Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 04:08:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779302.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_SRR1779302 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779302_1.fastq.gz SRR1779302_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 04:08:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779302.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,970,532
Mapped reads	18,226,877 / 96.08%
Unmapped reads	743,655 / 3.92%
Mapped paired reads	18,226,877 / 96.08%
Mapped reads, first in pair	9,184,069 / 48.41%
Mapped reads, second in pair	9,042,808 / 47.67%
Mapped reads, both in pair	18,056,066 / 95.18%
Mapped reads, singletons	170,811 / 0.9%
Secondary alignments	0
Supplementary alignments	46,060 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	499,781 / 2.63%
Duplication rate	2.55%
Clipped reads	569,404 / 3%

2.2. ACGT Content

Number/percentage of A's	446,365,513 / 30.77%
Number/percentage of C's	276,904,673 / 19.09%
Number/percentage of T's	446,026,792 / 30.74%
Number/percentage of G's	281,078,975 / 19.37%
Number/percentage of N's	389,183 / 0.03%

GC Percentage	38.46%

2.3. Coverage

Mean	0.4687
Standard Deviation	1.506

2.4. Mapping Quality

Mean Mapping Quality	52.71

2.5. Insert size

Mean	42,605.28
Standard Deviation	1,932,147.3
P25/Median/P75	160 / 212 / 287

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	5,043,329
Insertions	104,961
Mapped reads with at least one insertion	0.57%
Deletions	133,653
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.54%

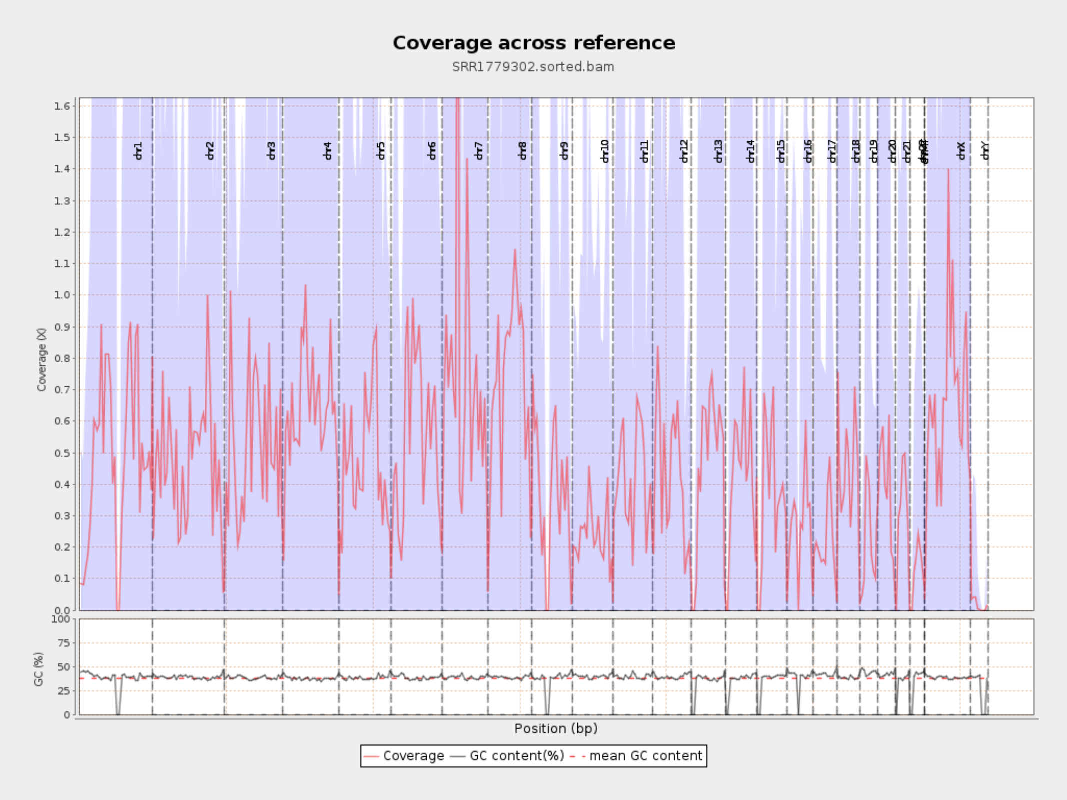
2.7. Chromosome stats

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

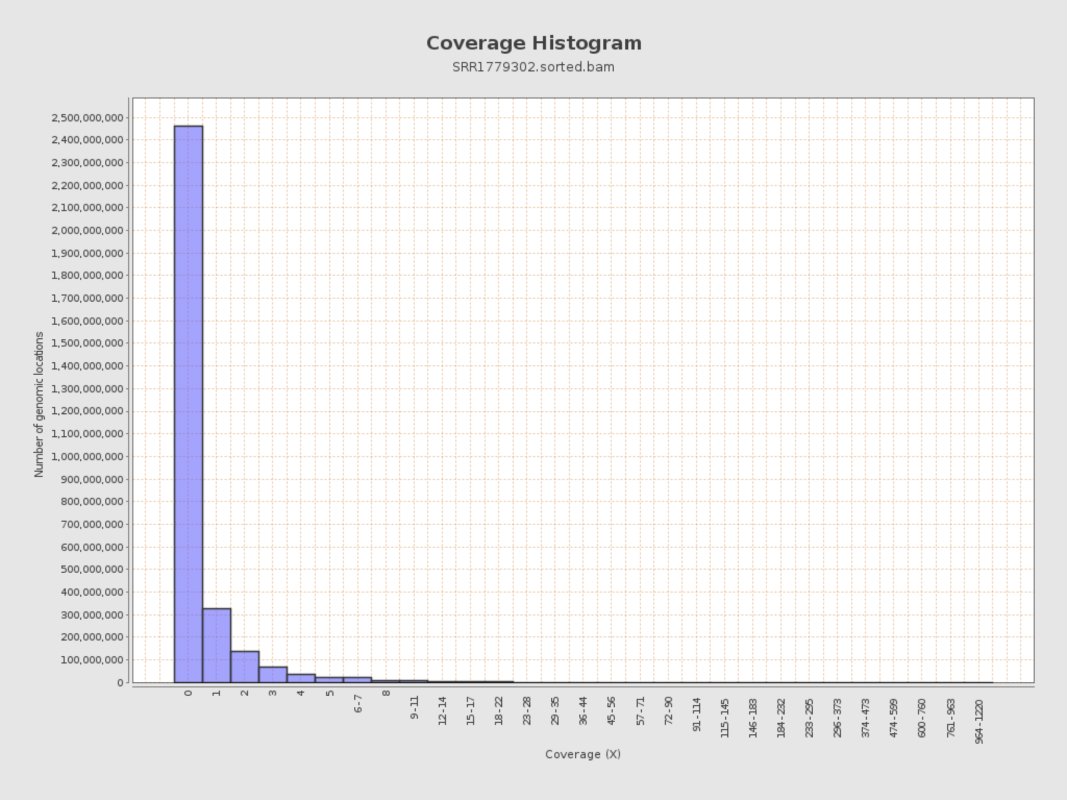
		bases	**coverage**	**deviation**
chr1	249250621	121969625	0.4893	1.835
chr2	243199373	114978512	0.4728	1.3357
chr3	198022430	103333091	0.5218	1.4089
chr4	191154276	124543936	0.6515	1.5206
chr5	180915260	85048515	0.4701	1.2987
chr6	171115067	96990167	0.5668	1.5313
chr7	159138663	121885243	0.7659	2.4952
chr8	146364022	110201067	0.7529	1.7425
chr9	141213431	50556898	0.358	1.1895
chr10	135534747	33349363	0.2461	1.8177
chr11	135006516	55663241	0.4123	1.2612
chr12	133851895	57140034	0.4269	1.3079
chr13	115169878	54904391	0.4767	1.3198
chr14	107349540	45037019	0.4195	1.2808
chr15	102531392	37296837	0.3638	1.1604
chr16	90354753	23646773	0.2617	0.9529
chr17	81195210	17577798	0.2165	0.8729
chr18	78077248	35407883	0.4535	1.4162
chr19	59128983	11744861	0.1986	1.0612
chr20	63025520	24003020	0.3808	1.2017
chr21	48129895	15140321	0.3146	1.0167
chr22	51304566	6410658	0.125	0.5864
chrMT	16571	580	0.035	0.1931
chrX	155270560	103191824	0.6646	1.886

chrY	59373566	1020892	0.0172	0.22

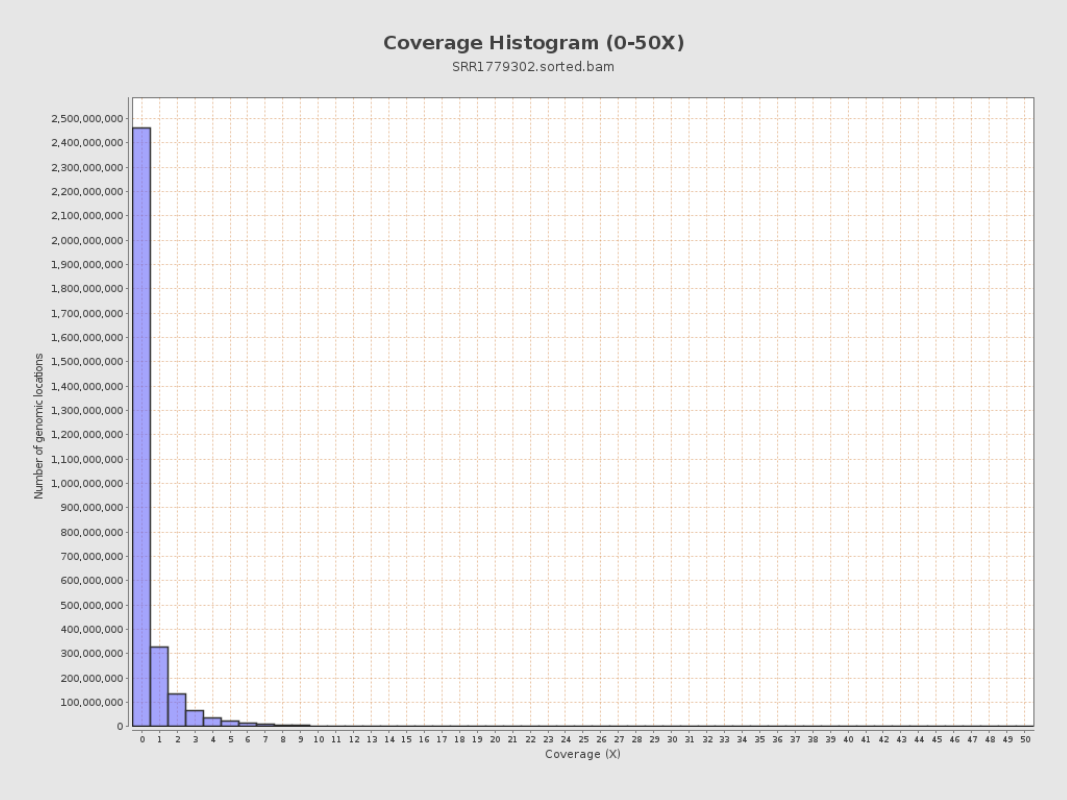
3. Results : Coverage across reference



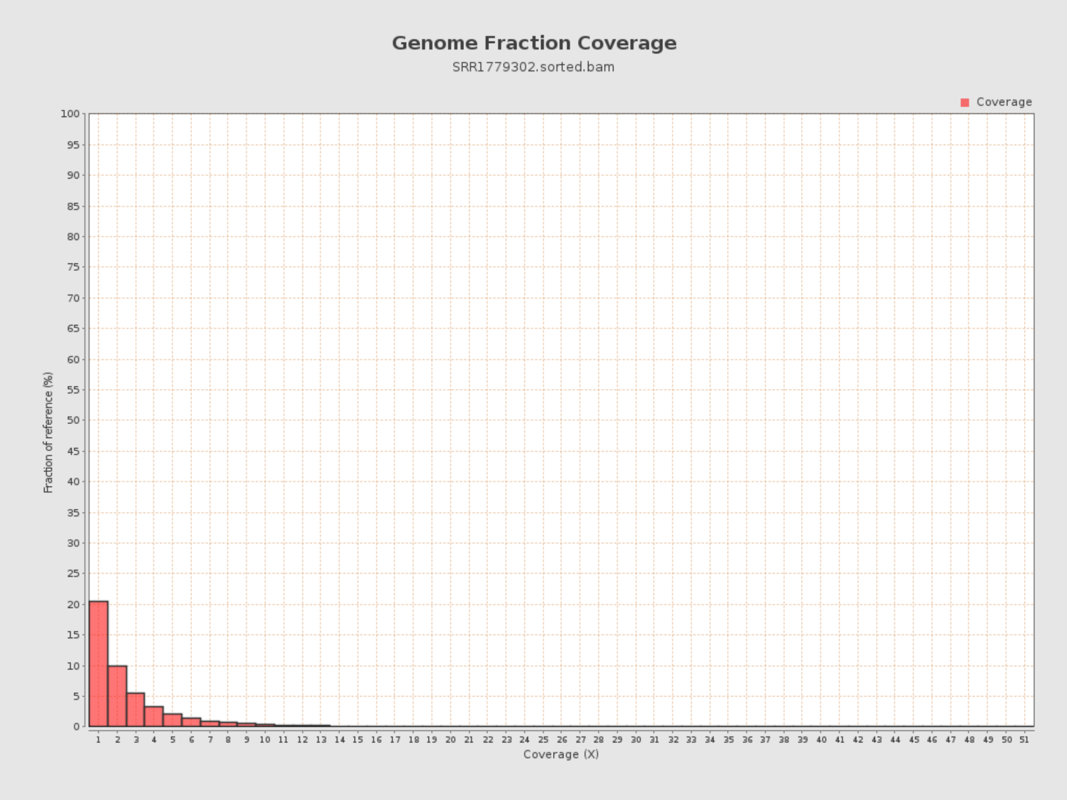
4. Results : Coverage Histogram



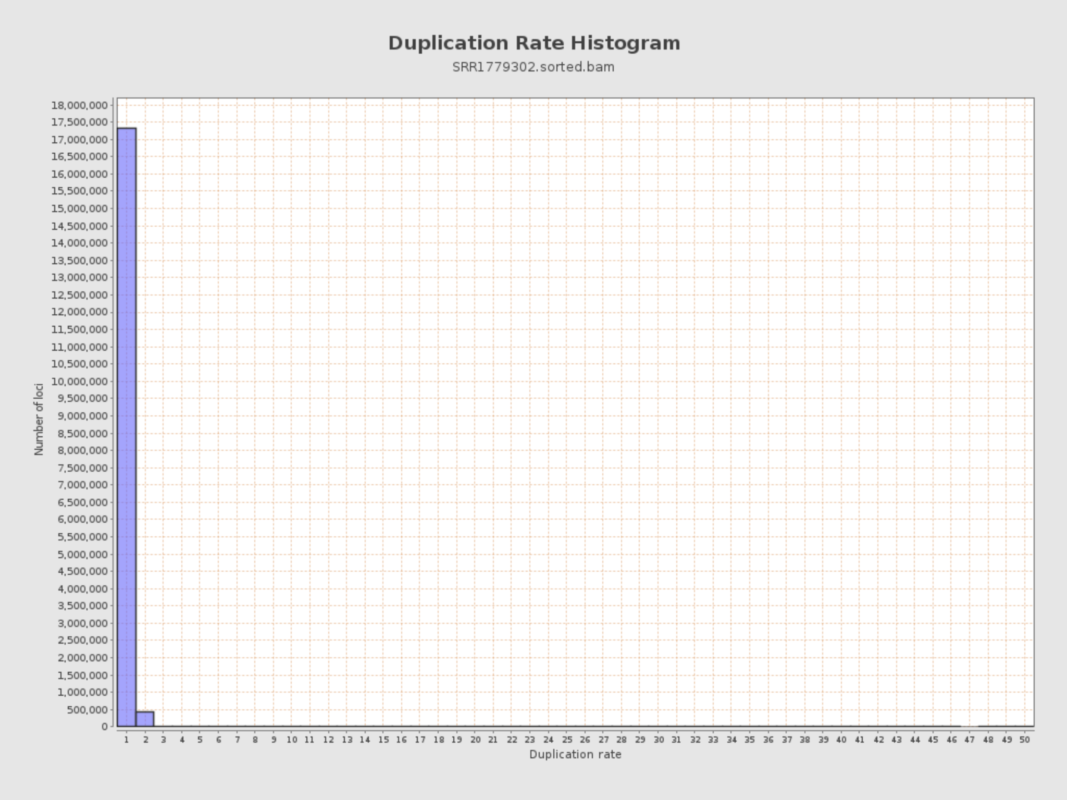
5. Results : Coverage Histogram (0-50X)



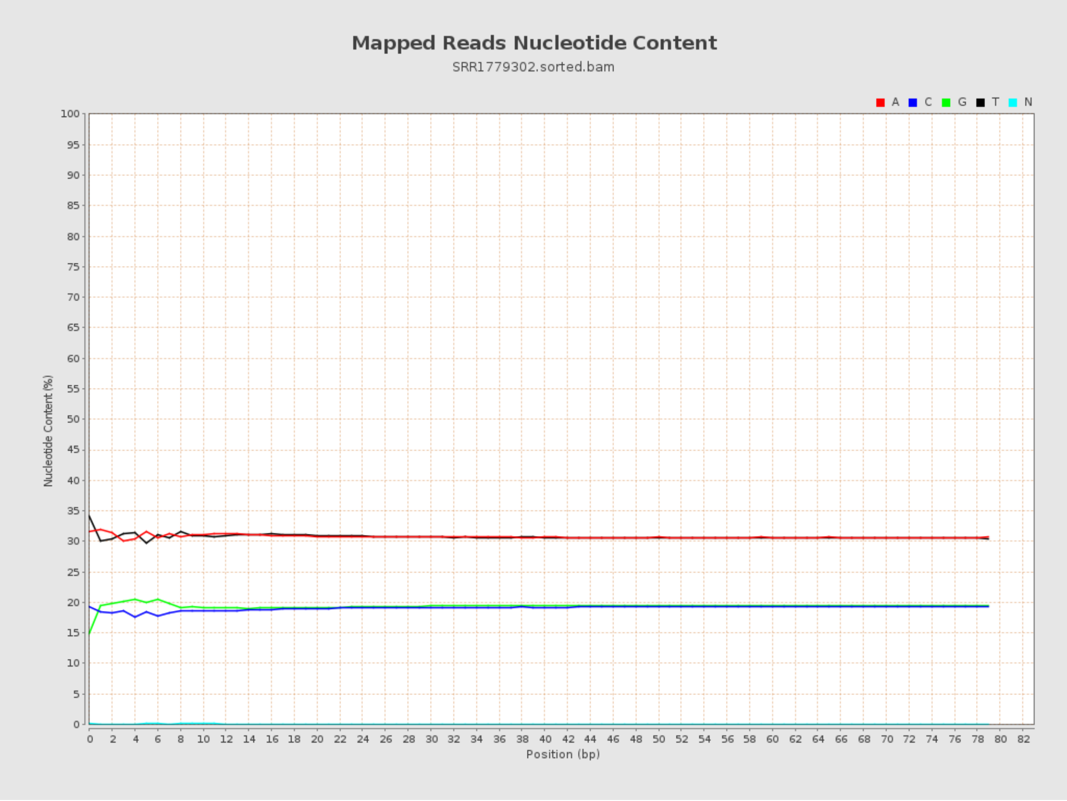
6. Results : Genome Fraction Coverage



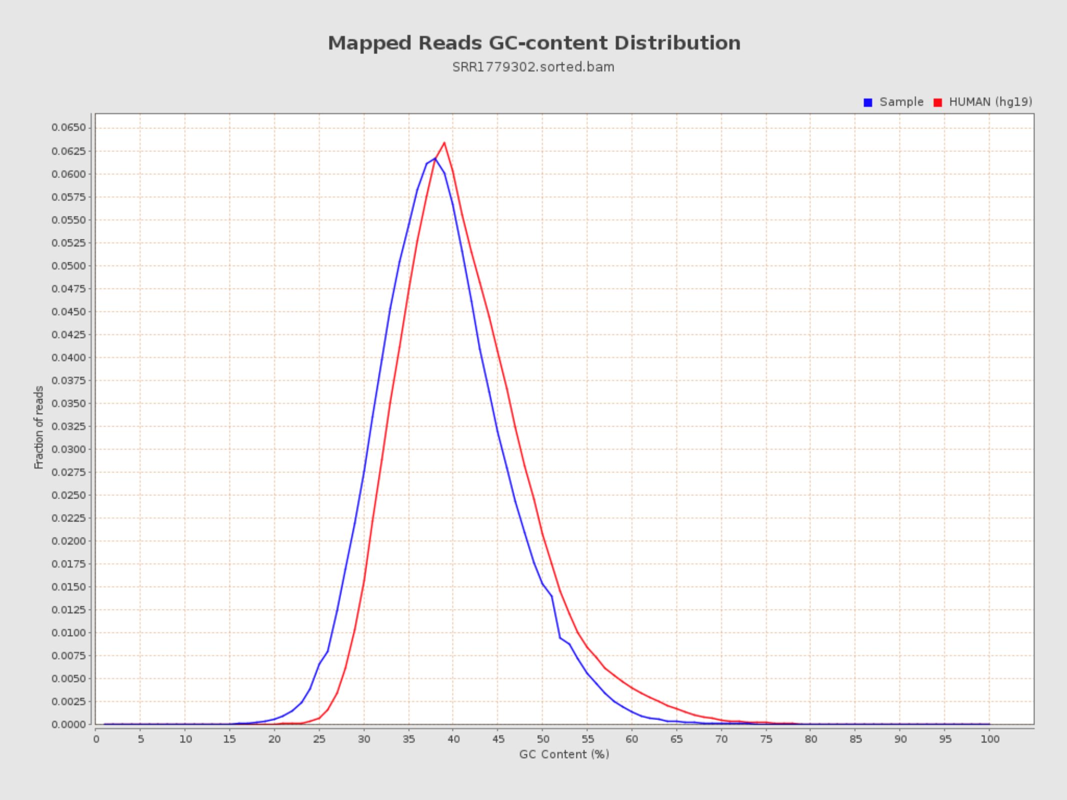
7. Results : Duplication Rate Histogram



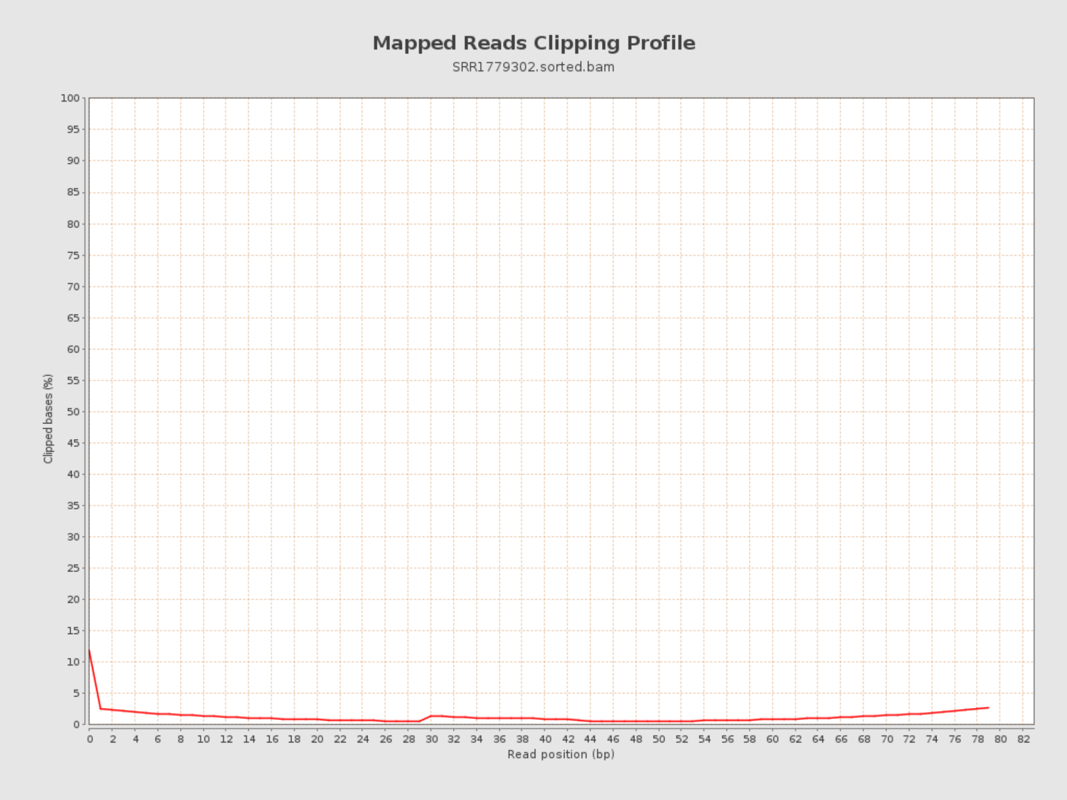
8. Results : Mapped Reads Nucleotide Content



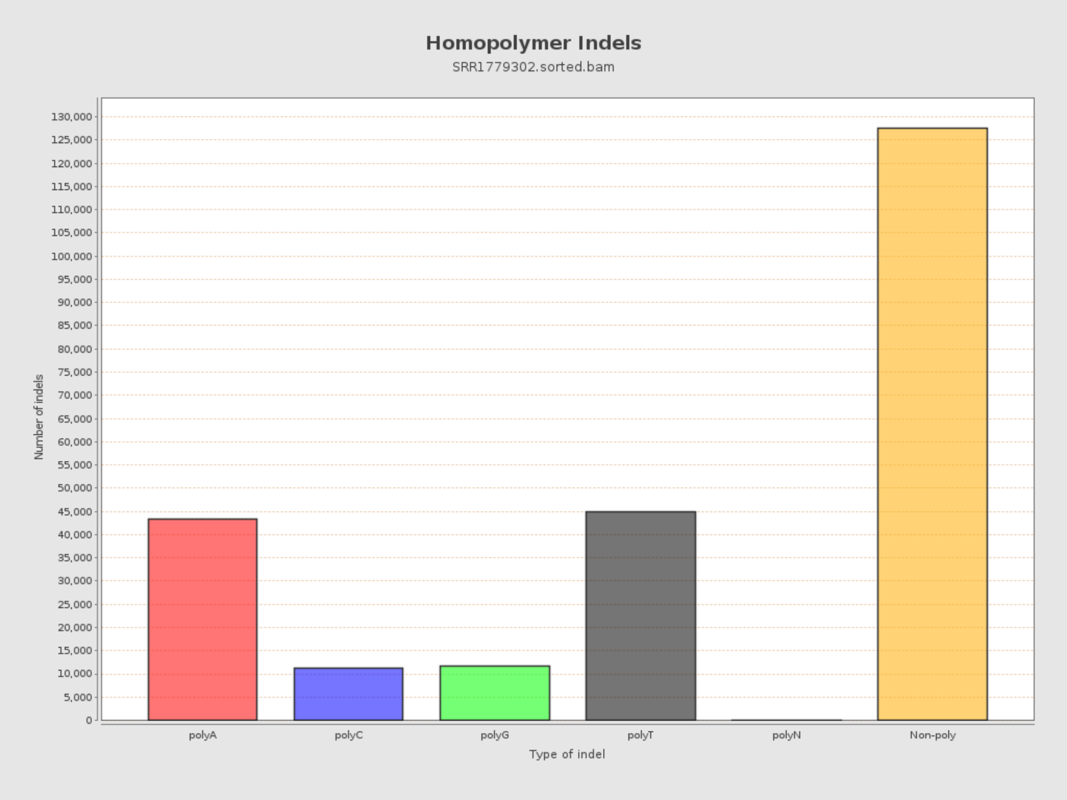
9. Results : Mapped Reads GC-content Distribution



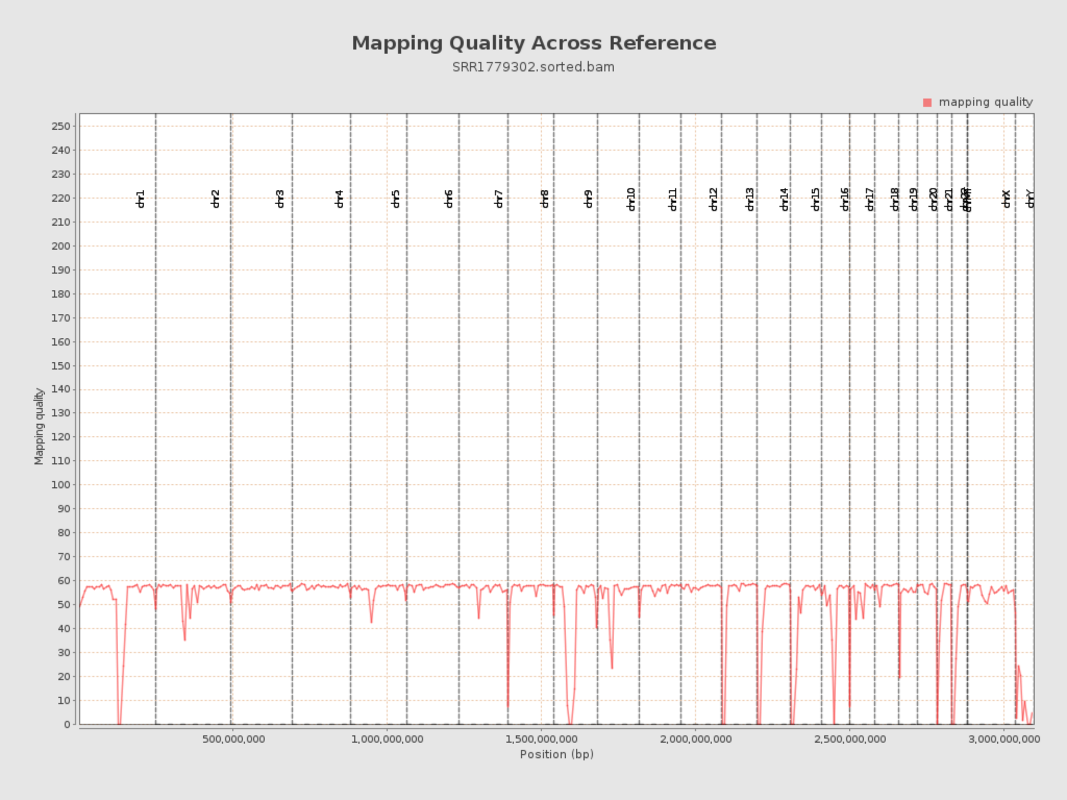
10. Results : Mapped Reads Clipping Profile



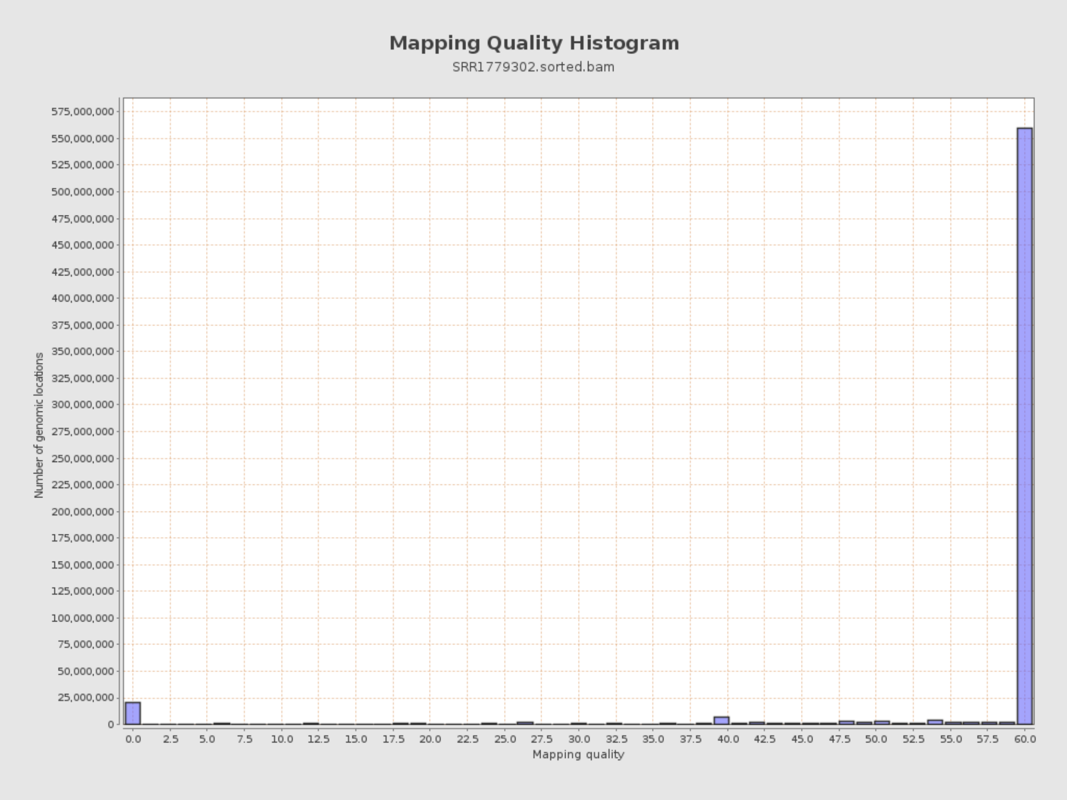
11. Results : Homopolymer Indels



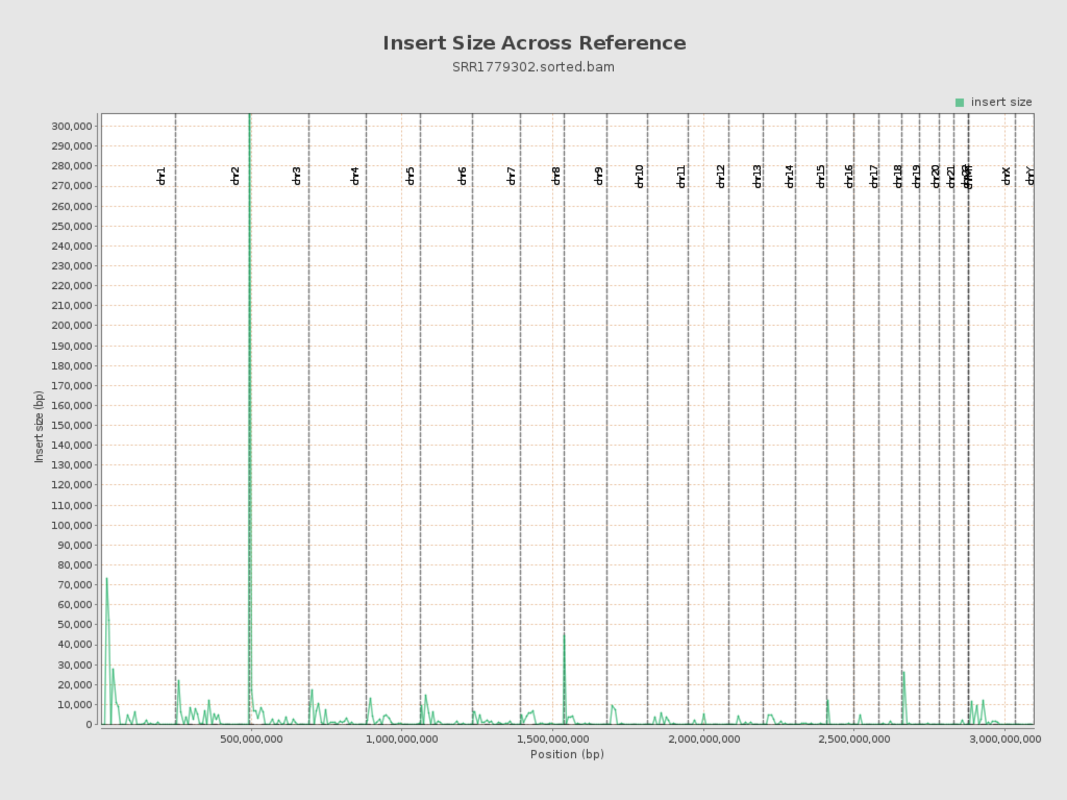
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram