Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 15:11:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779383.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_SRR1779383 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779383_1.fastq.gz SRR1779383_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 15:11:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779383.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,114,892
Mapped reads	12,414,721 / 94.66%
Unmapped reads	700,171 / 5.34%
Mapped paired reads	12,414,721 / 94.66%
Mapped reads, first in pair	6,245,786 / 47.62%
Mapped reads, second in pair	6,168,935 / 47.04%
Mapped reads, both in pair	12,292,272 / 93.73%
Mapped reads, singletons	122,449 / 0.93%
Secondary alignments	0
Supplementary alignments	90,035 / 0.69%
Read min/max/mean length	30 / 80 / 80.25
Duplicated reads (estimated)	2,252,944 / 17.18%
Duplication rate	8.57%
Clipped reads	709,512 / 5.41%

2.2. ACGT Content

Number/percentage of A's	305,001,474 / 30.95%
Number/percentage of C's	187,143,453 / 18.99%
Number/percentage of T's	301,575,195 / 30.6%
Number/percentage of G's	191,467,167 / 19.43%
Number/percentage of N's	219,452 / 0.02%

GC Percentage	38.42%

2.3. Coverage

Mean	0.3184
Standard Deviation	9.0245

2.4. Mapping Quality

Mean Mapping Quality	52.74

2.5. Insert size

Mean	89,056.26
Standard Deviation	2,821,243.39
P25/Median/P75	171 / 221 / 278

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	3,762,003
Insertions	95,638
Mapped reads with at least one insertion	0.76%
Deletions	106,983
Mapped reads with at least one deletion	0.85%
Homopolymer indels	47.09%

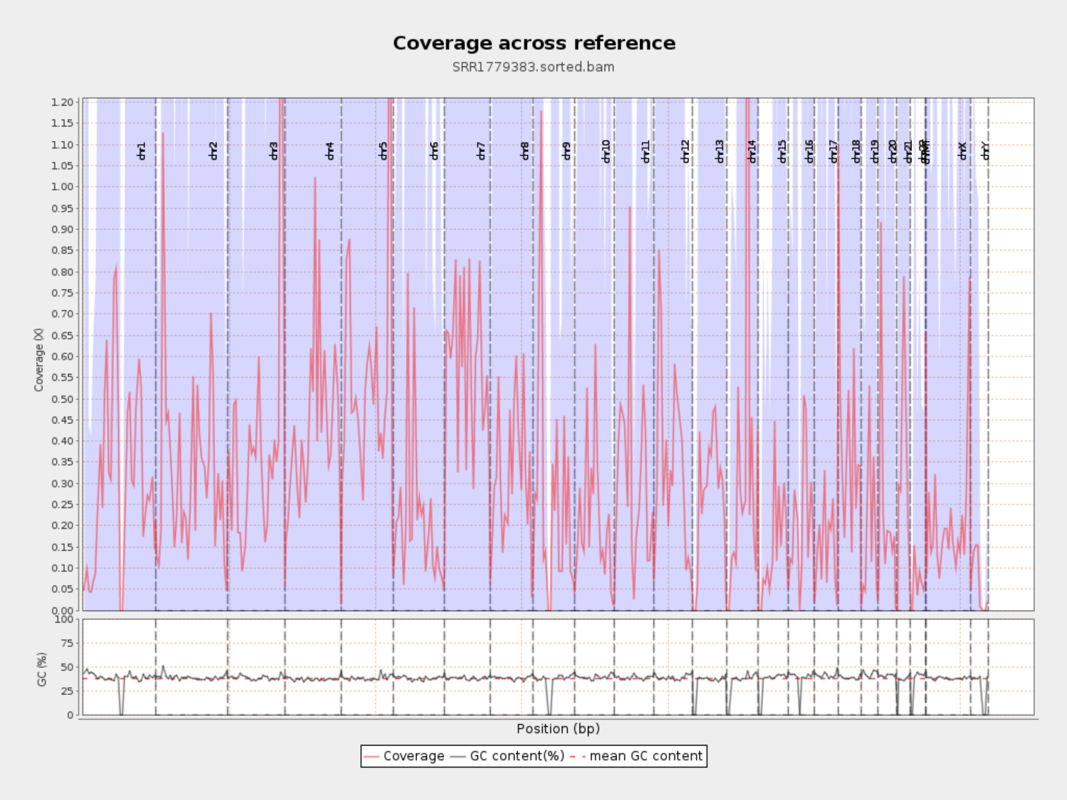
2.7. Chromosome stats

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

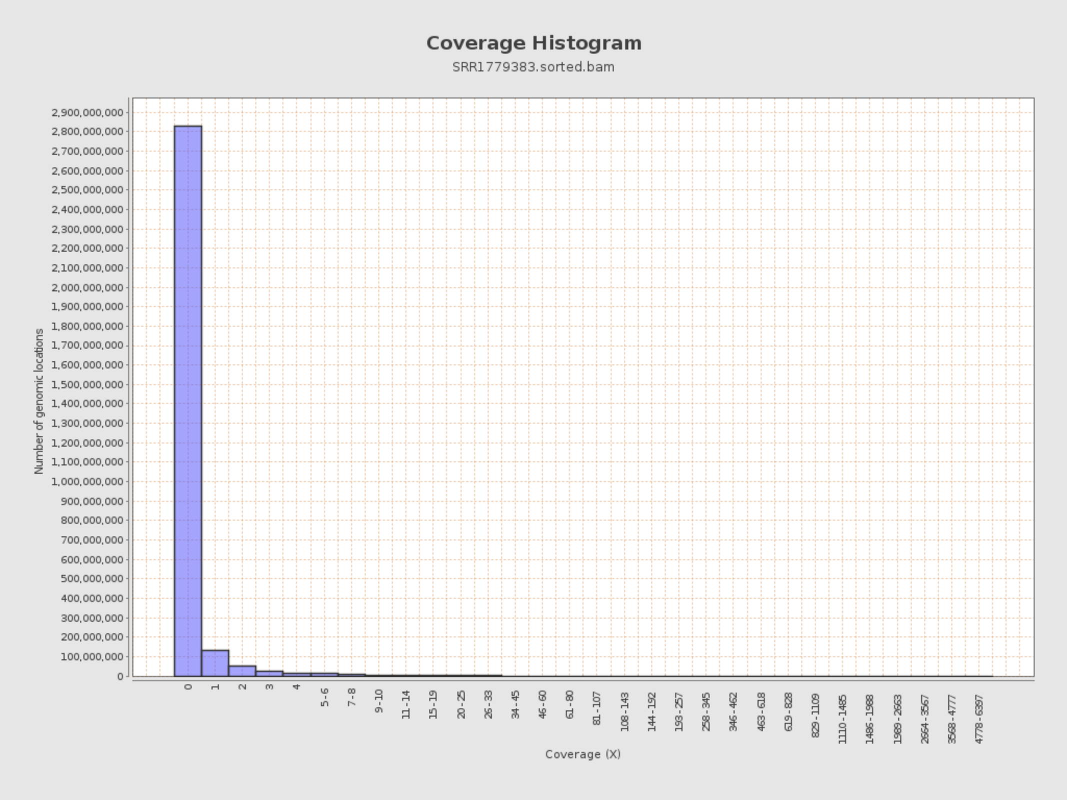
		bases	coverage	deviation
chr1	249250621	76721214	0.3078	9.5195
chr2	243199373	79776391	0.328	7.5811
chr3	198022430	78819315	0.398	15.5173
chr4	191154276	83561383	0.4371	3.5804
chr5	180915260	97748275	0.5403	8.4999
chr6	171115067	38171055	0.2231	5.2641
chr7	159138663	90962162	0.5716	6.3
chr8	146364022	48222271	0.3295	3.178
chr9	141213431	39848539	0.2822	2.3536
chr10	135534747	30009048	0.2214	6.8576
chr11	135006516	43159811	0.3197	3.0414
chr12	133851895	46288220	0.3458	2.1618
chr13	115169878	32030754	0.2781	2.2422
chr14	107349540	41078687	0.3827	29.9052
chr15	102531392	15271621	0.1489	5.1636
chr16	90354753	19068188	0.211	10.3113
chr17	81195210	12422901	0.153	2.9728
chr18	78077248	30404815	0.3894	5.7348
chr19	59128983	11269136	0.1906	6.4159
chr20	63025520	15537098	0.2465	7.1228
chr21	48129895	16082413	0.3341	2.0264
chr22	51304566	3263745	0.0636	1.295
chrMT	16571	10915	0.6587	0.983
chrX	155270560	31777373	0.2047	9.005

chrY	59373566	4114459	0.0693	0.6397

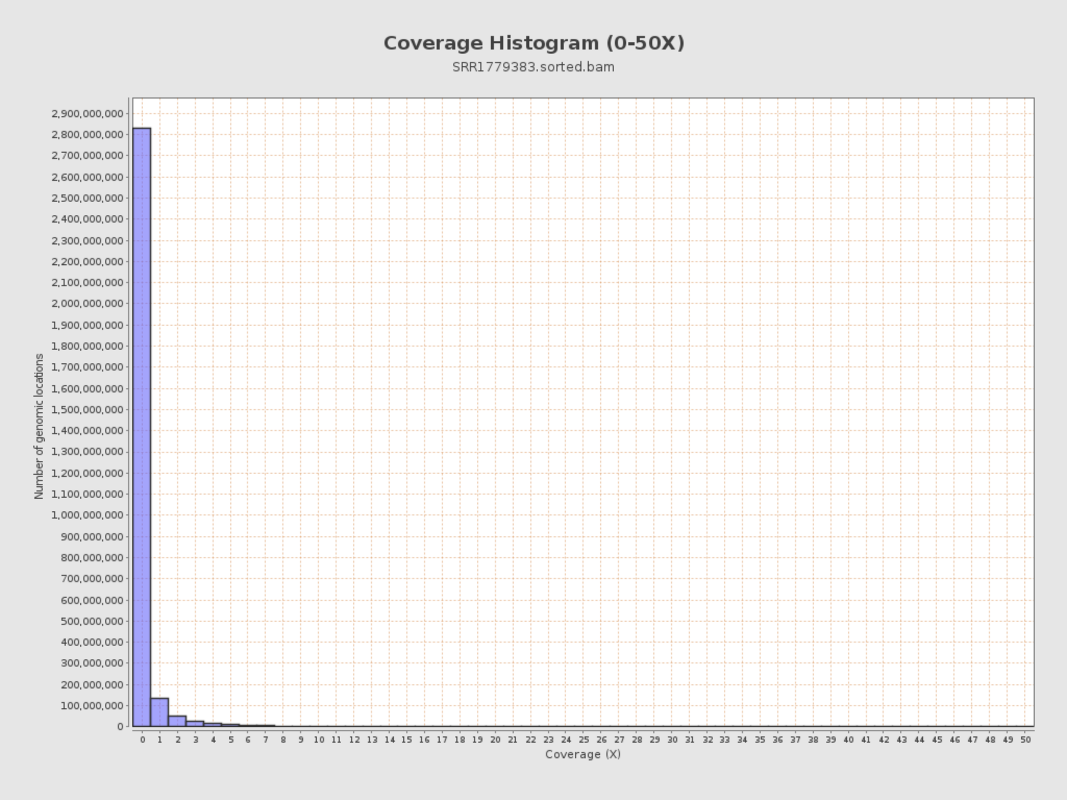
3. Results : Coverage across reference



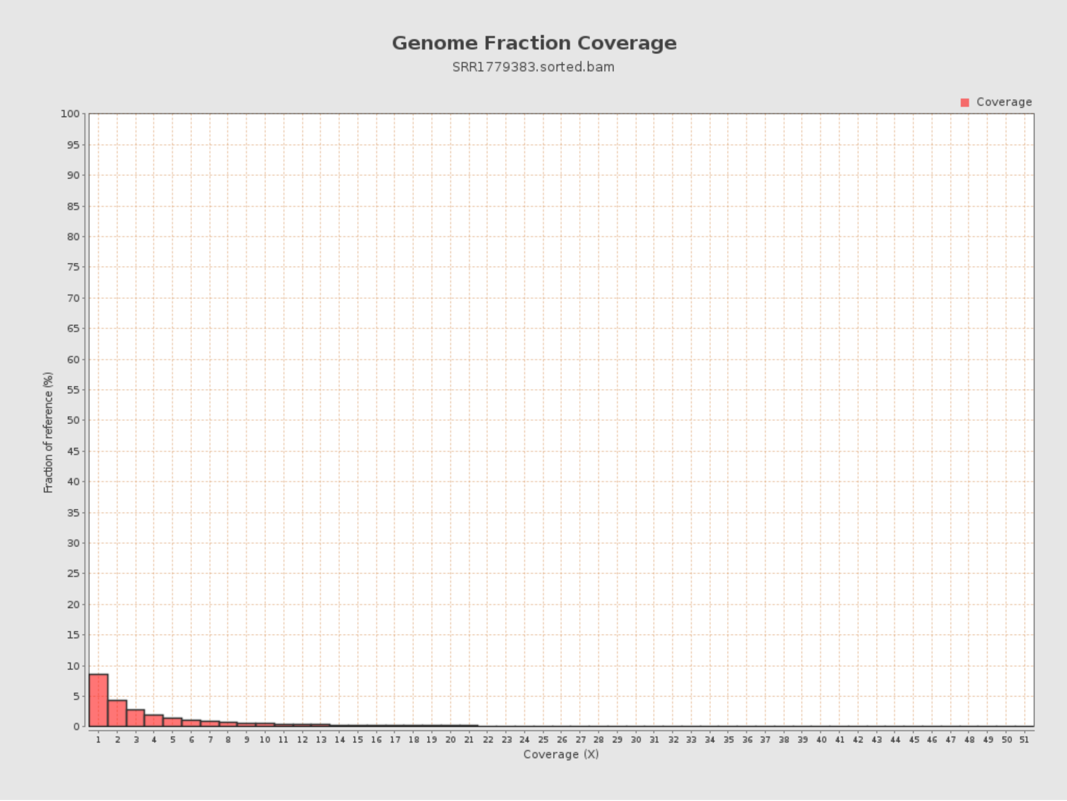
4. Results : Coverage Histogram



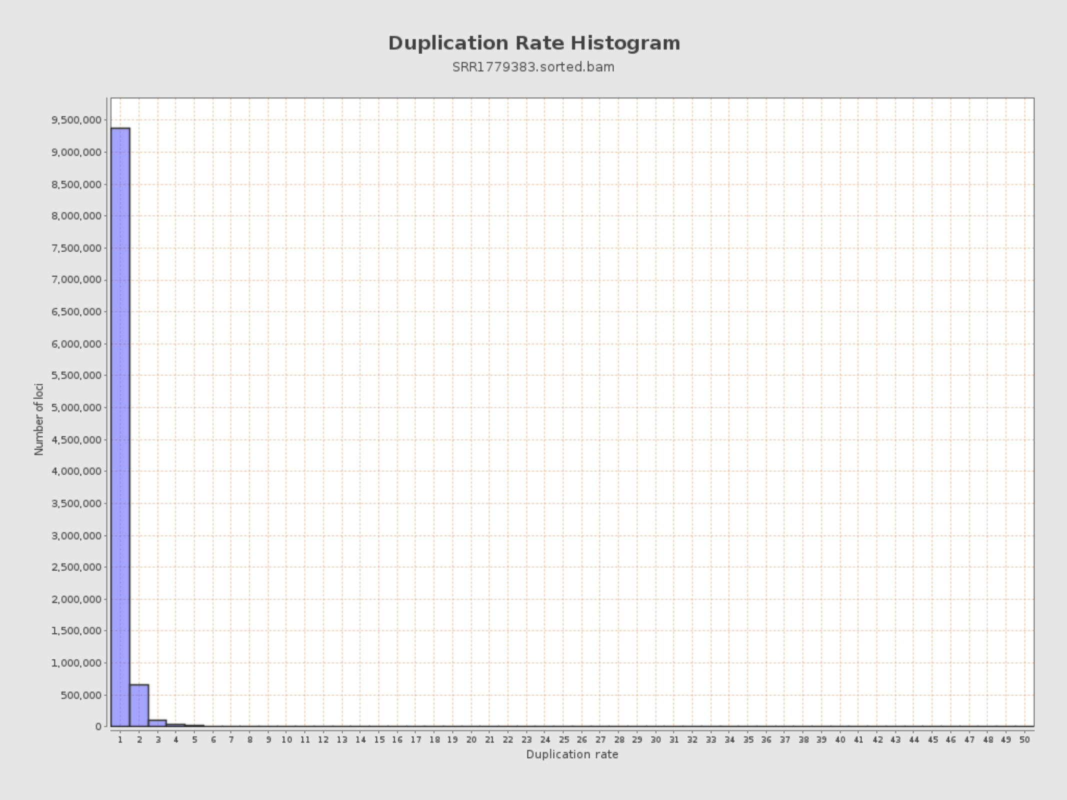
5. Results : Coverage Histogram (0-50X)



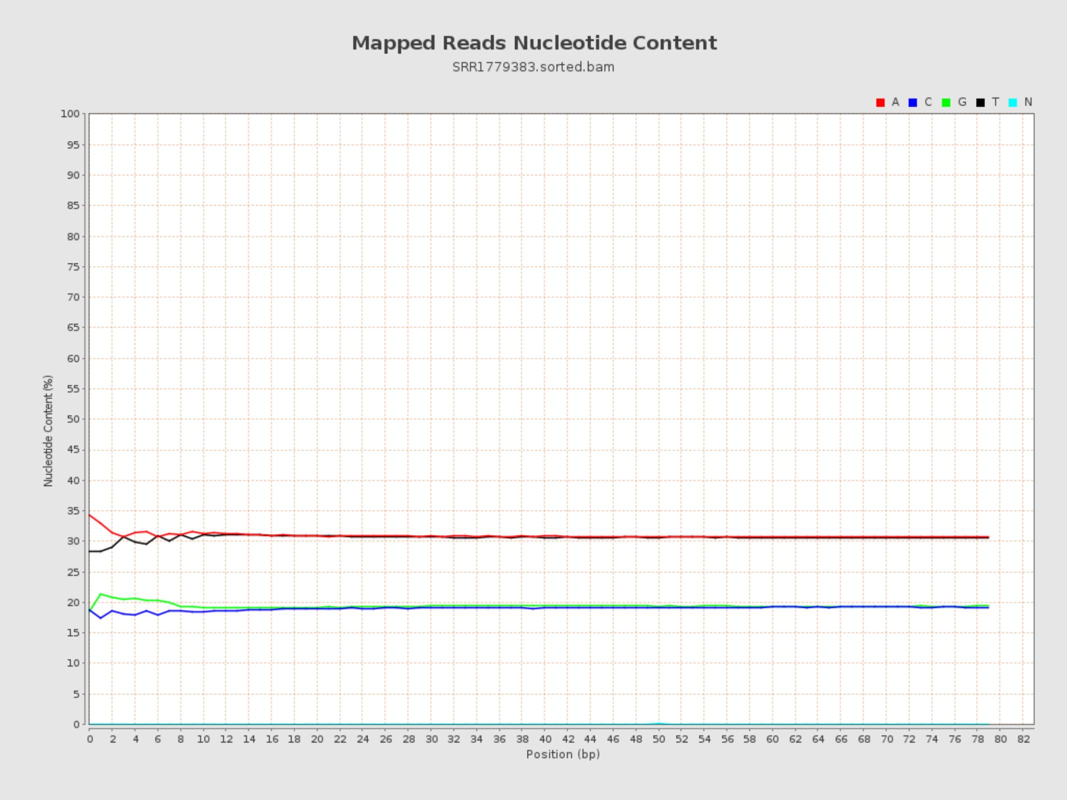
6. Results : Genome Fraction Coverage



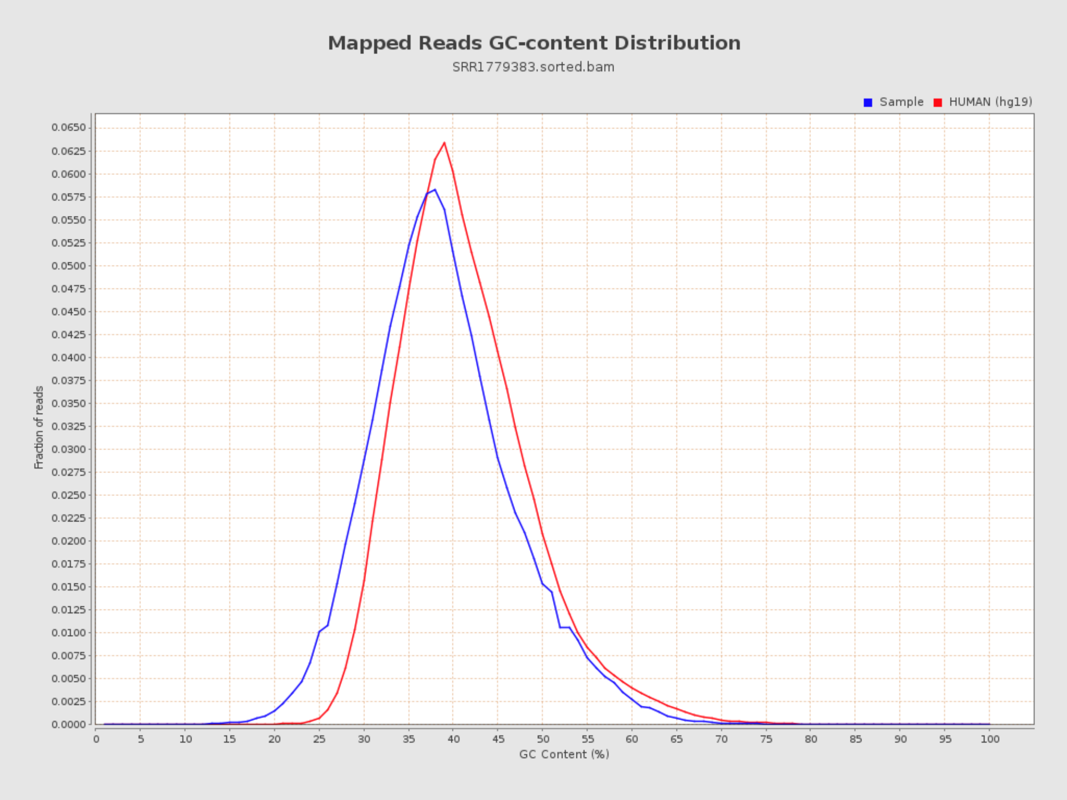
7. Results : Duplication Rate Histogram



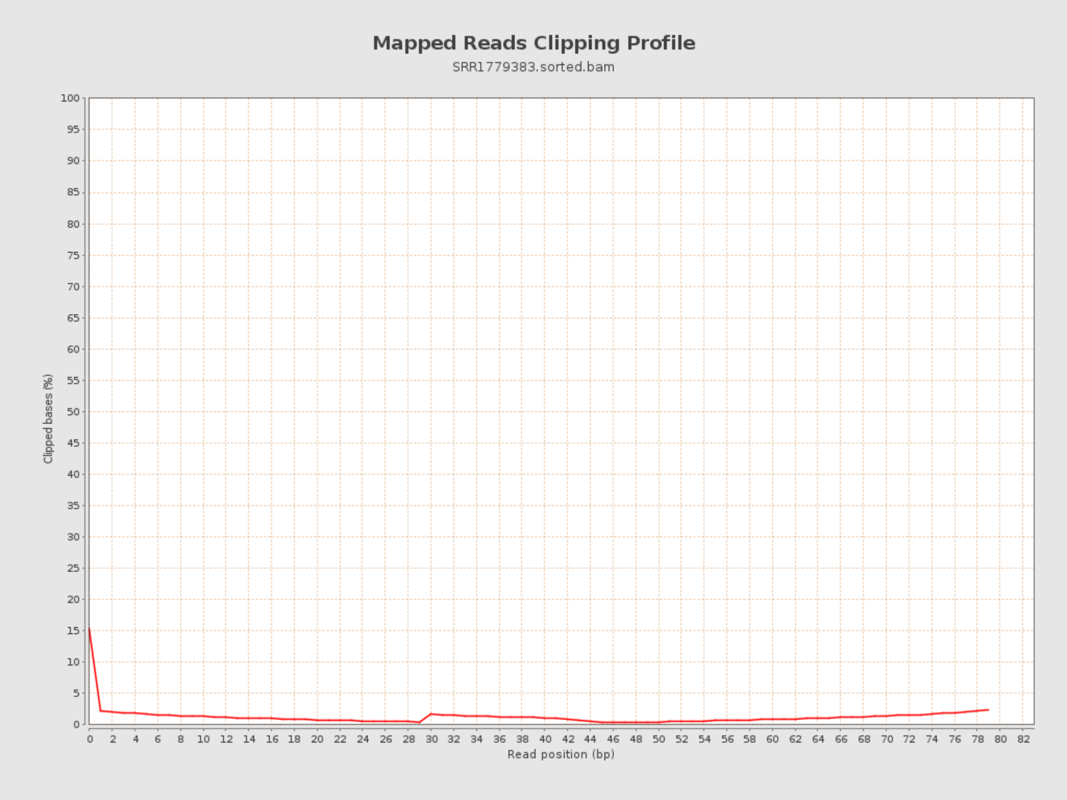
8. Results : Mapped Reads Nucleotide Content



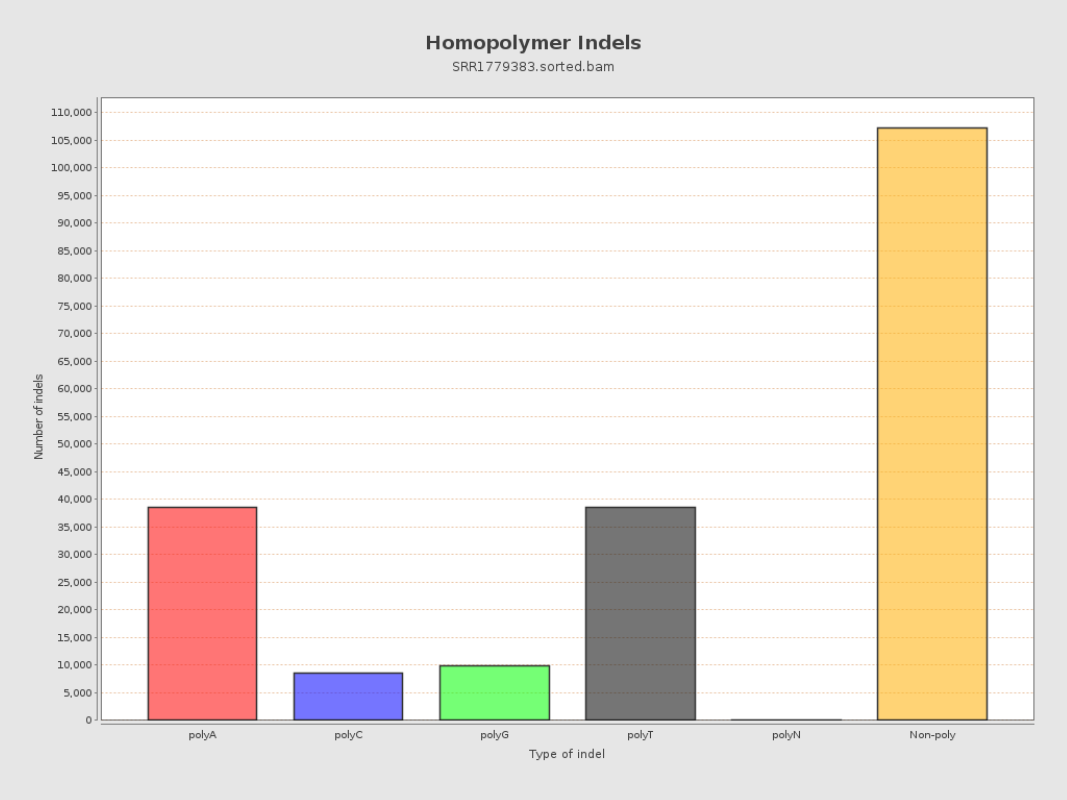
9. Results : Mapped Reads GC-content Distribution



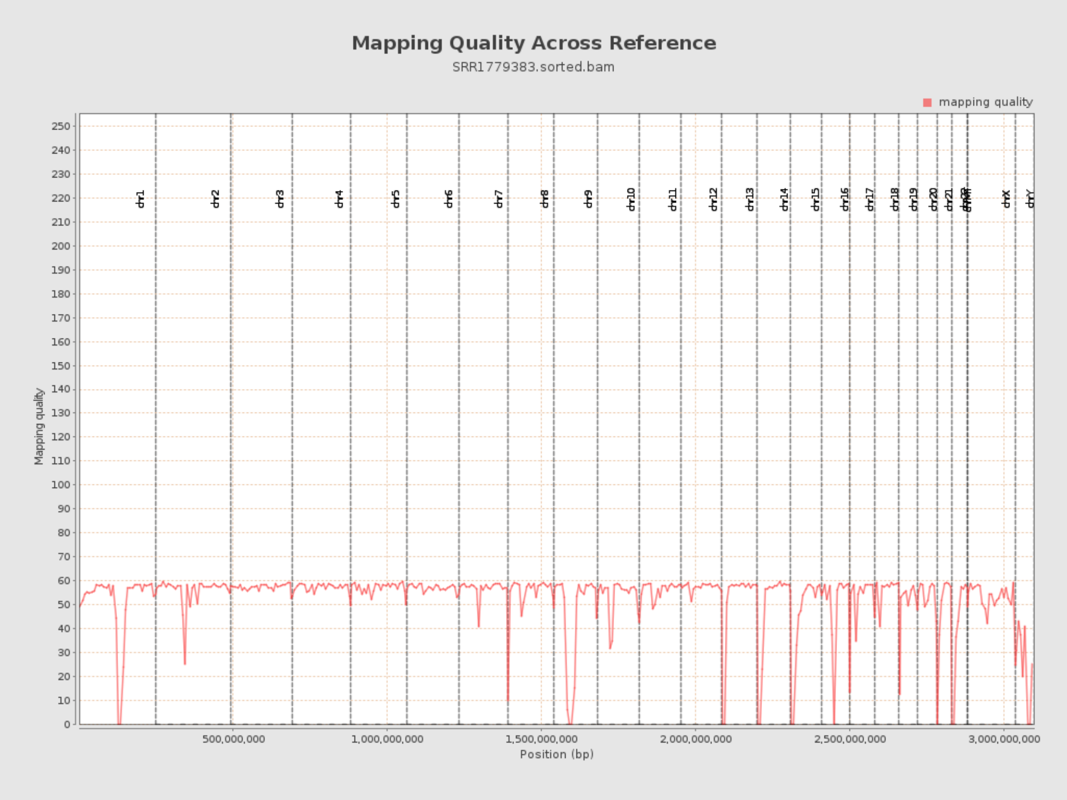
10. Results : Mapped Reads Clipping Profile



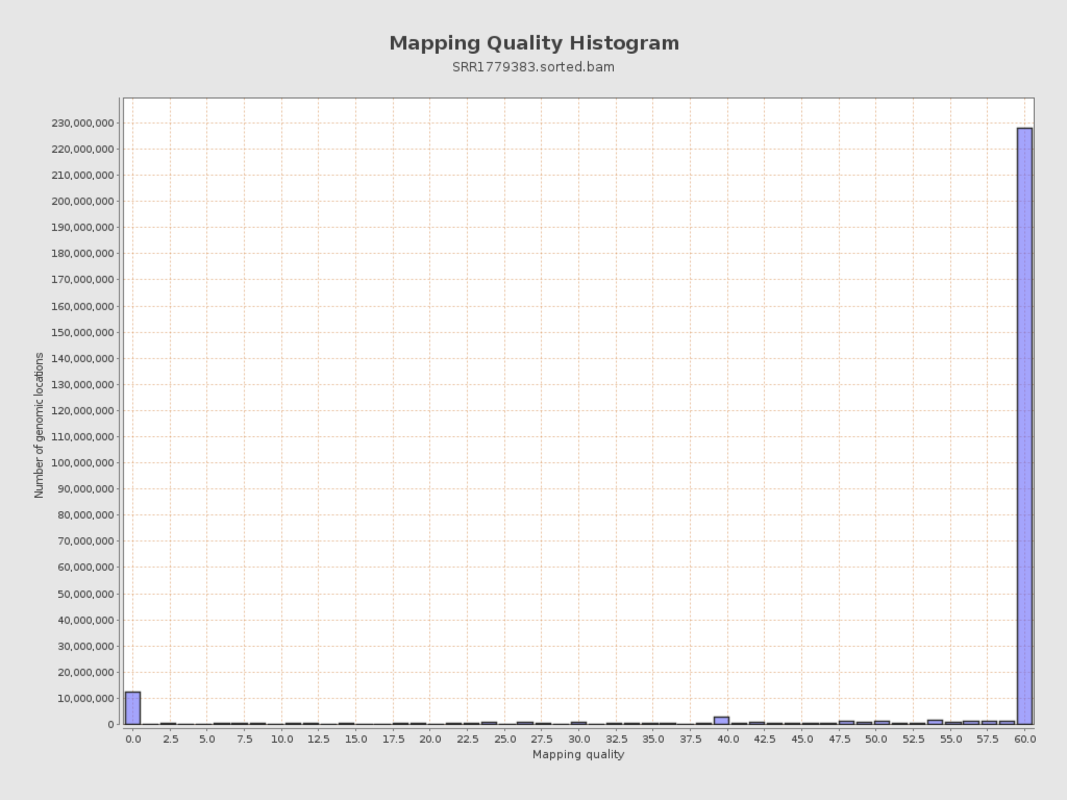
11. Results : Homopolymer Indels



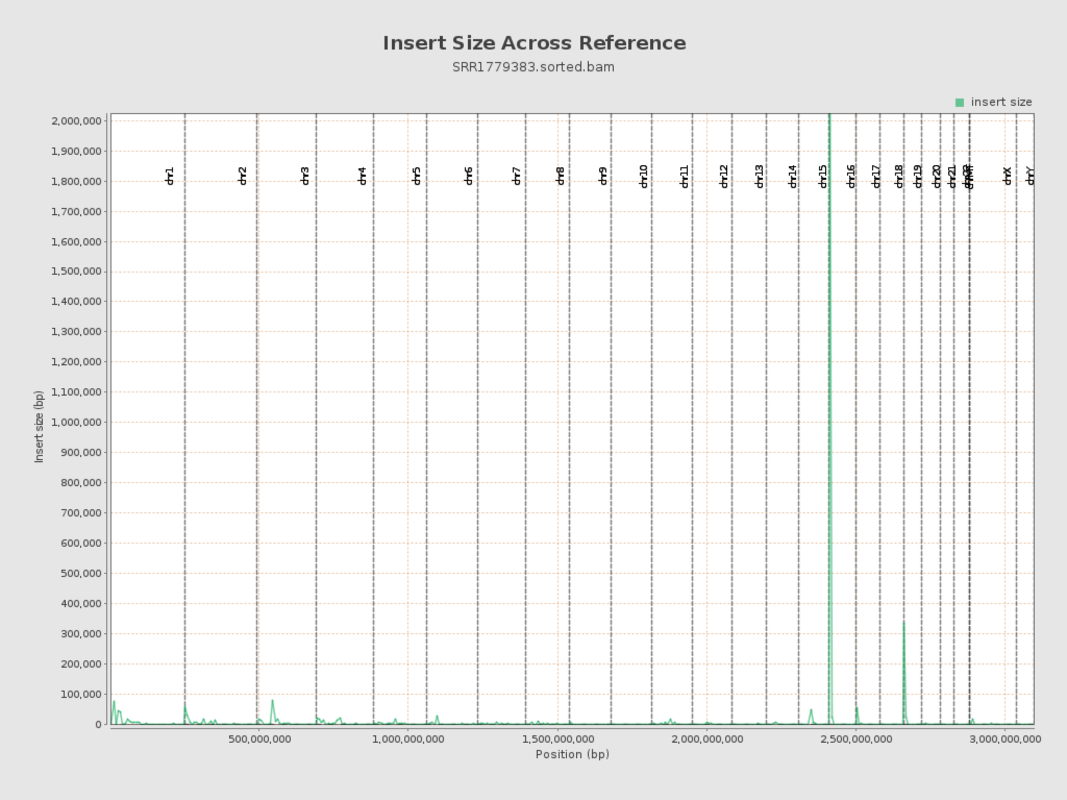
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram