Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 13:17:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779345.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_SRR1779345 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779345_1.fastq.gz SRR1779345_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 13:17:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779345.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	304,893,820
Mapped reads	272,562,416 / 89.4%
Unmapped reads	32,331,404 / 10.6%
Mapped paired reads	272,562,416 / 89.4%
Mapped reads, first in pair	138,135,067 / 45.31%
Mapped reads, second in pair	134,427,349 / 44.09%
Mapped reads, both in pair	265,157,444 / 86.97%
Mapped reads, singletons	7,404,972 / 2.43%
Secondary alignments	0
Supplementary alignments	1,650,642 / 0.54%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	36,090,887 / 11.84%
Duplication rate	10.75%
Clipped reads	14,149,517 / 4.64%

2.2. ACGT Content

Number/percentage of A's	8,204,294,557 / 30.07%
Number/percentage of C's	5,403,870,959 / 19.81%
Number/percentage of T's	8,134,848,641 / 29.82%
Number/percentage of G's	5,533,099,707 / 20.28%
Number/percentage of N's	5,715,382 / 0.02%

GC Percentage	40.09%

2.3. Coverage

Mean	8.8152
Standard Deviation	31.5245

2.4. Mapping Quality

Mean Mapping Quality	53.9

2.5. Insert size

Mean	52,071.5
Standard Deviation	2,212,467.1
P25/Median/P75	246 / 313 / 394

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	114,612,010
Insertions	2,741,651
Mapped reads with at least one insertion	0.99%
Deletions	3,322,103
Mapped reads with at least one deletion	1.2%
Homopolymer indels	48.09%

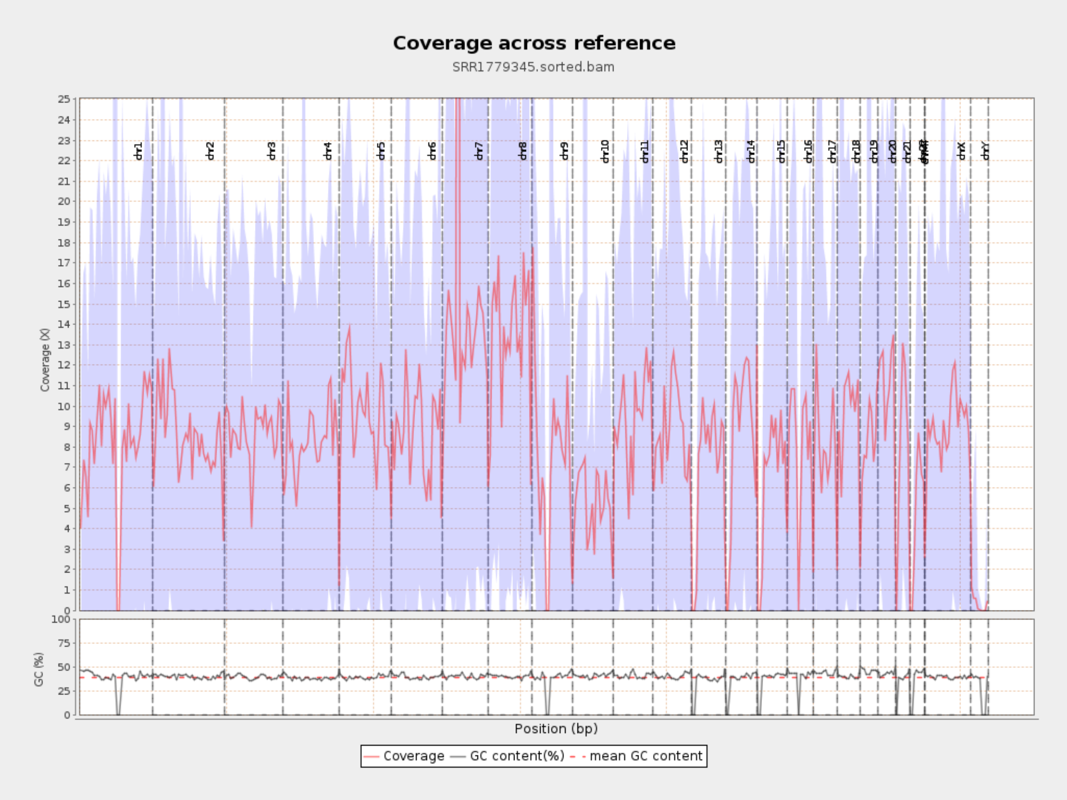
2.7. Chromosome stats

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

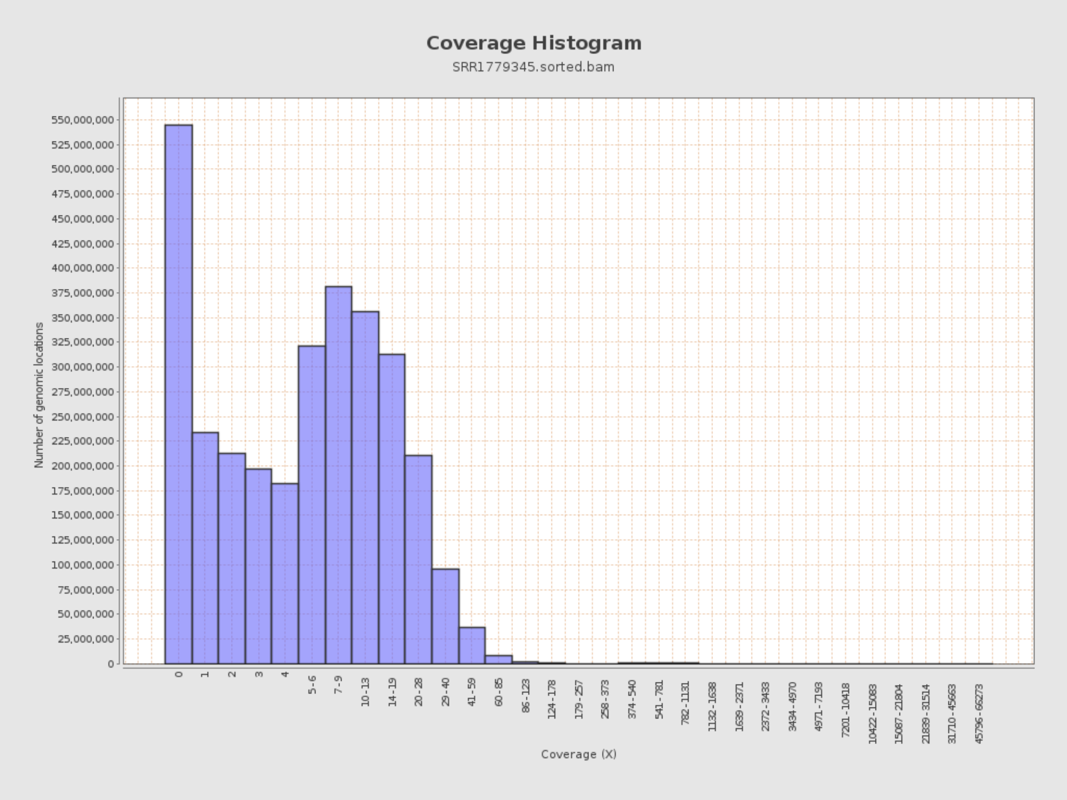
		bases	coverage	deviation
chr1	249250621	2057972910	8.2566	71.4406
chr2	243199373	2081127334	8.5573	16.8762
chr3	198022430	1727206914	8.7223	9.3367
chr4	191154276	1581825953	8.2751	11.1189
chr5	180915260	1733548931	9.5821	10.0343
chr6	171115067	1522809194	8.8993	13.4272
chr7	159138663	2670443785	16.7806	63.6745
chr8	146364022	1977189995	13.5087	14.3408
chr9	141213431	1058399173	7.495	20.5186
chr10	135534747	718320533	5.2999	61.3154
chr11	135006516	1283918399	9.51	11.2032
chr12	133851895	1175932720	8.7853	22.8704
chr13	115169878	815610515	7.0818	9.0747
chr14	107349540	908362598	8.4617	10.4741
chr15	102531392	659693410	6.4341	10.3615
chr16	90354753	689367020	7.6296	10.628
chr17	81195210	639835835	7.8802	22.0298
chr18	78077248	760557079	9.7411	22.8916
chr19	59128983	471565762	7.9752	46.4101
chr20	63025520	696509232	11.0512	12.4605
chr21	48129895	391435750	8.1329	11.4759
chr22	51304566	244877206	4.773	8.0506
chrMT	16571	48935	2.9531	2.5864
chrX	155270560	1402865273	9.035	11.62

chrY	59373566	19782346	0.3332	4.17

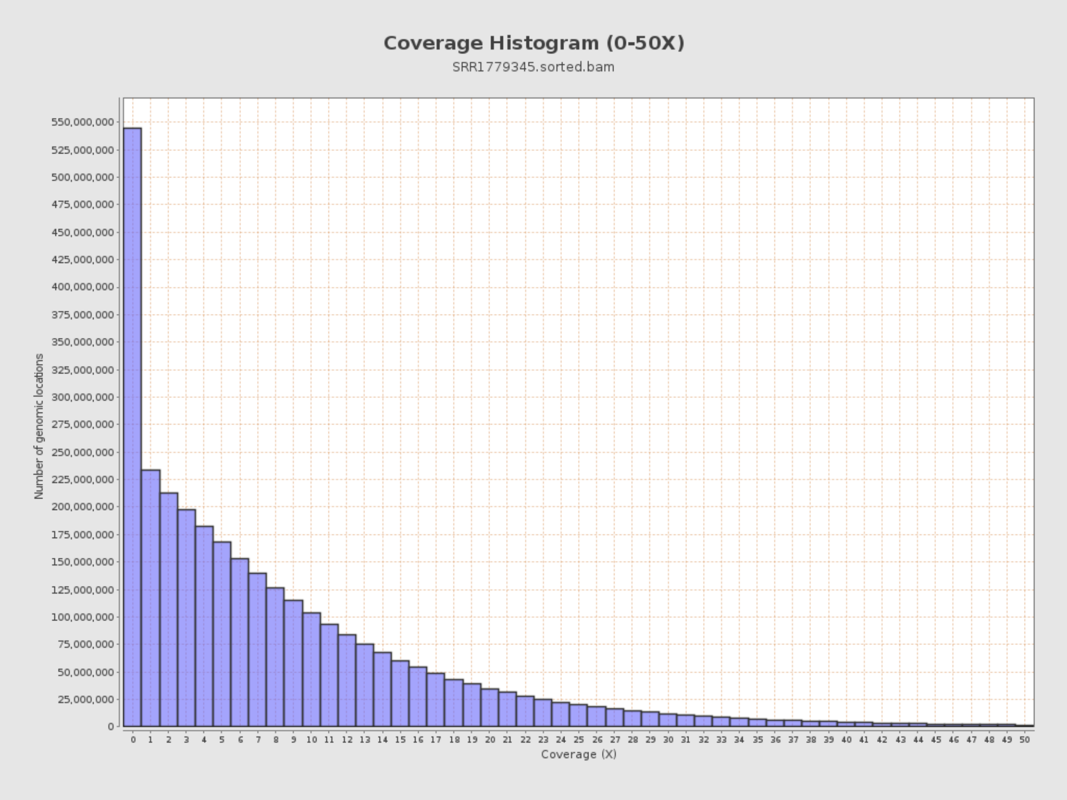
3. Results : Coverage across reference



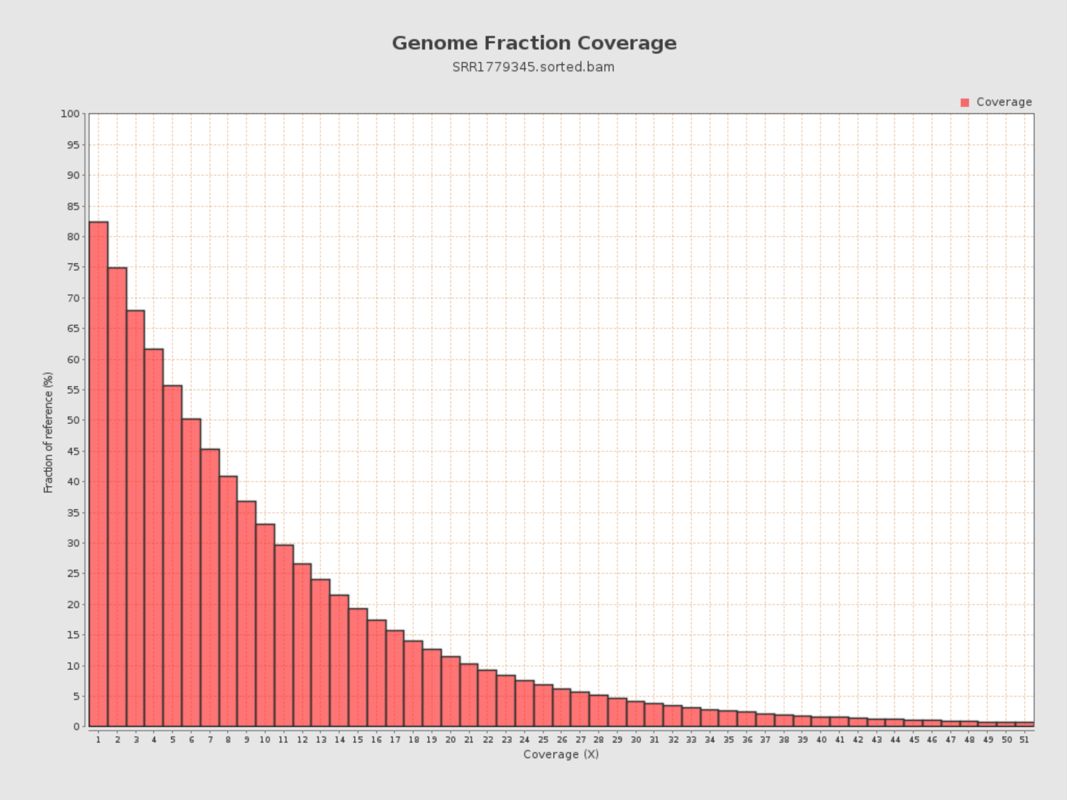
4. Results : Coverage Histogram



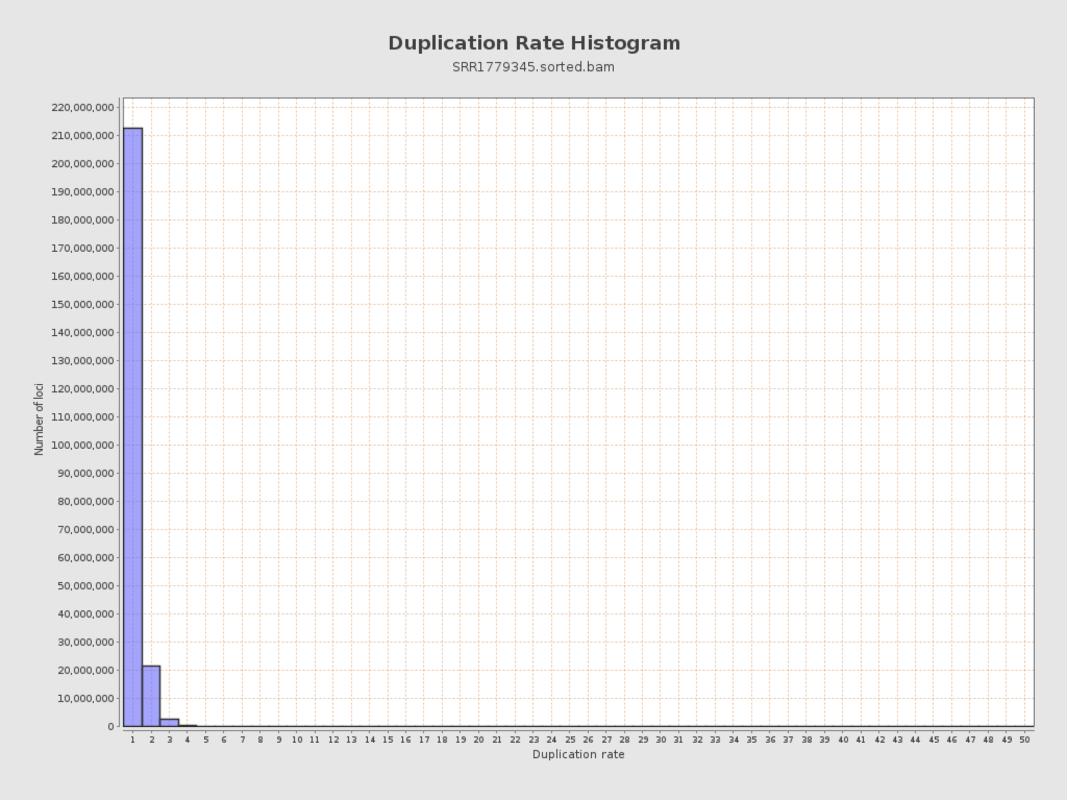
5. Results : Coverage Histogram (0-50X)



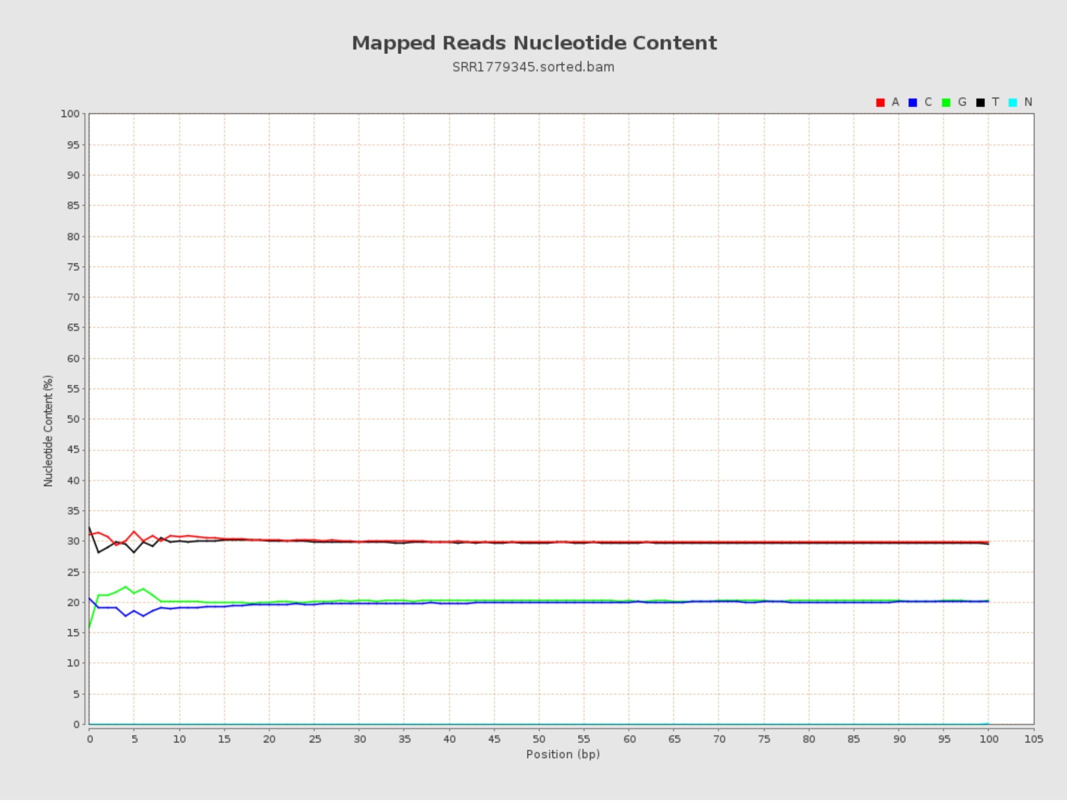
6. Results : Genome Fraction Coverage



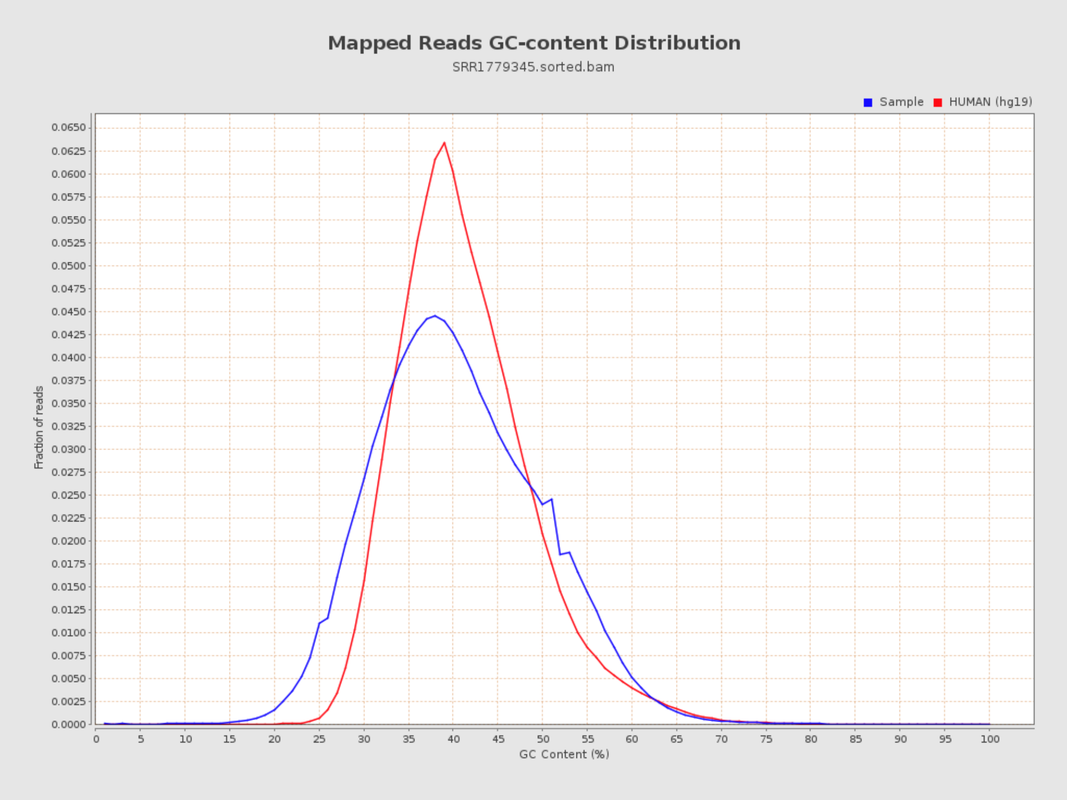
7. Results : Duplication Rate Histogram



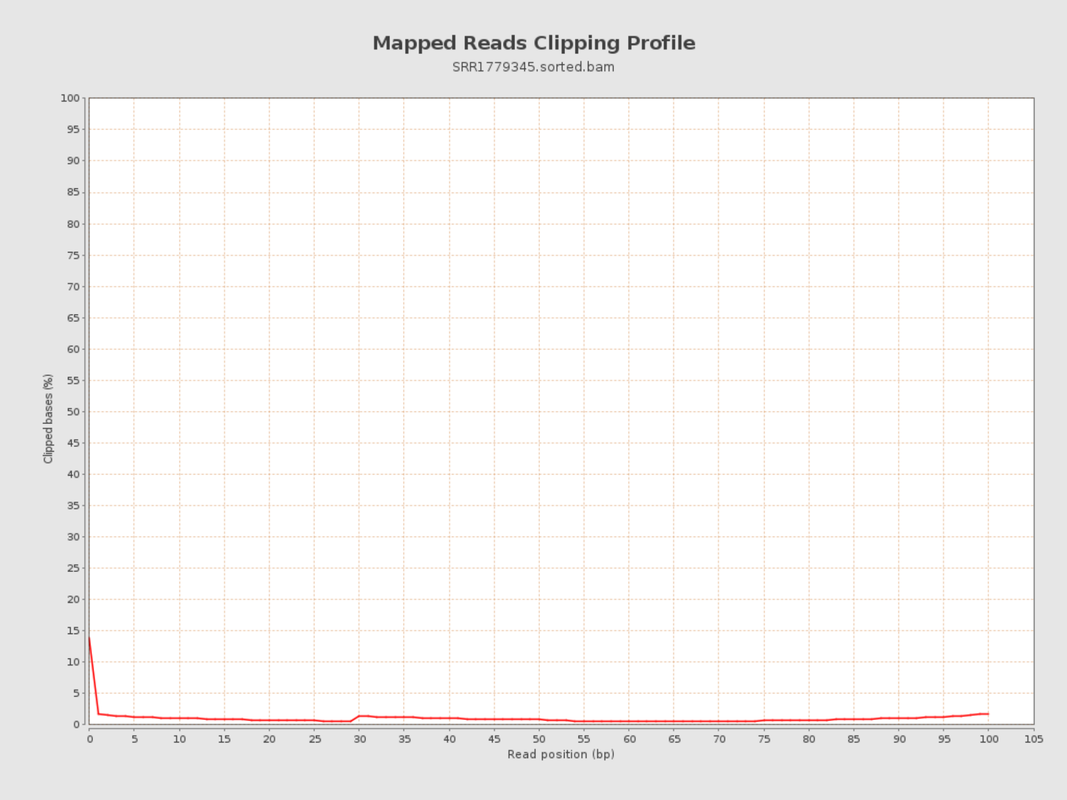
8. Results : Mapped Reads Nucleotide Content



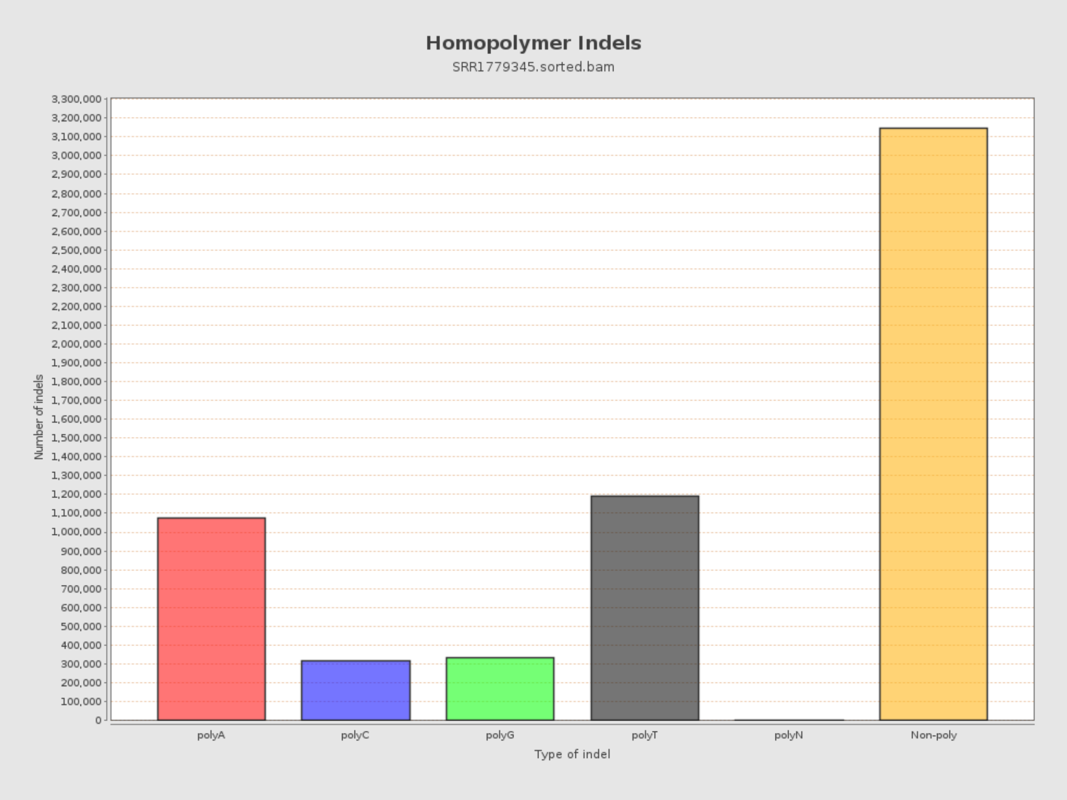
9. Results : Mapped Reads GC-content Distribution



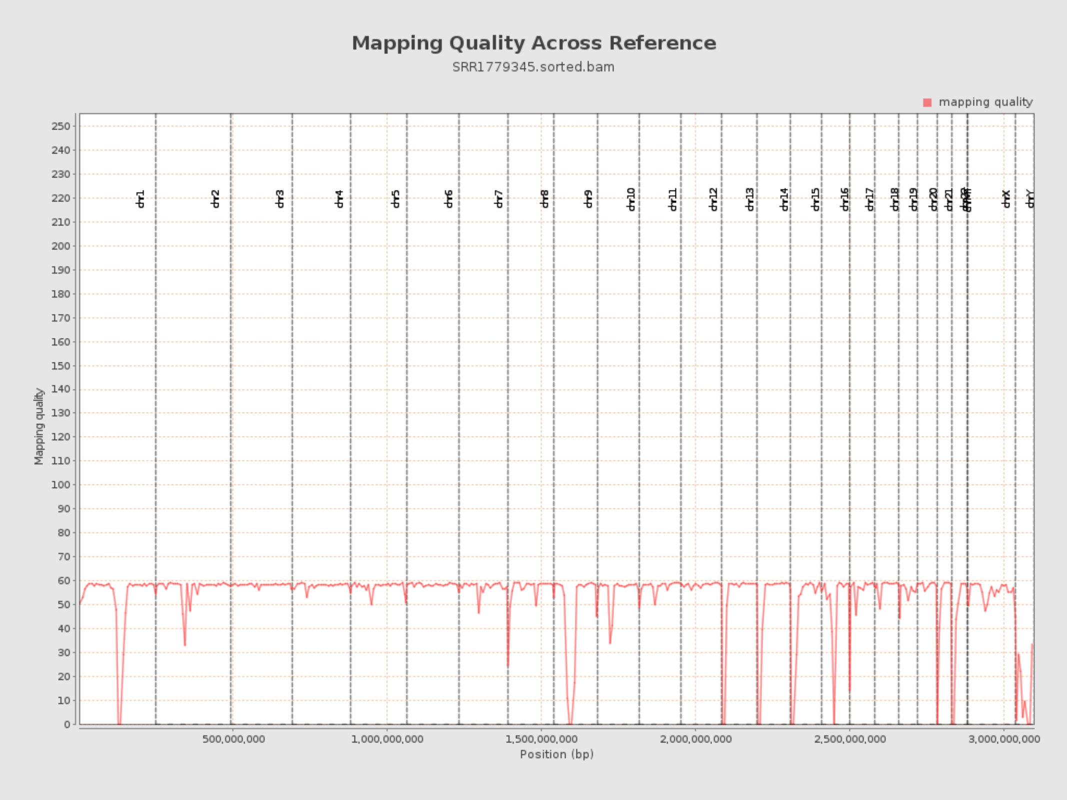
10. Results : Mapped Reads Clipping Profile



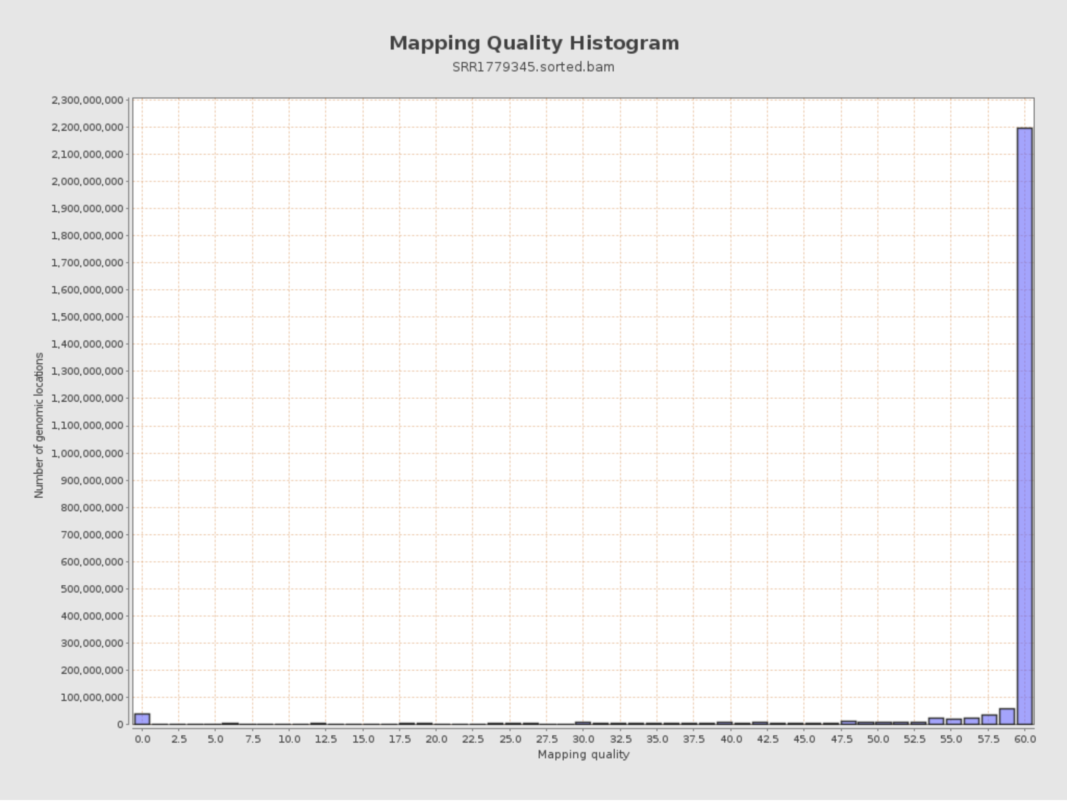
11. Results : Homopolymer Indels



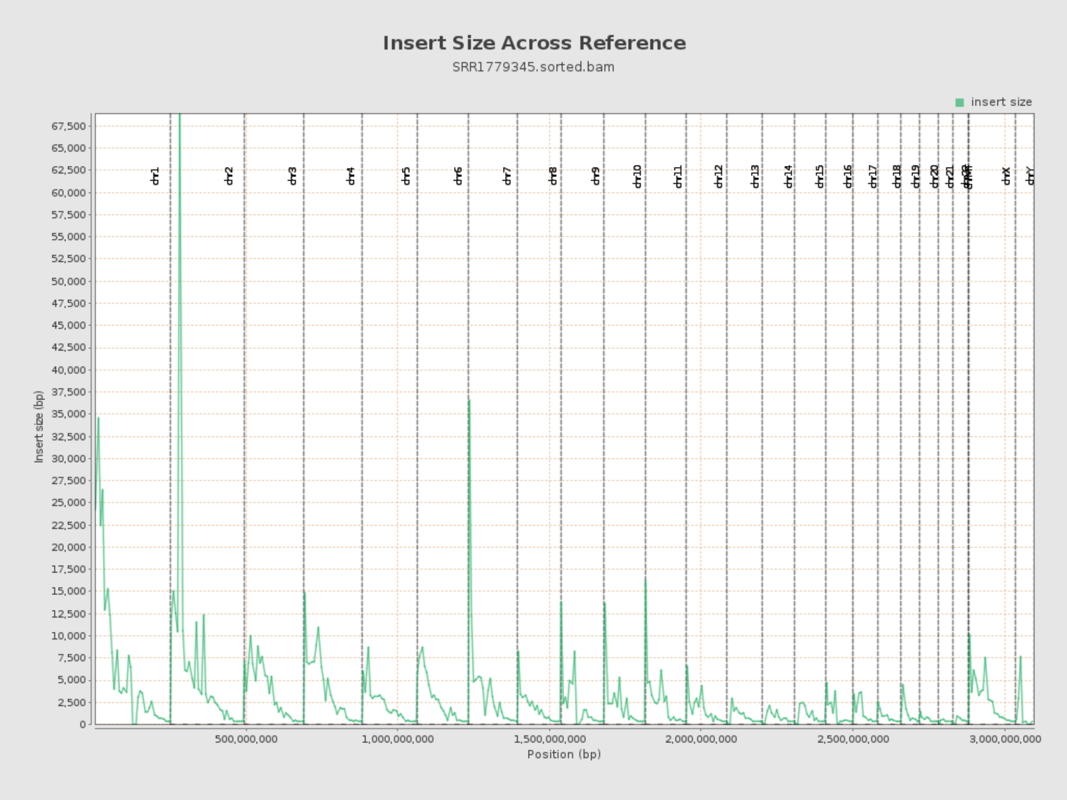
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram