Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 02:42:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779425.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_SRR1779425 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779425_1.fastq.gz SRR1779425_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 02:42:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779425.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,574,366
Mapped reads	16,236,161 / 97.96%
Unmapped reads	338,205 / 2.04%
Mapped paired reads	16,236,161 / 97.96%
Mapped reads, first in pair	8,184,473 / 49.38%
Mapped reads, second in pair	8,051,688 / 48.58%
Mapped reads, both in pair	16,074,622 / 96.98%
Mapped reads, singletons	161,539 / 0.97%
Secondary alignments	0
Supplementary alignments	66,419 / 0.4%
Read min/max/mean length	30 / 80 / 80.15
Duplicated reads (estimated)	659,949 / 3.98%
Duplication rate	3.69%
Clipped reads	636,413 / 3.84%

2.2. ACGT Content

Number/percentage of A's	390,661,123 / 30.26%
Number/percentage of C's	253,591,013 / 19.64%
Number/percentage of T's	389,847,478 / 30.19%
Number/percentage of G's	256,820,957 / 19.89%
Number/percentage of N's	285,210 / 0.02%

GC Percentage	39.53%

2.3. Coverage

Mean	0.4172
Standard Deviation	1.7615

2.4. Mapping Quality

Mean Mapping Quality	53.19

2.5. Insert size

Mean	34,785.07
Standard Deviation	1,757,992.71
P25/Median/P75	143 / 183 / 234

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	4,315,796
Insertions	116,025
Mapped reads with at least one insertion	0.71%
Deletions	133,395
Mapped reads with at least one deletion	0.81%
Homopolymer indels	47.07%

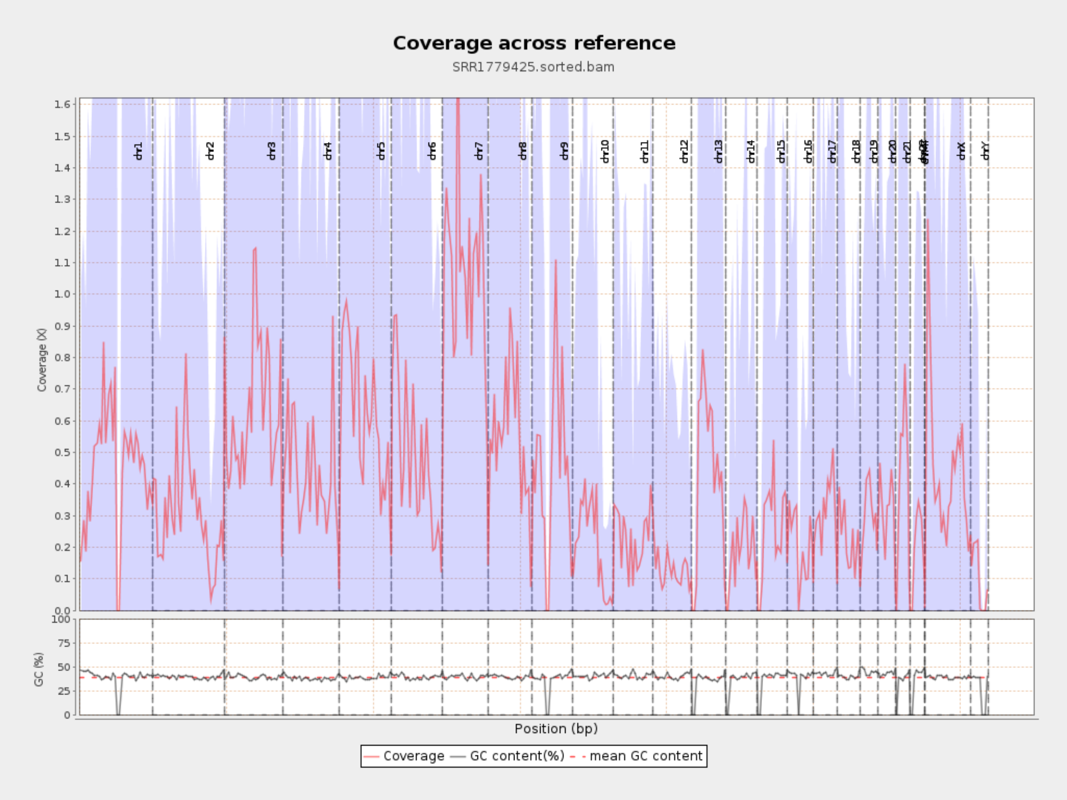
2.7. Chromosome stats

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

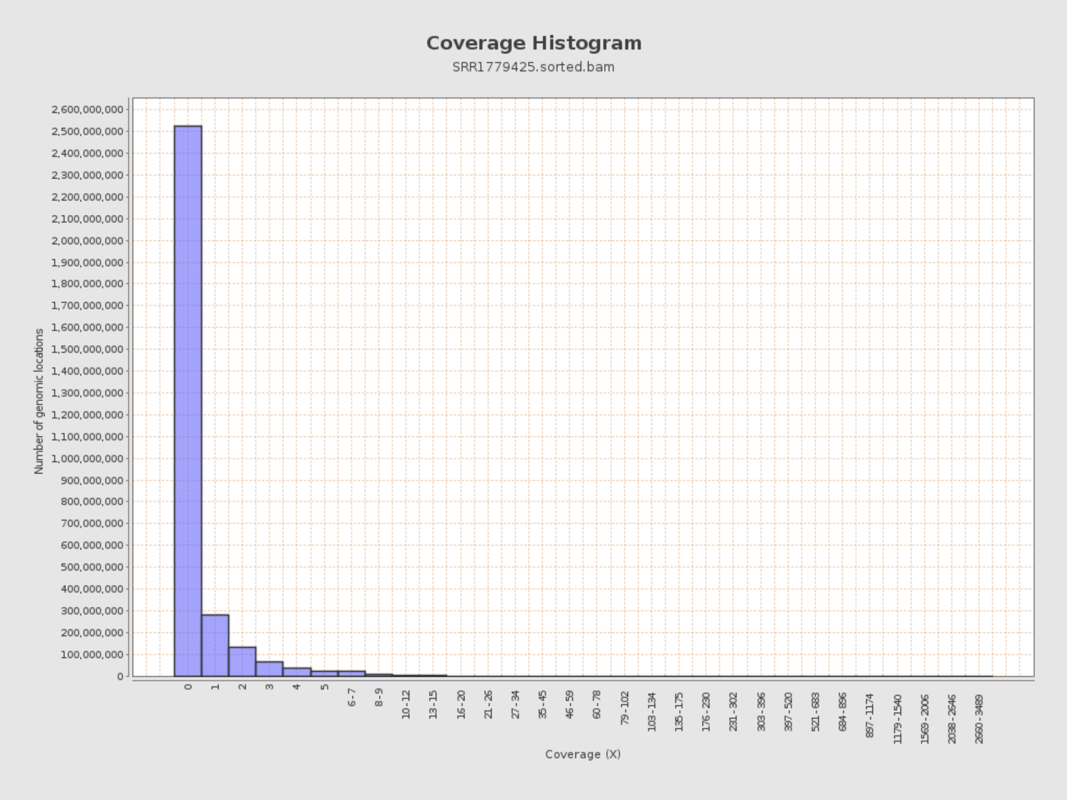
		bases	coverage	deviation
chr1	249250621	113209718	0.4542	3.821
chr2	243199373	74840729	0.3077	1.0706
chr3	198022430	125927169	0.6359	1.484
chr4	191154276	84729720	0.4433	1.241
chr5	180915260	111886960	0.6184	1.447
chr6	171115067	82755937	0.4836	1.3567
chr7	159138663	171613930	1.0784	2.7123
chr8	146364022	83029783	0.5673	1.4919
chr9	141213431	62624431	0.4435	1.3709
chr10	135534747	28161446	0.2078	2.3559
chr11	135006516	30745667	0.2277	0.884
chr12	133851895	17541787	0.1311	0.6162
chr13	115169878	52010817	0.4516	1.5302
chr14	107349540	19799128	0.1844	0.7973
chr15	102531392	26575266	0.2592	0.9486
chr16	90354753	18179774	0.2012	0.7954
chr17	81195210	25409482	0.3129	1.142
chr18	78077248	17951972	0.2299	1.1633
chr19	59128983	17913822	0.303	2.2484
chr20	63025520	20503648	0.3253	1.0691
chr21	48129895	20953500	0.4354	1.2086
chr22	51304566	10056670	0.196	0.7527
chrMT	16571	160	0.0097	0.0978
chrX	155270560	68728673	0.4426	1.2969

chrY	59373566	6329664	0.1066	0.5973

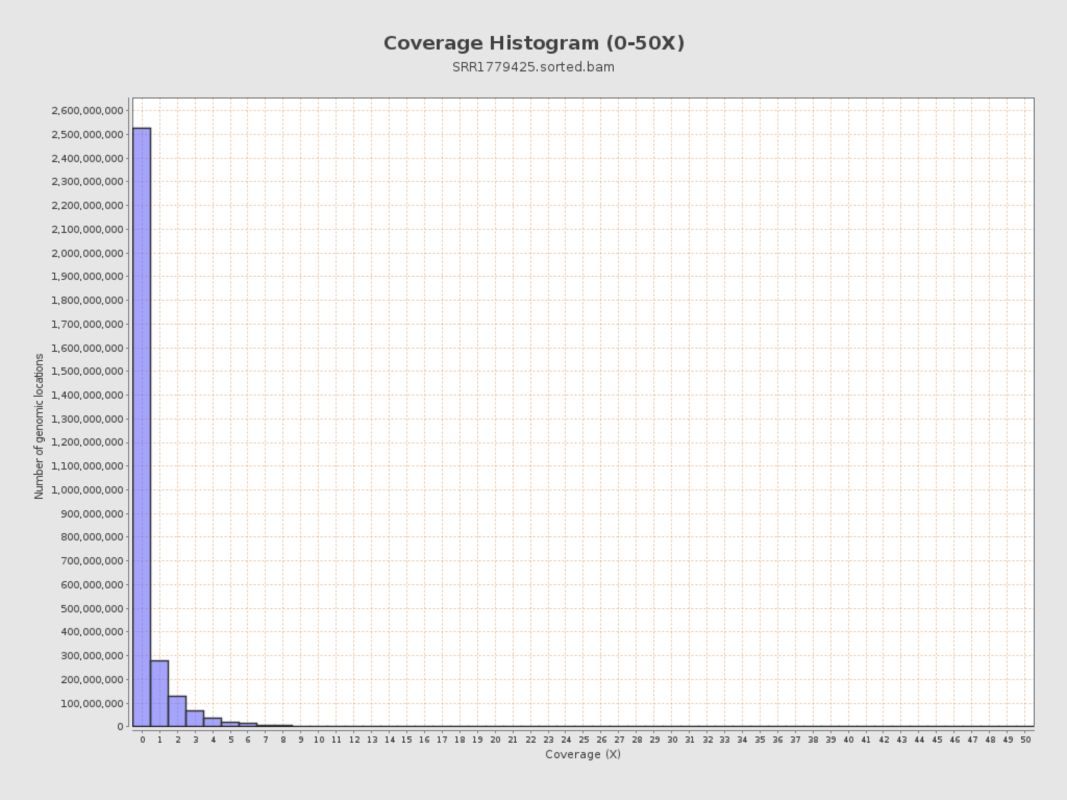
3. Results : Coverage across reference



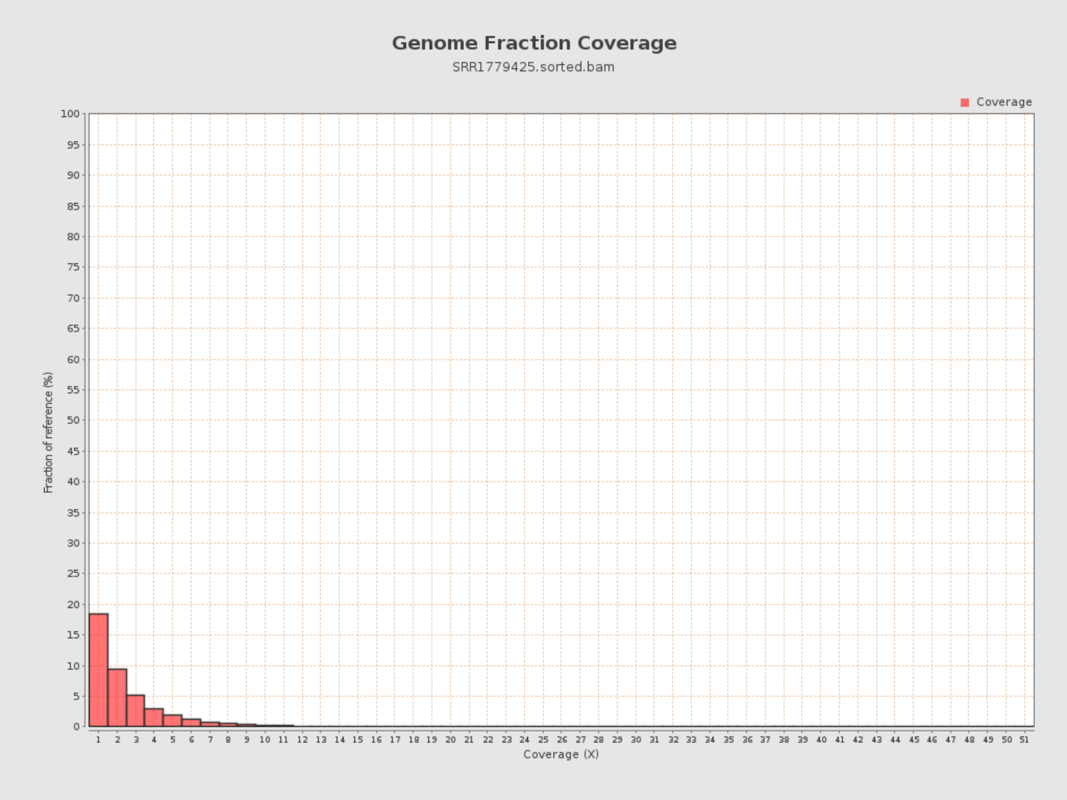
4. Results : Coverage Histogram



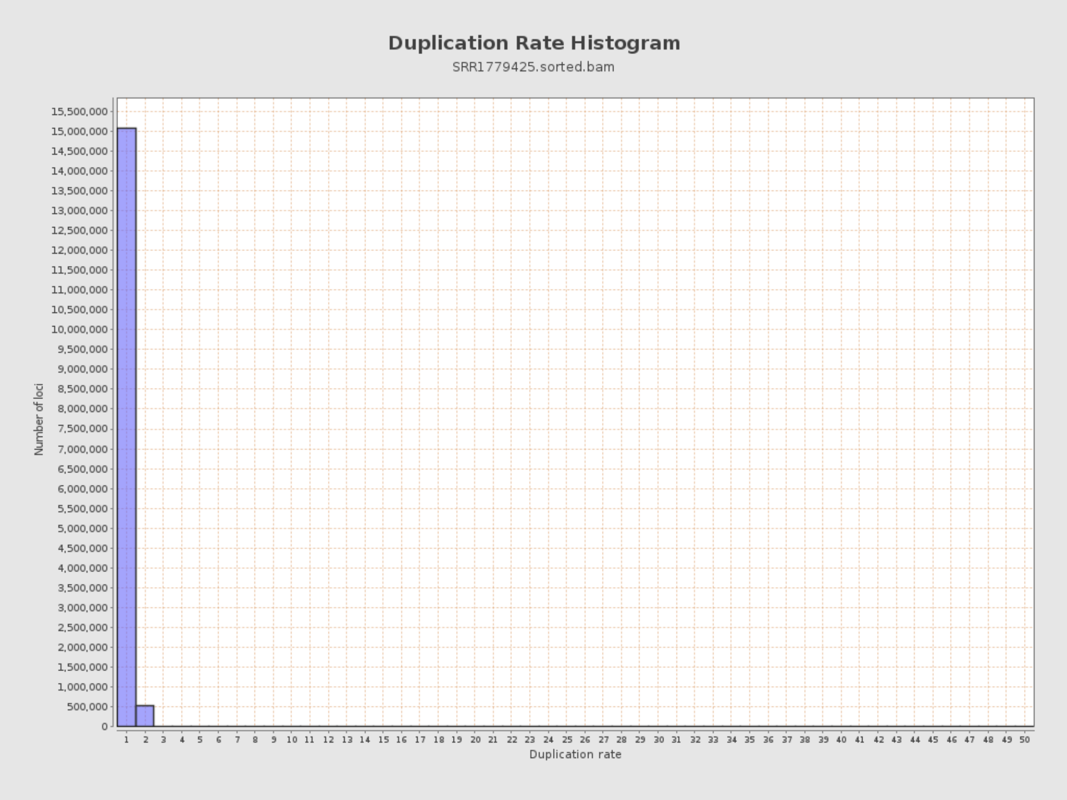
5. Results : Coverage Histogram (0-50X)



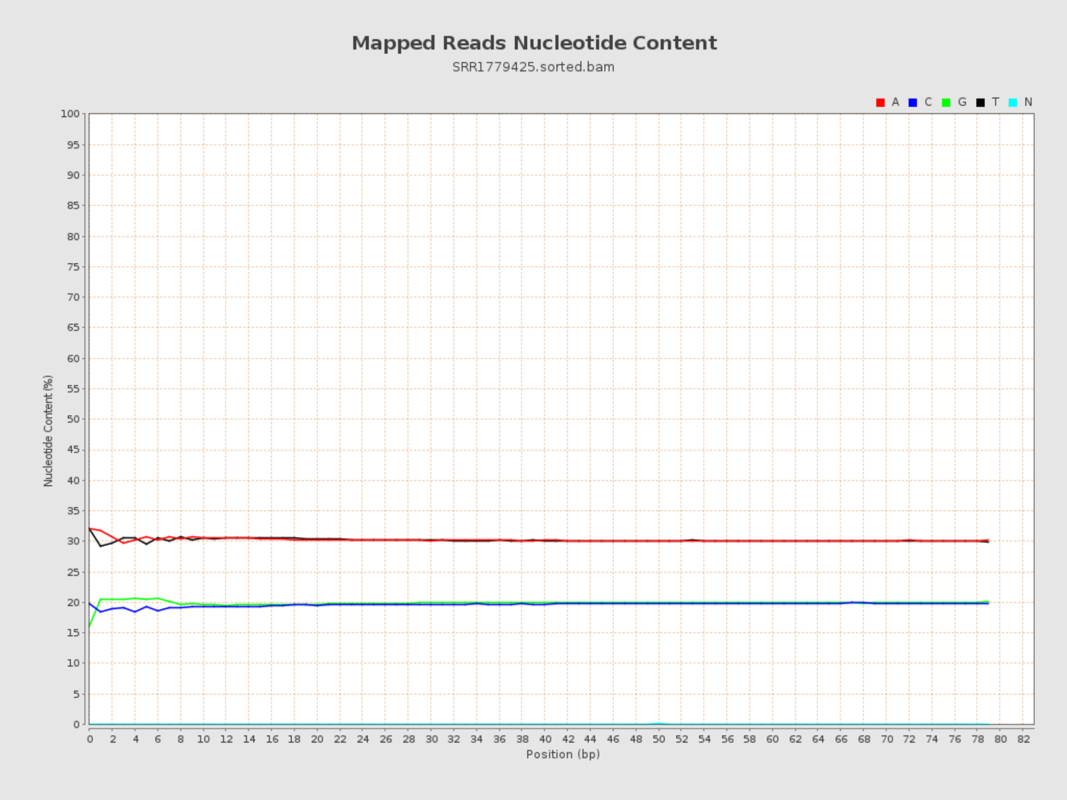
6. Results : Genome Fraction Coverage



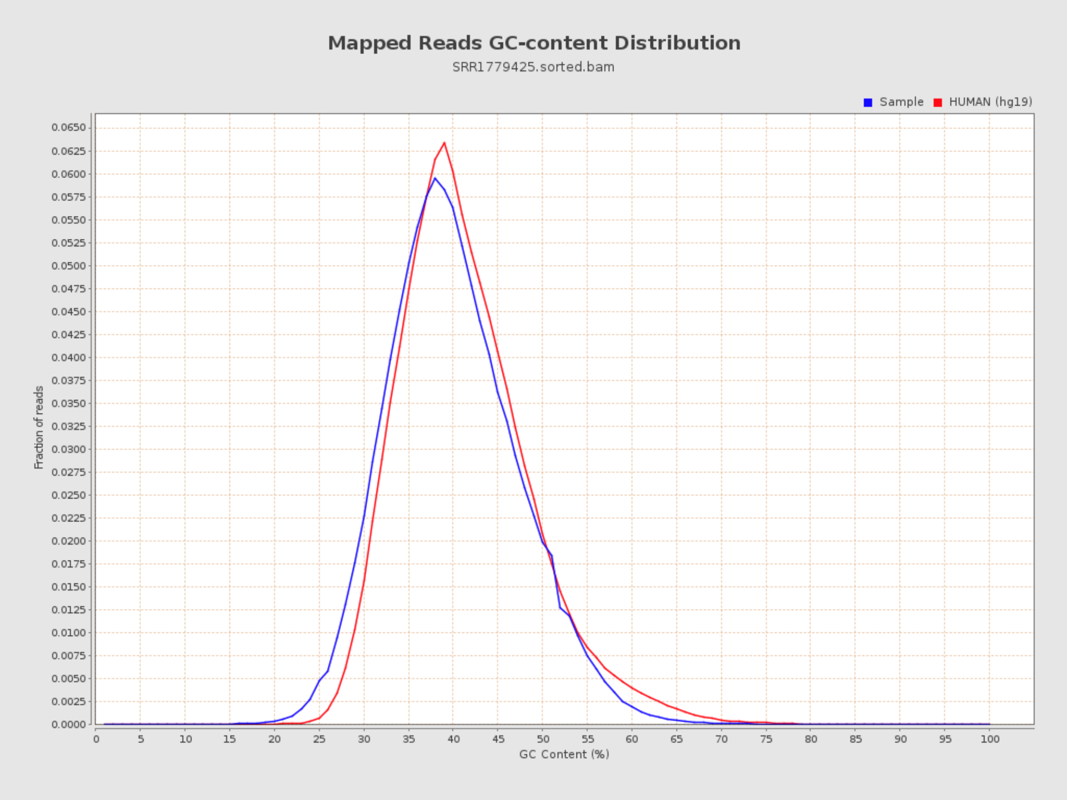
7. Results : Duplication Rate Histogram



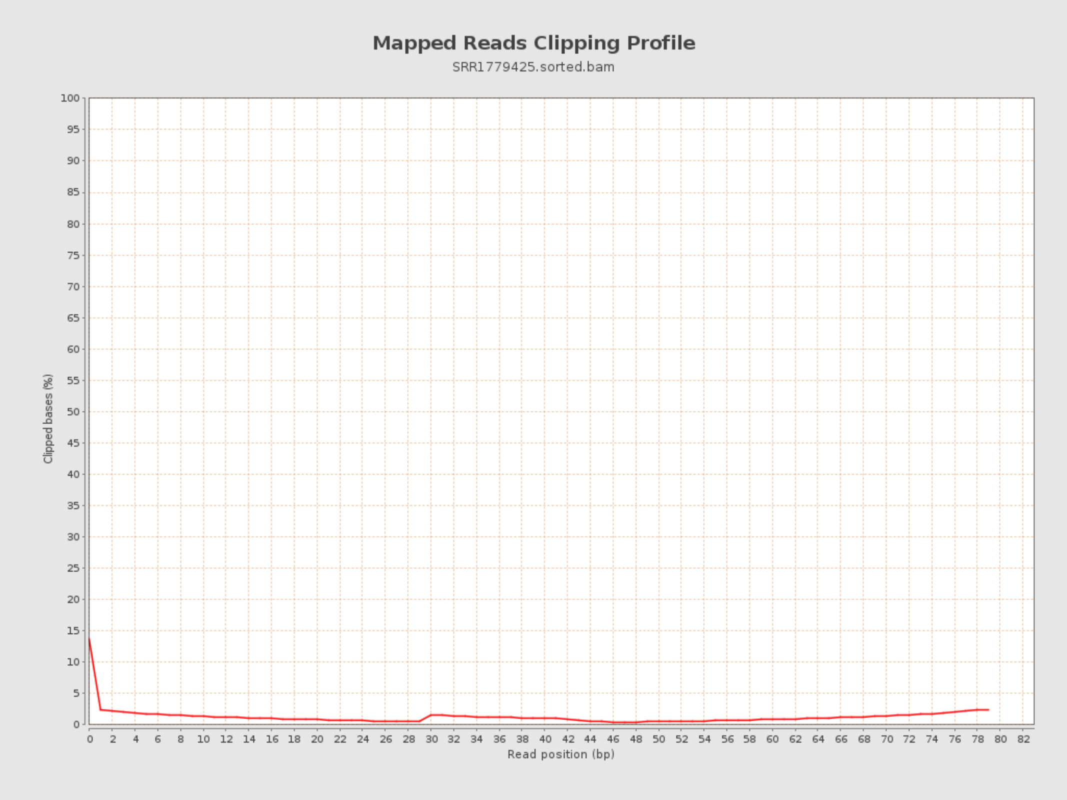
8. Results : Mapped Reads Nucleotide Content



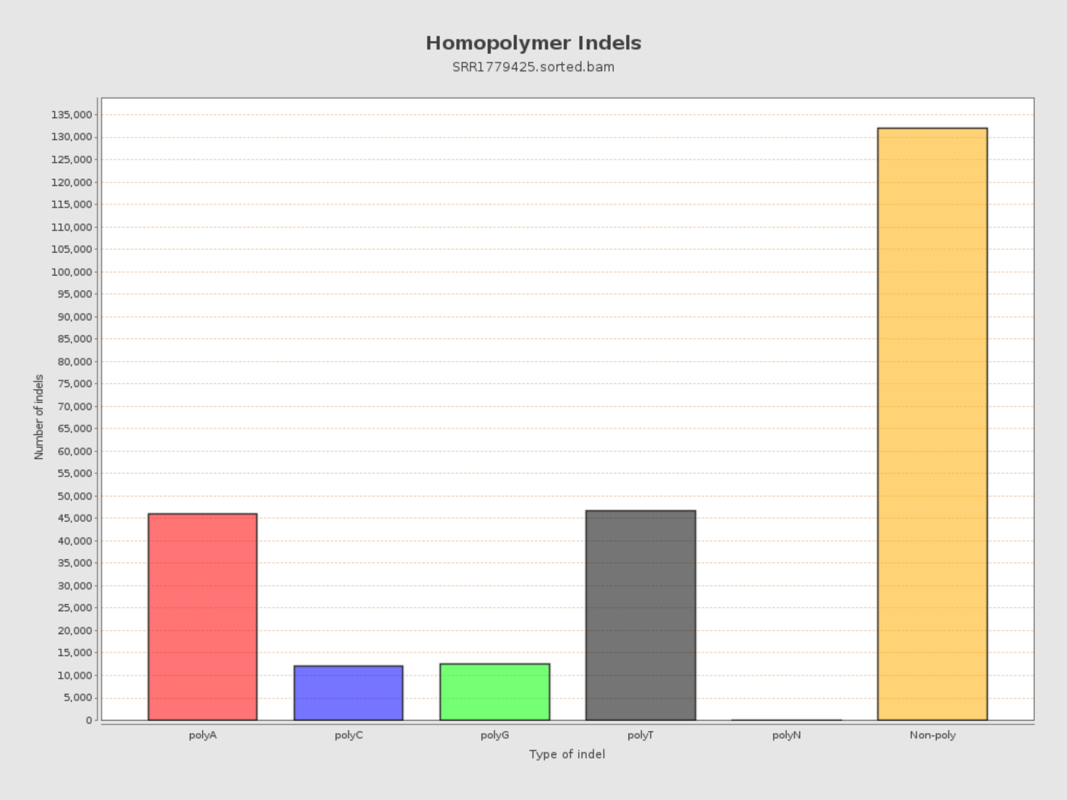
9. Results : Mapped Reads GC-content Distribution



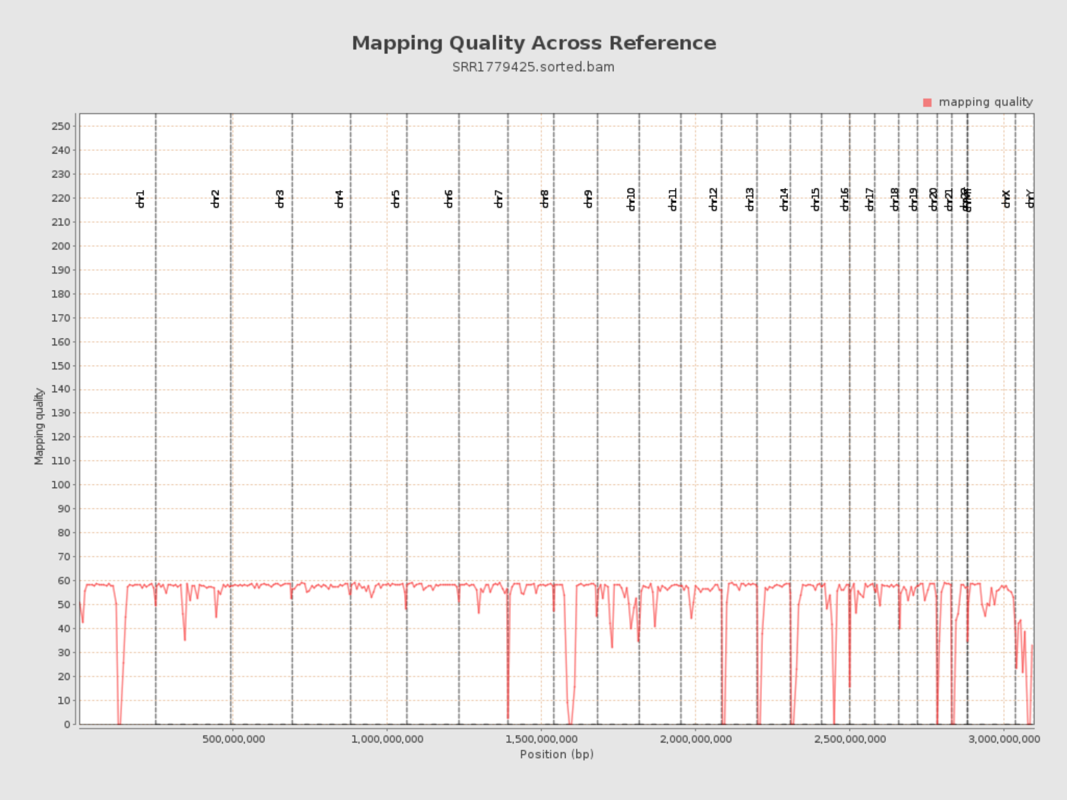
10. Results : Mapped Reads Clipping Profile



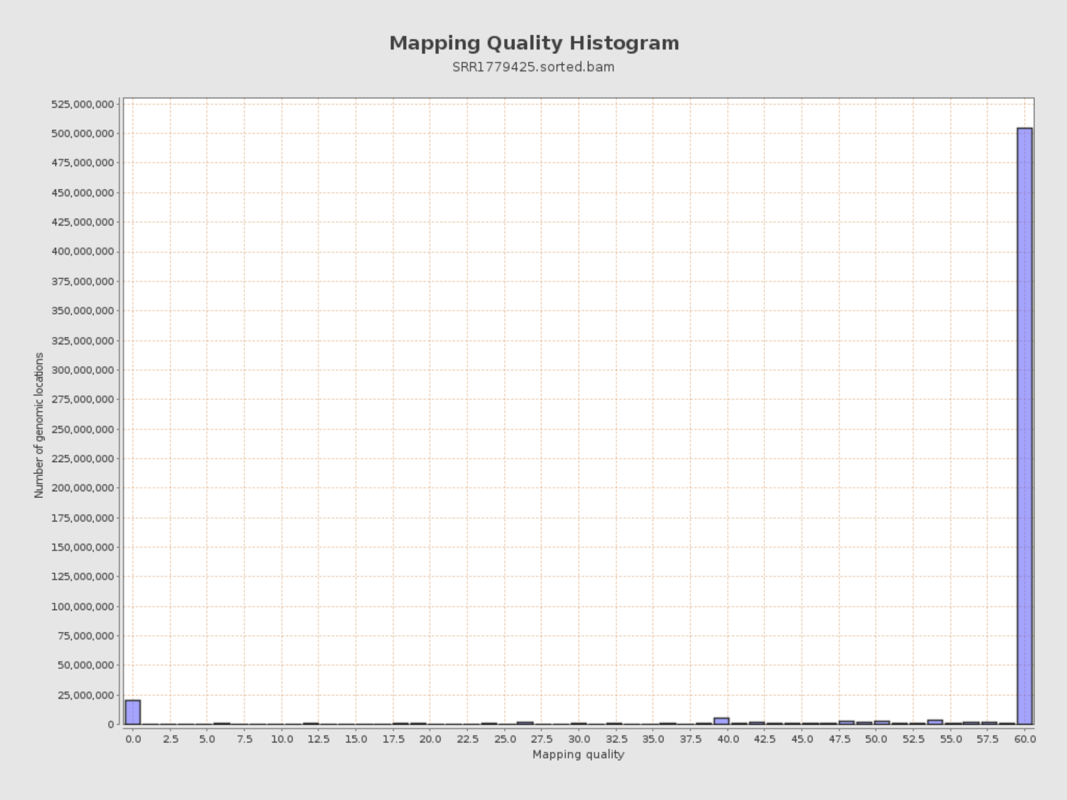
11. Results : Homopolymer Indels



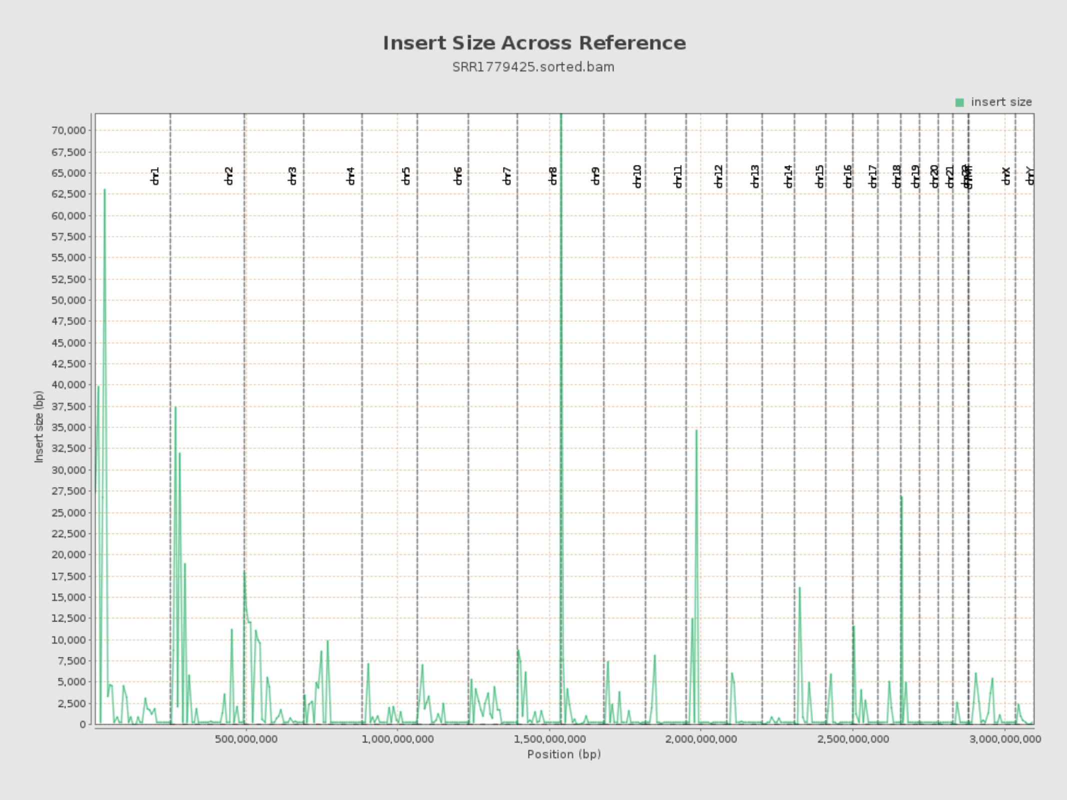
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram