Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 02:59:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779299.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_SRR1779299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779299_1.fastq.gz SRR1779299_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 02:59:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,110,006
Mapped reads	24,145,197 / 92.47%
Unmapped reads	1,964,809 / 7.53%
Mapped paired reads	24,145,197 / 92.47%
Mapped reads, first in pair	12,168,739 / 46.61%
Mapped reads, second in pair	11,976,458 / 45.87%
Mapped reads, both in pair	23,900,928 / 91.54%
Mapped reads, singletons	244,269 / 0.94%
Secondary alignments	0
Supplementary alignments	60,332 / 0.23%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	1,215,572 / 4.66%
Duplication rate	4.63%
Clipped reads	754,693 / 2.89%

2.2. ACGT Content

Number/percentage of A's	594,032,061 / 30.91%
Number/percentage of C's	363,662,335 / 18.92%
Number/percentage of T's	592,879,726 / 30.85%
Number/percentage of G's	370,562,941 / 19.28%
Number/percentage of N's	511,278 / 0.03%

GC Percentage	38.21%

2.3. Coverage

Mean	0.6209
Standard Deviation	2.3657

2.4. Mapping Quality

Mean Mapping Quality	53.23

2.5. Insert size

Mean	30,267.27
Standard Deviation	1,634,384.21
P25/Median/P75	164 / 226 / 314

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	6,885,402
Insertions	139,899
Mapped reads with at least one insertion	0.57%
Deletions	175,825
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.96%

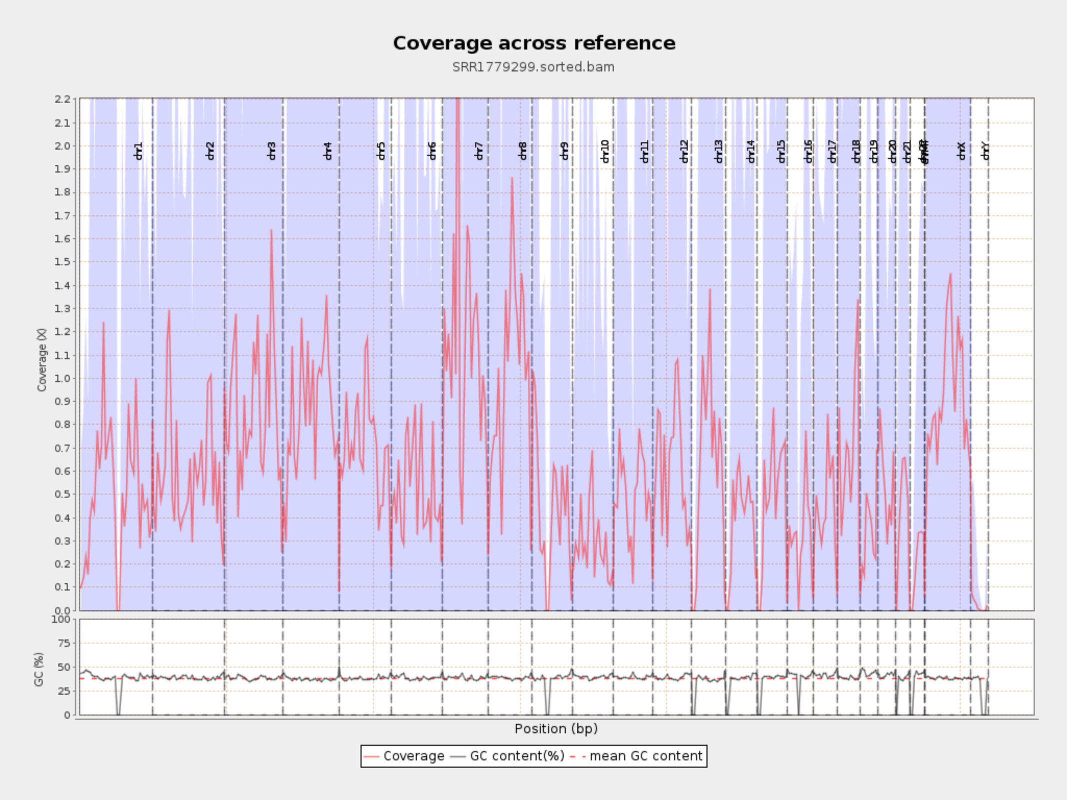
2.7. Chromosome stats

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

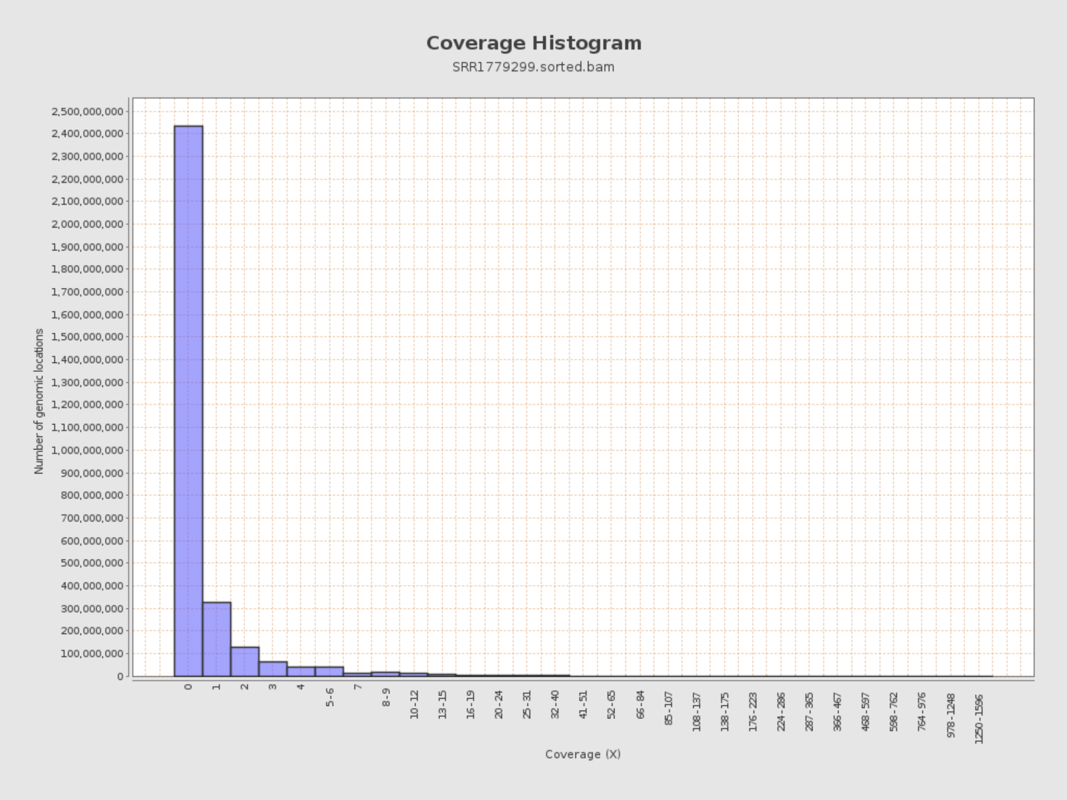
		bases	coverage	deviation
chr1	249250621	125903934	0.5051	2.447
chr2	243199373	141978907	0.5838	2.0103
chr3	198022430	170839087	0.8627	2.9352
chr4	191154276	166839000	0.8728	2.8312
chr5	180915260	126318108	0.6982	2.1166
chr6	171115067	90897760	0.5312	1.7682
chr7	159138663	185904672	1.1682	3.9776
chr8	146364022	150689772	1.0296	2.8241
chr9	141213431	60239246	0.4266	1.7453
chr10	135534747	38813898	0.2864	2.2845
chr11	135006516	67454233	0.4996	1.9865
chr12	133851895	82889332	0.6193	2.1075
chr13	115169878	74198820	0.6443	2.3967
chr14	107349540	41986965	0.3911	1.574
chr15	102531392	49897499	0.4867	1.8327
chr16	90354753	27858753	0.3083	1.3391
chr17	81195210	35465189	0.4368	1.7088
chr18	78077248	54981678	0.7042	2.6862
chr19	59128983	18050534	0.3053	1.4815
chr20	63025520	33656723	0.534	1.6855
chr21	48129895	20533484	0.4266	1.5551
chr22	51304566	10464475	0.204	1.0178
chrMT	16571	3468	0.2093	0.734
chrX	155270560	144843241	0.9328	3.0039

chrY	59373566	1302382	0.0219	0.2874

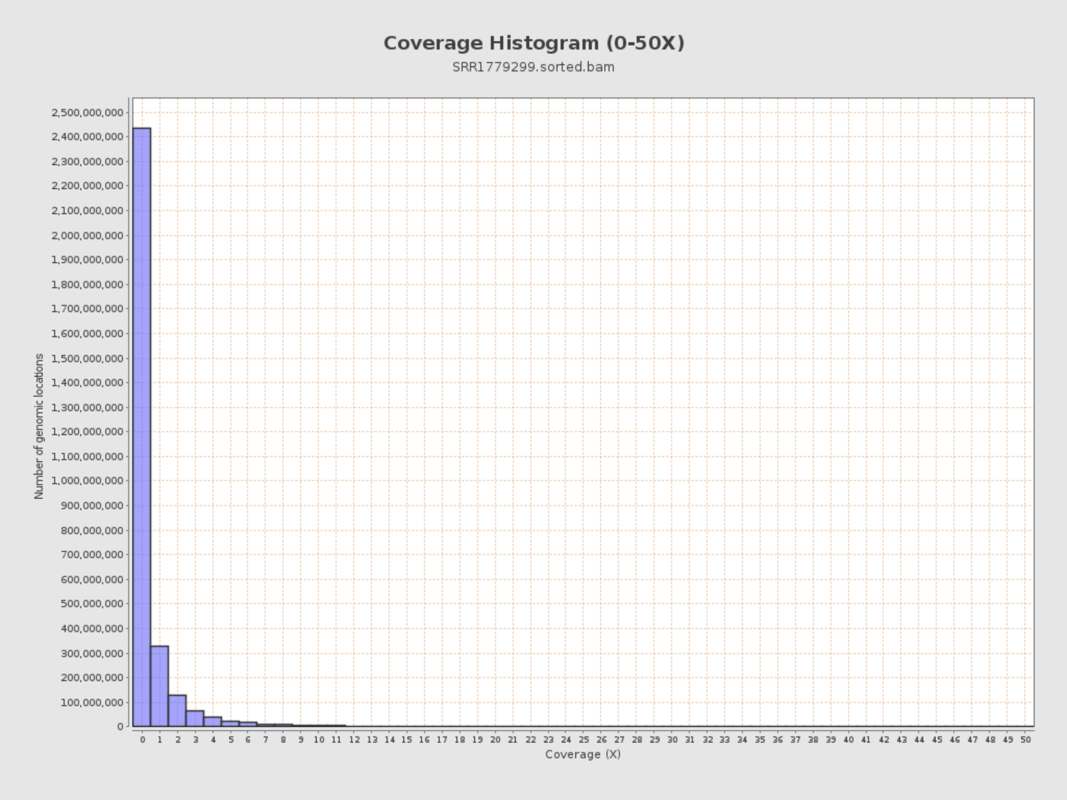
3. Results : Coverage across reference



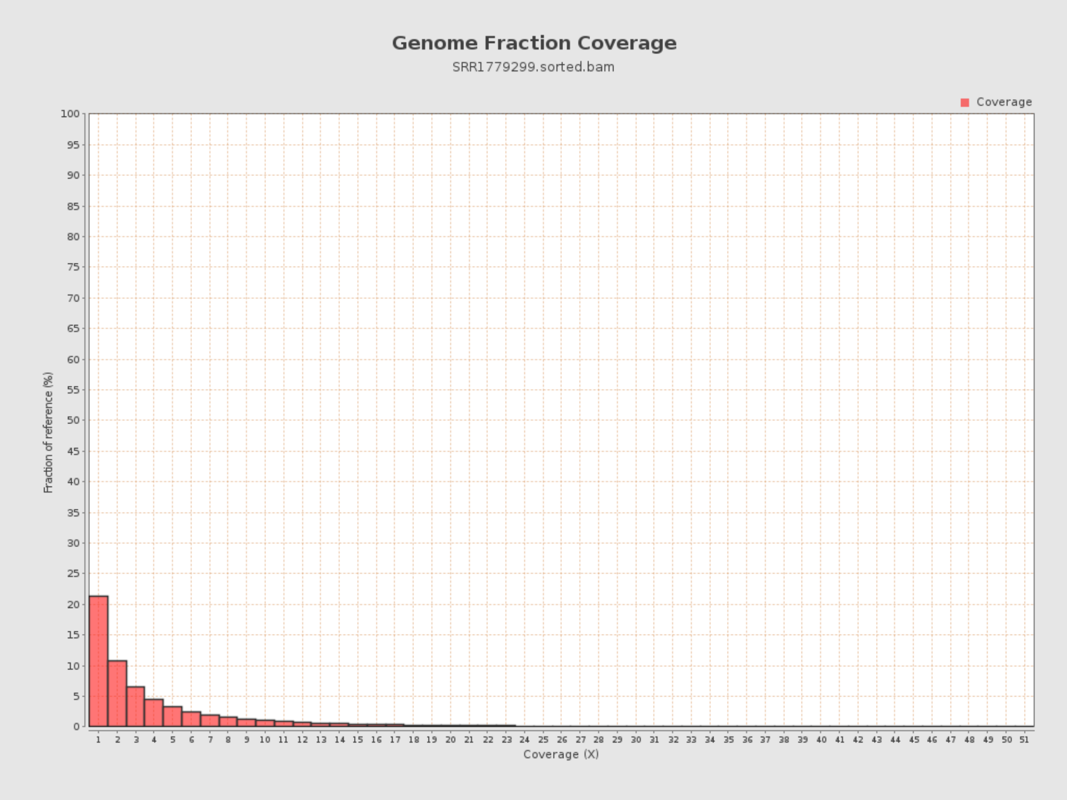
4. Results : Coverage Histogram



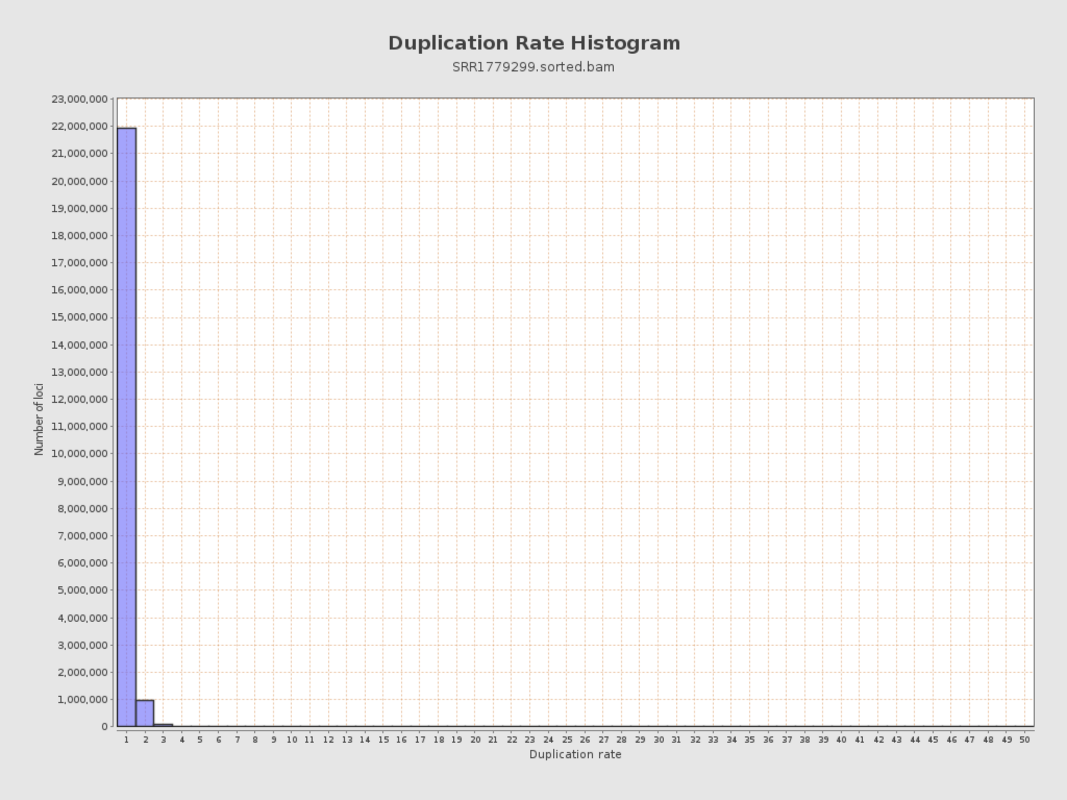
5. Results : Coverage Histogram (0-50X)



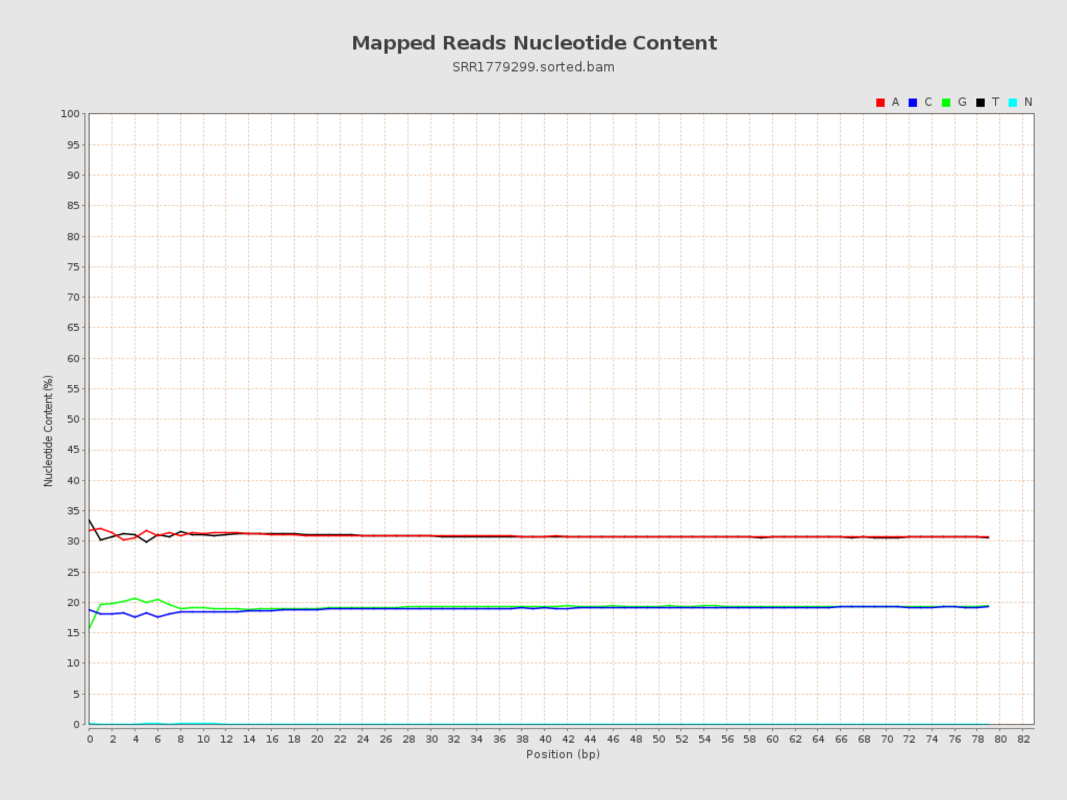
6. Results : Genome Fraction Coverage



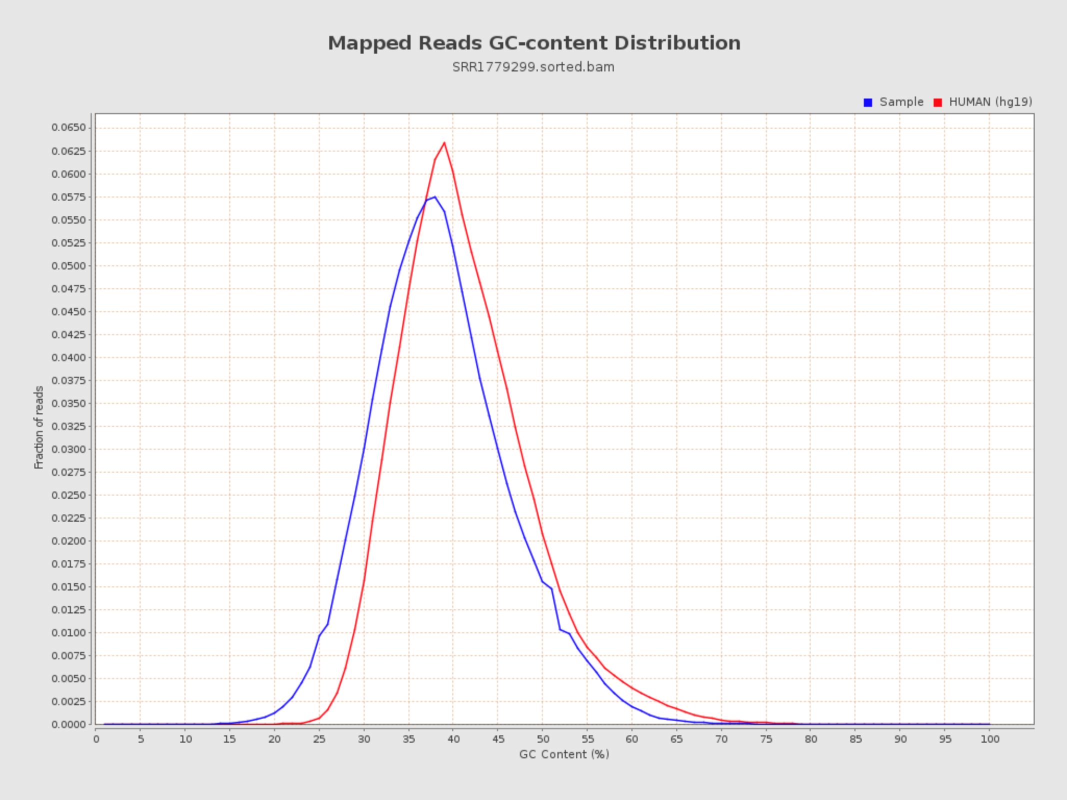
7. Results : Duplication Rate Histogram



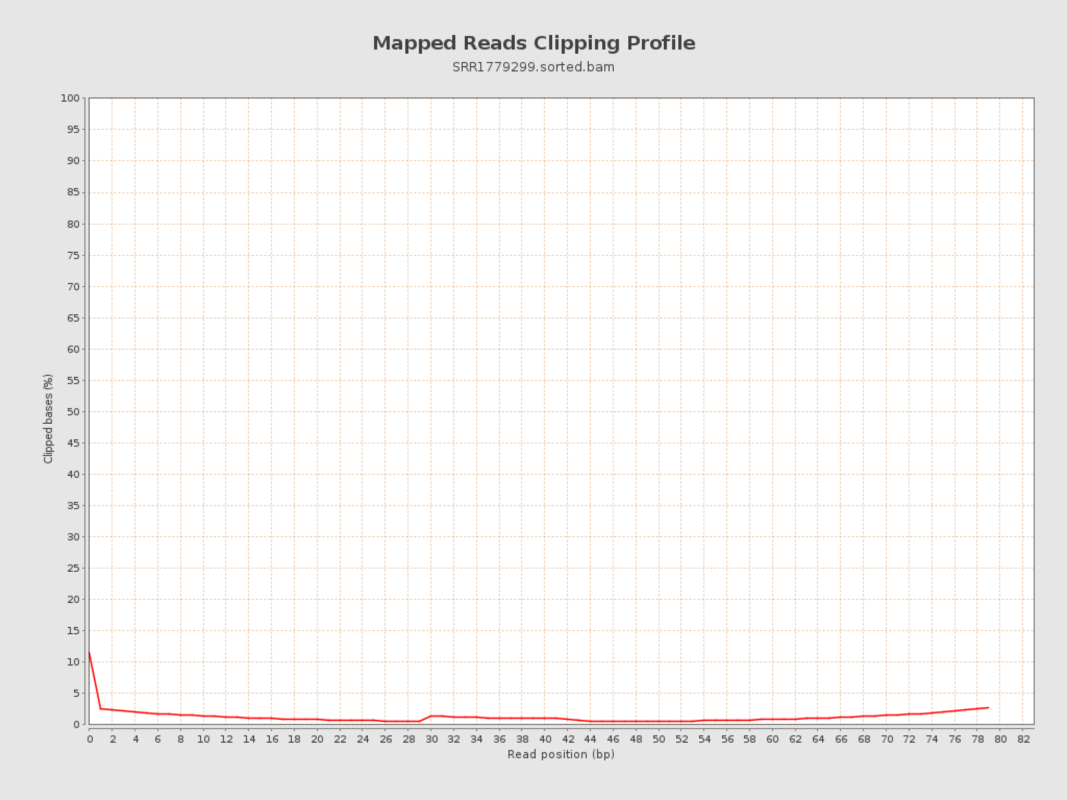
8. Results : Mapped Reads Nucleotide Content



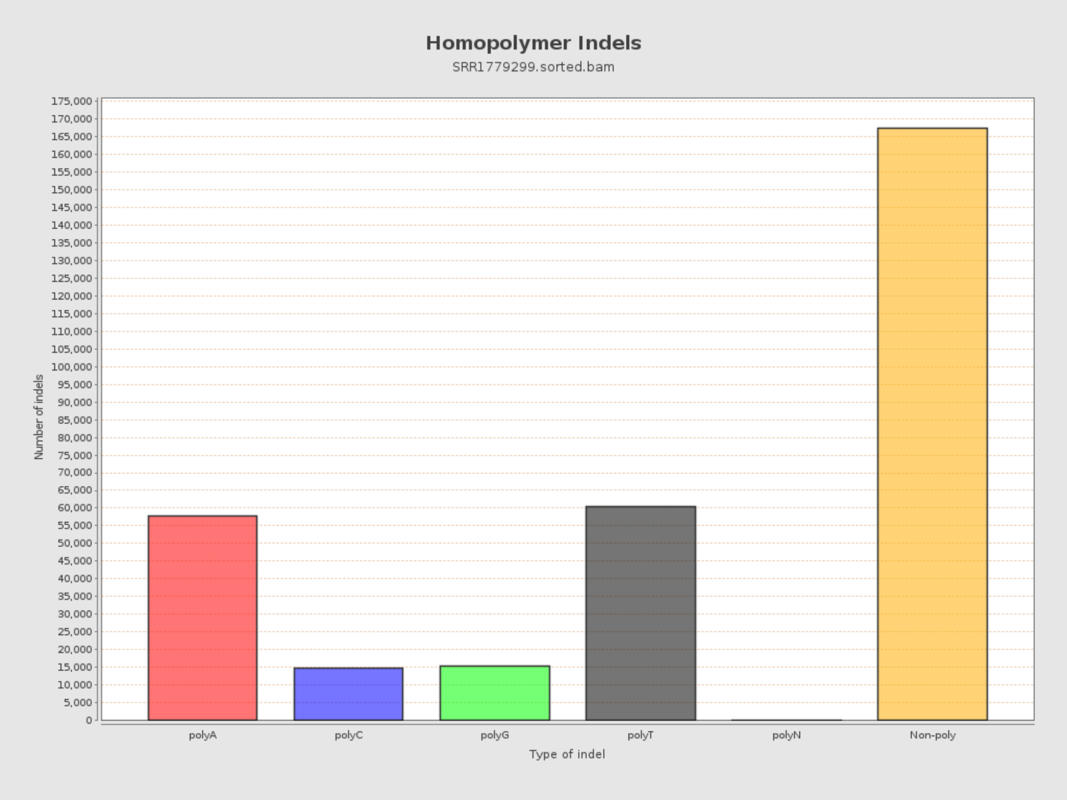
9. Results : Mapped Reads GC-content Distribution



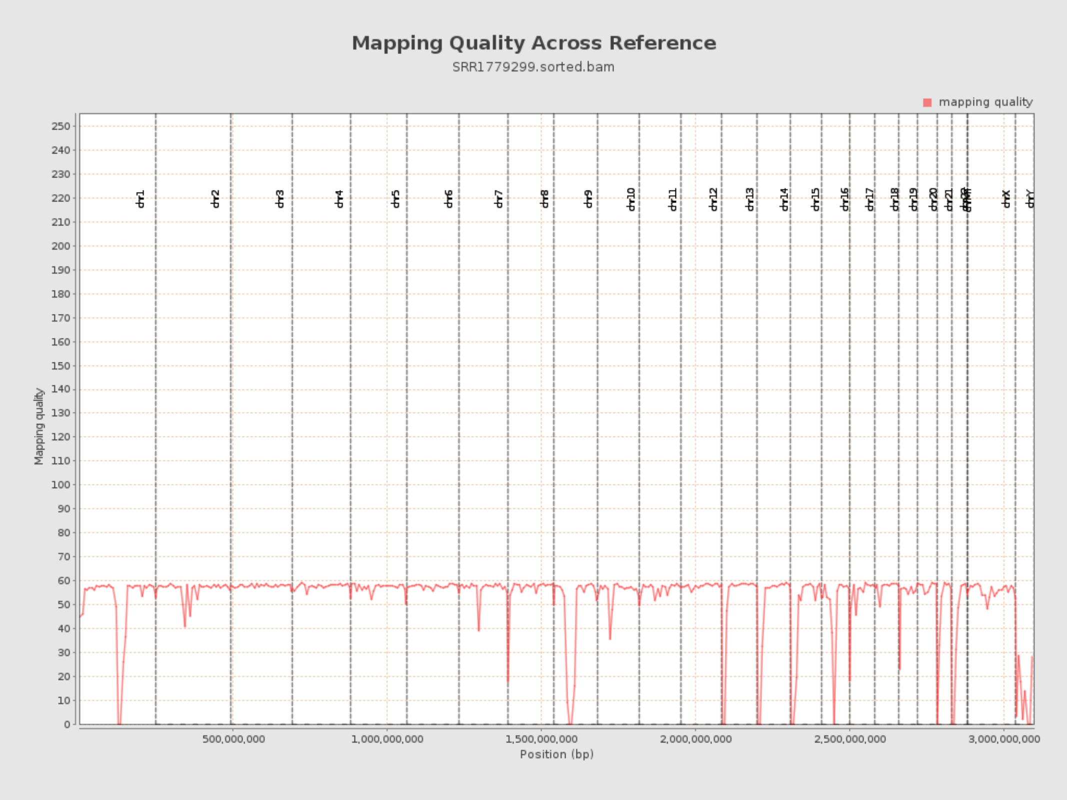
10. Results : Mapped Reads Clipping Profile



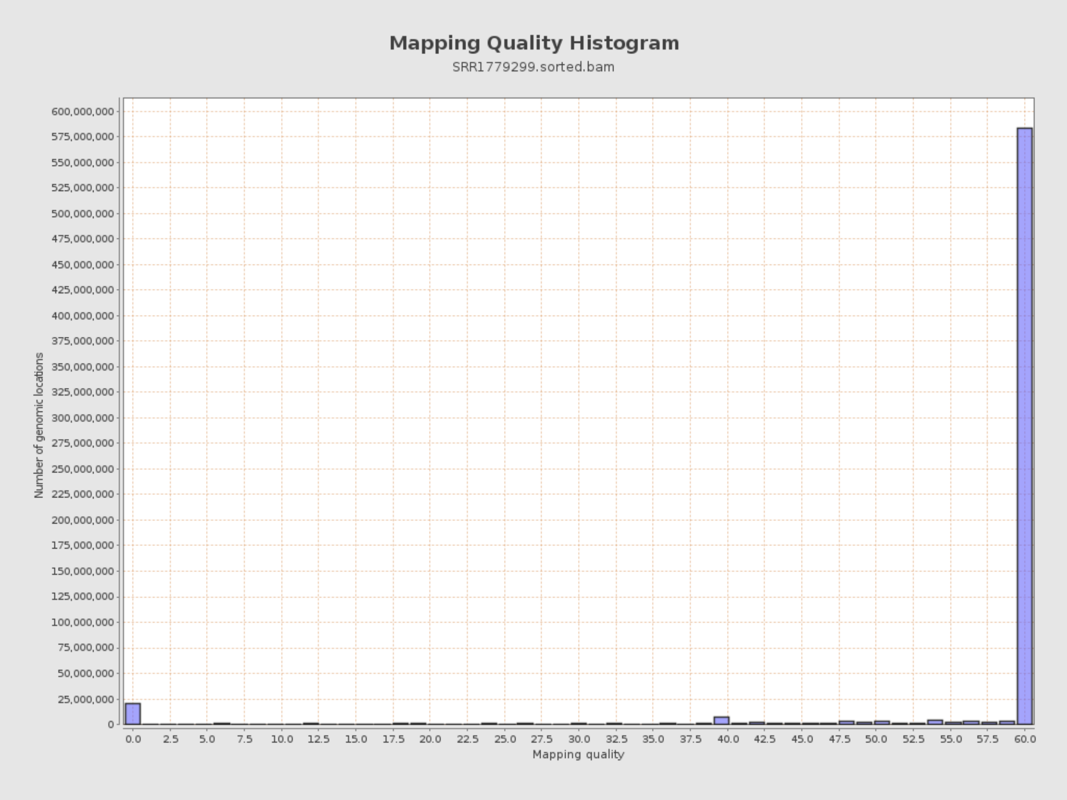
11. Results : Homopolymer Indels



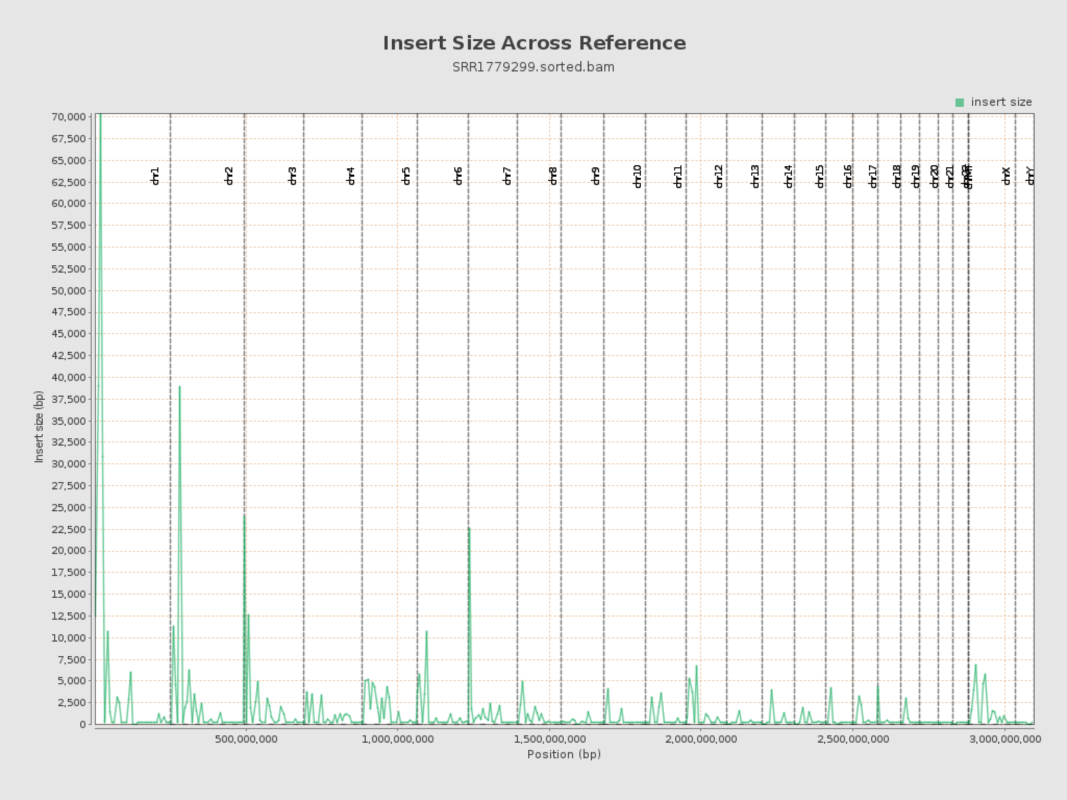
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram