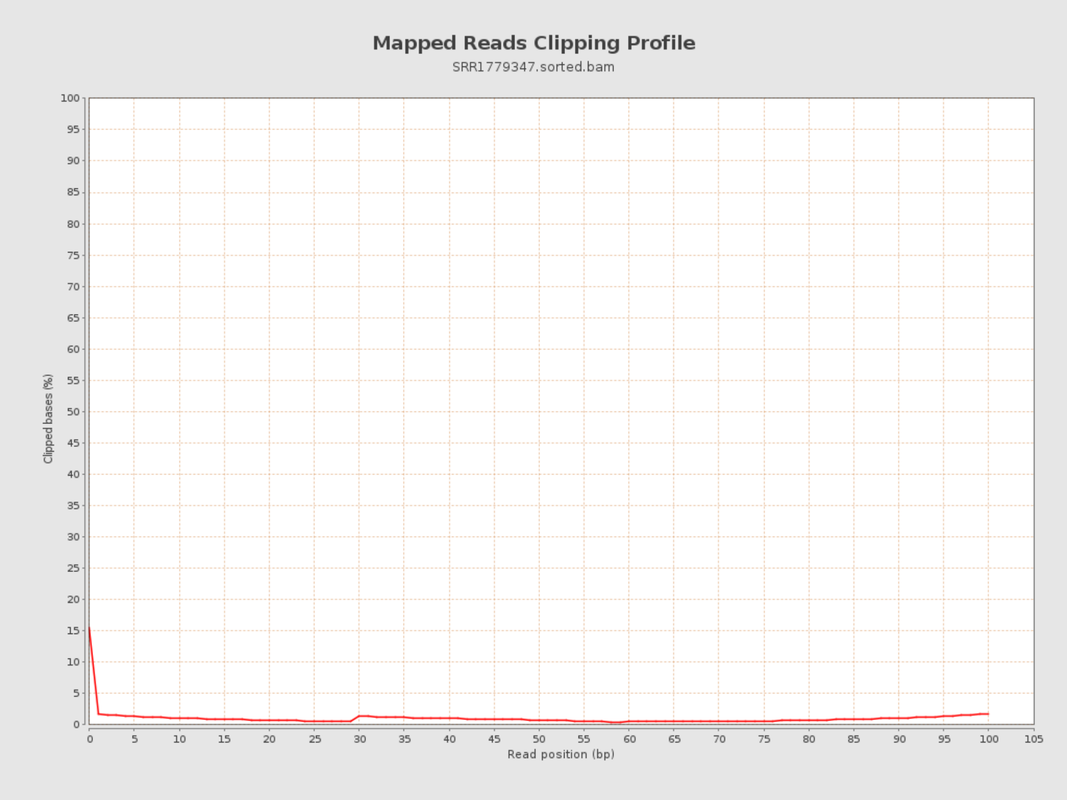
8. Results : Mapped Reads Nucleotide Content



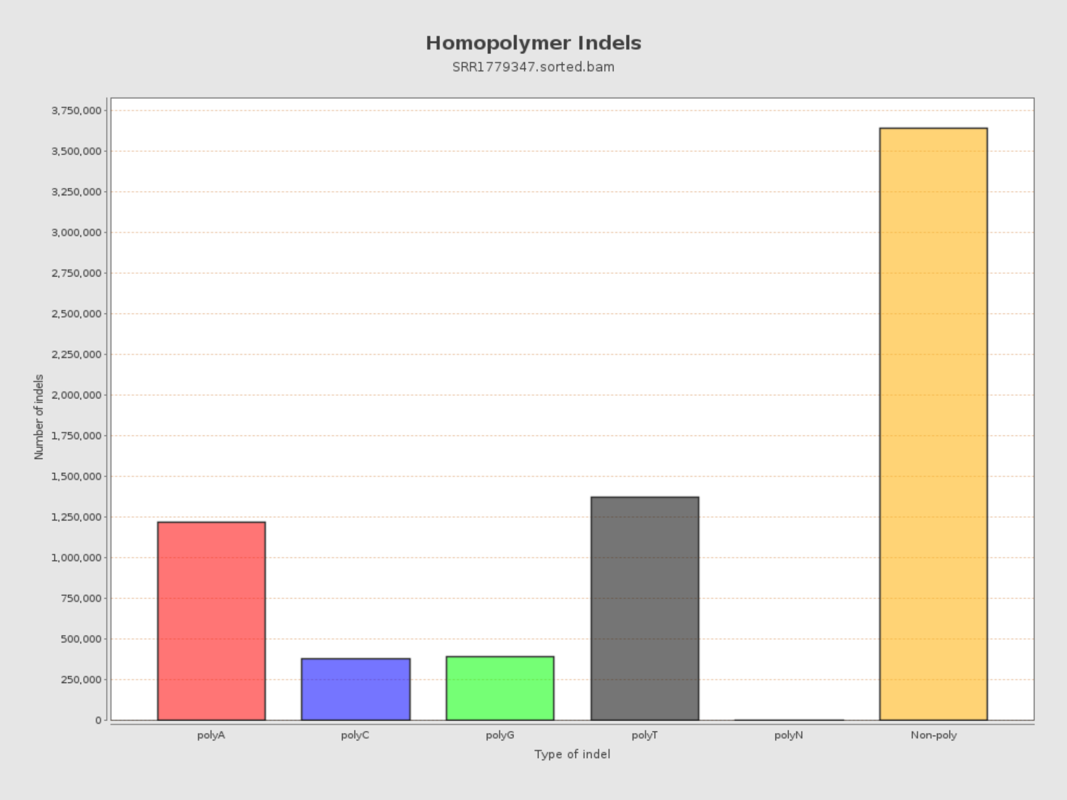
9. Results : Mapped Reads GC-content Distribution



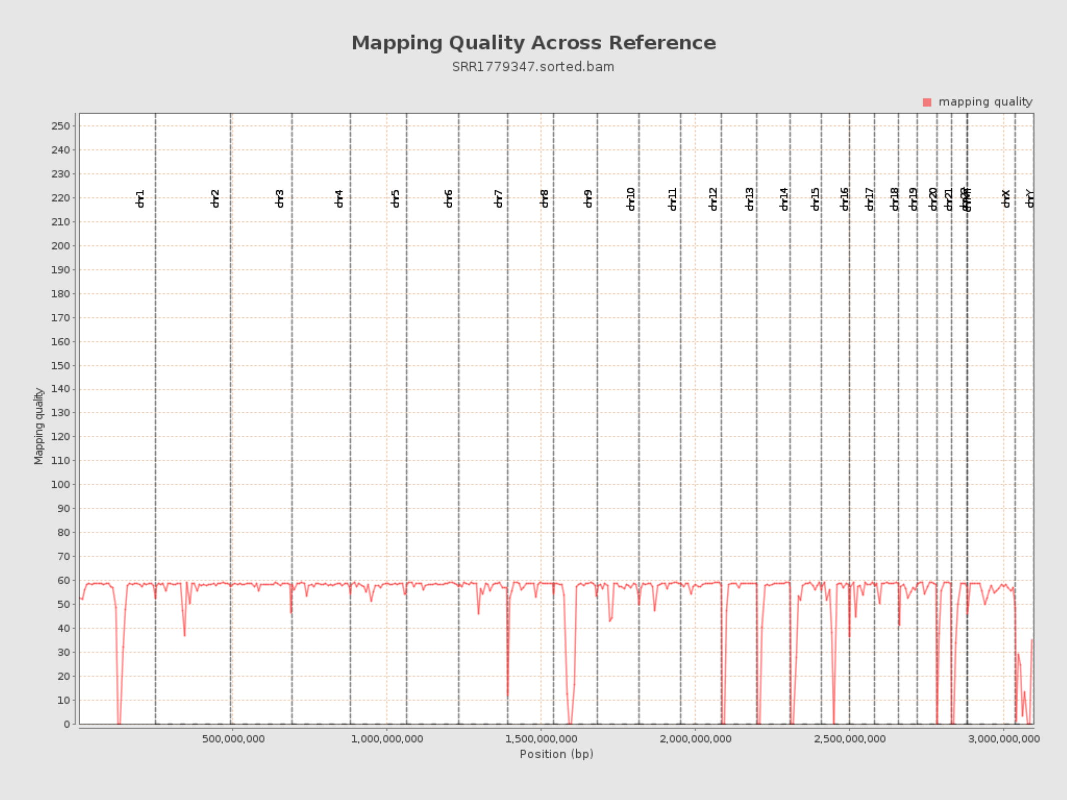
10. Results : Mapped Reads Clipping Profile



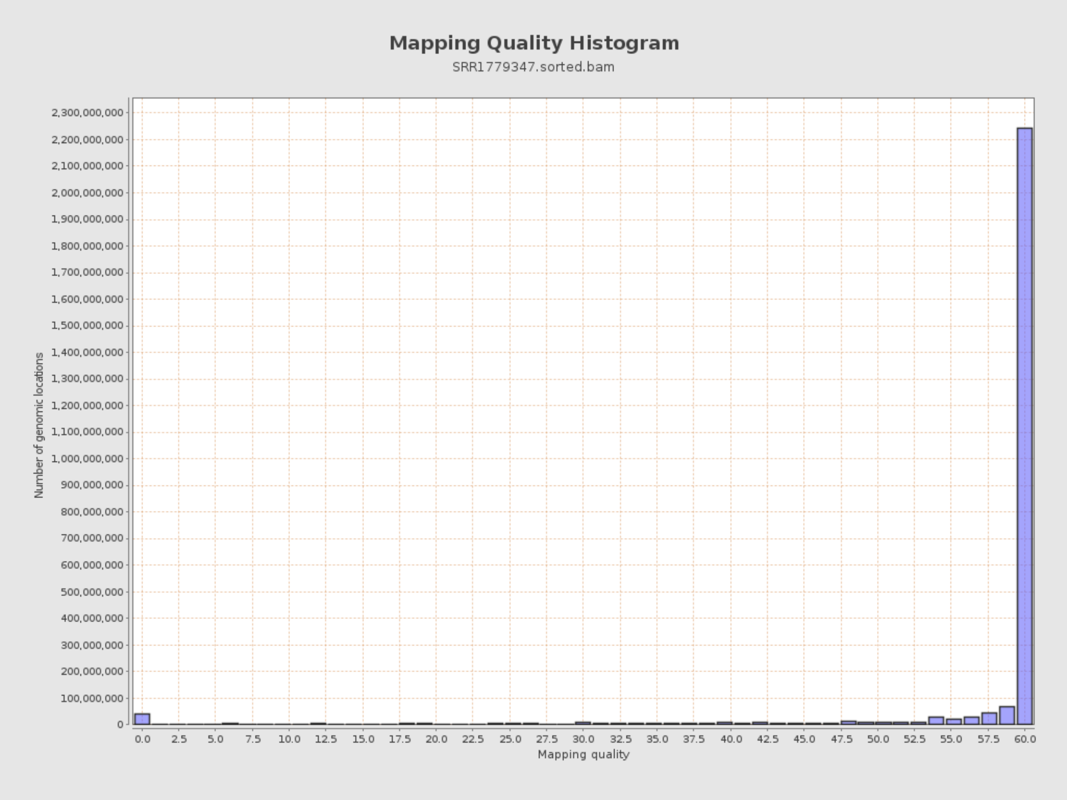
11. Results : Homopolymer Indels



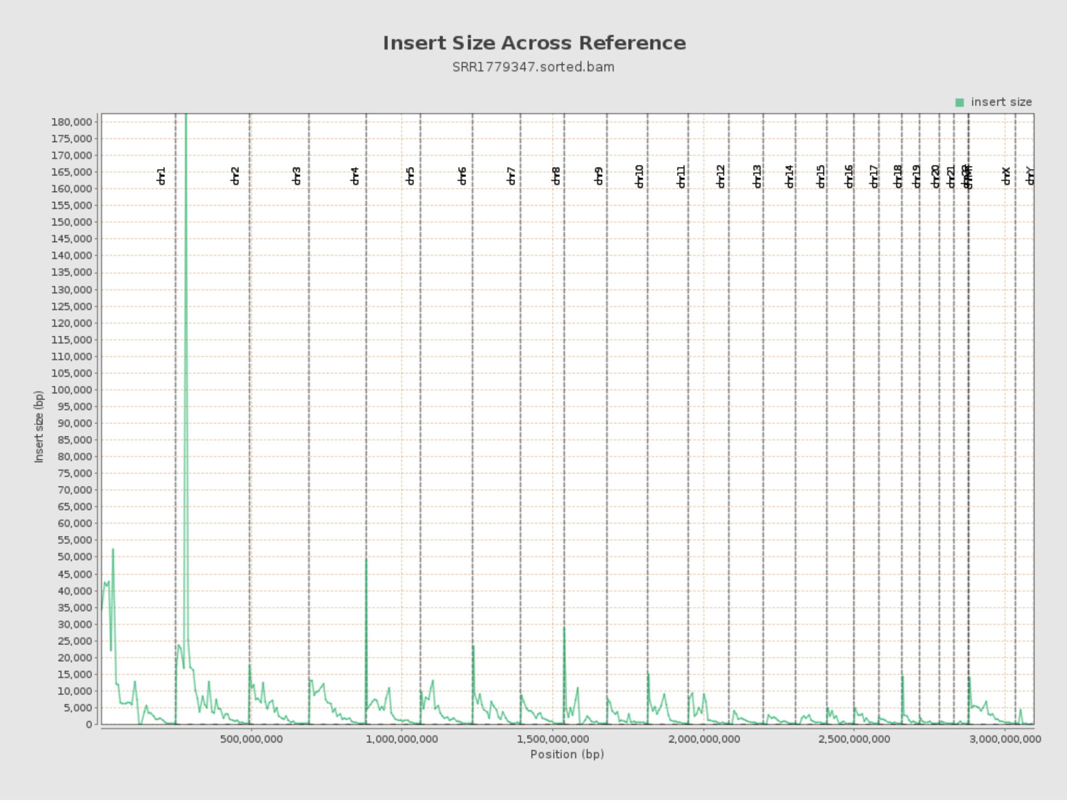
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram