Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 04:48:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779161.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_SRR1779161 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779161_1.fastq.gz SRR1779161_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 04:48:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,682,430
Mapped reads	24,205,969 / 94.25%
Unmapped reads	1,476,461 / 5.75%
Mapped paired reads	24,205,969 / 94.25%
Mapped reads, first in pair	12,174,684 / 47.4%
Mapped reads, second in pair	12,031,285 / 46.85%
Mapped reads, both in pair	23,942,576 / 93.23%
Mapped reads, singletons	263,393 / 1.03%
Secondary alignments	0
Supplementary alignments	144,105 / 0.56%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	1,306,055 / 5.09%
Duplication rate	4.88%
Clipped reads	1,796,828 / 7%

2.2. ACGT Content

Number/percentage of A's	741,231,467 / 30.71%
Number/percentage of C's	463,017,718 / 19.19%
Number/percentage of T's	737,203,607 / 30.55%
Number/percentage of G's	470,904,832 / 19.51%
Number/percentage of N's	969,945 / 0.04%

GC Percentage	38.7%

2.3. Coverage

Mean	0.7798
Standard Deviation	2.7754

2.4. Mapping Quality

Mean Mapping Quality	53.56

2.5. Insert size

Mean	54,705.57
Standard Deviation	2,252,386.72
P25/Median/P75	153 / 213 / 295

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	9,948,750
Insertions	203,372
Mapped reads with at least one insertion	0.83%
Deletions	249,732
Mapped reads with at least one deletion	1.01%
Homopolymer indels	46.71%

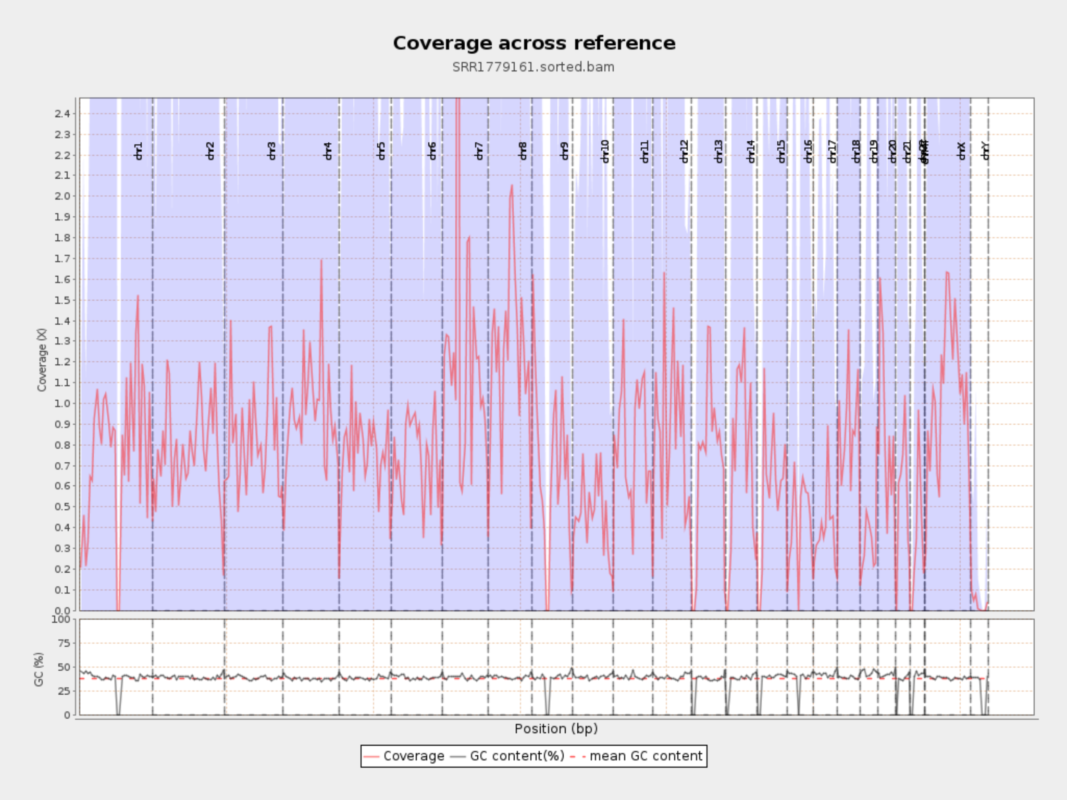
2.7. Chromosome stats

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

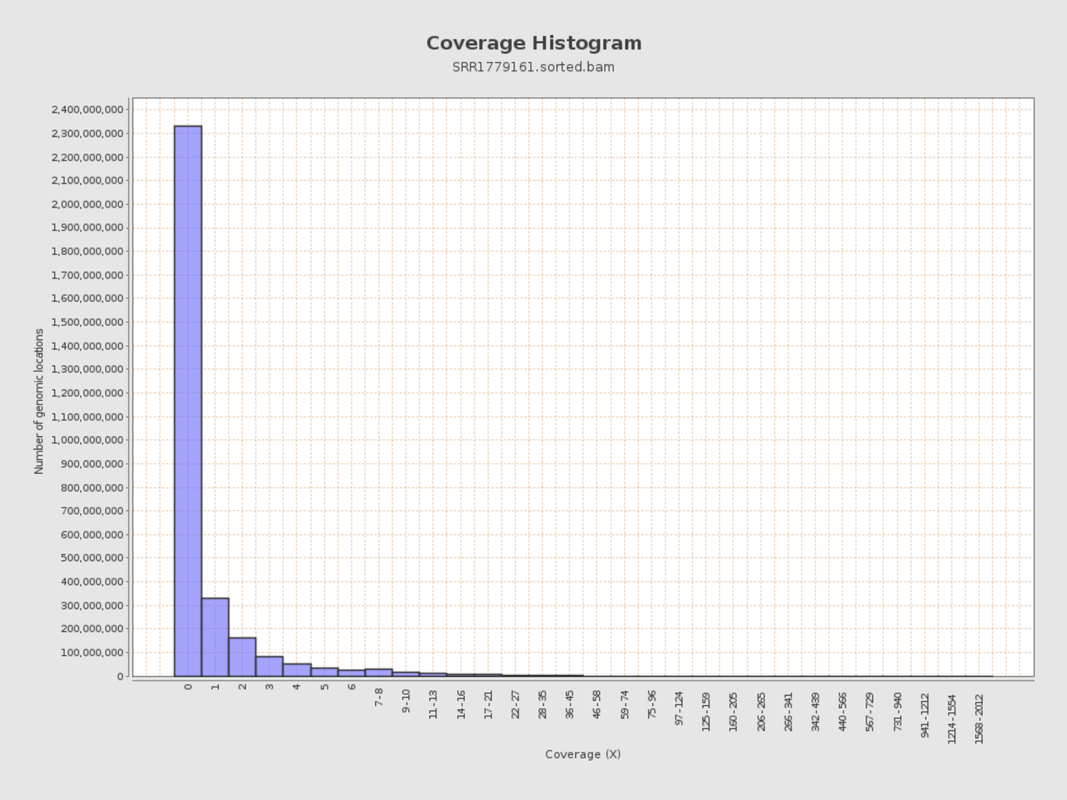
		bases	coverage	deviation
chr1	249250621	191889167	0.7699	3.2942
chr2	243199373	190164614	0.7819	2.5516
chr3	198022430	165297924	0.8347	2.4867
chr4	191154276	182822347	0.9564	2.6259
chr5	180915260	136165661	0.7526	2.2425
chr6	171115067	126271969	0.7379	2.1584
chr7	159138663	207425448	1.3034	4.9923
chr8	146364022	185730207	1.269	3.2451
chr9	141213431	94917131	0.6722	2.2622
chr10	135534747	63562301	0.469	3.1589
chr11	135006516	110310308	0.8171	2.7607
chr12	133851895	115381486	0.862	2.6058
chr13	115169878	85122977	0.7391	2.3244
chr14	107349540	76868188	0.7161	2.4879
chr15	102531392	59831847	0.5835	1.9337
chr16	90354753	37420296	0.4141	1.7402
chr17	81195210	32095163	0.3953	1.6001
chr18	78077248	70451840	0.9023	2.5708
chr19	59128983	18947803	0.3204	1.6473
chr20	63025520	53600171	0.8505	2.6913
chr21	48129895	27671281	0.5749	2.4047
chr22	51304566	16950325	0.3304	1.9581
chrMT	16571	3794	0.229	0.7062
chrX	155270560	163154650	1.0508	3.418

chrY	59373566	1823165	0.0307	0.4691

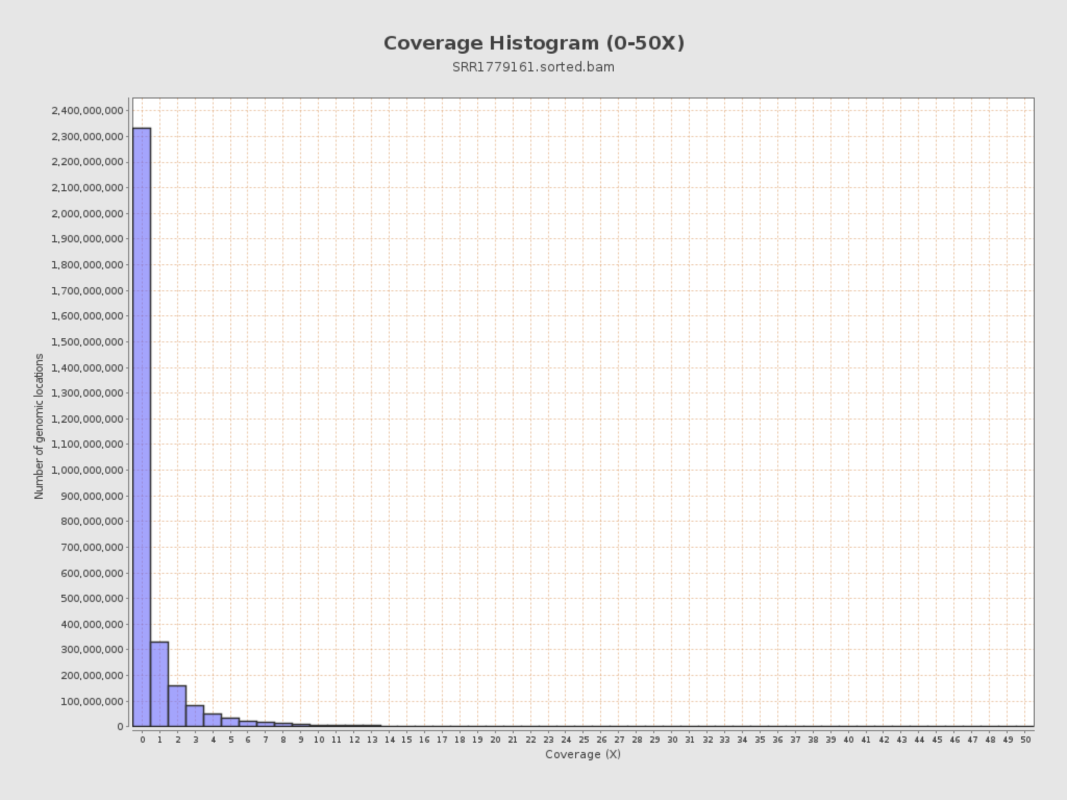
3. Results : Coverage across reference



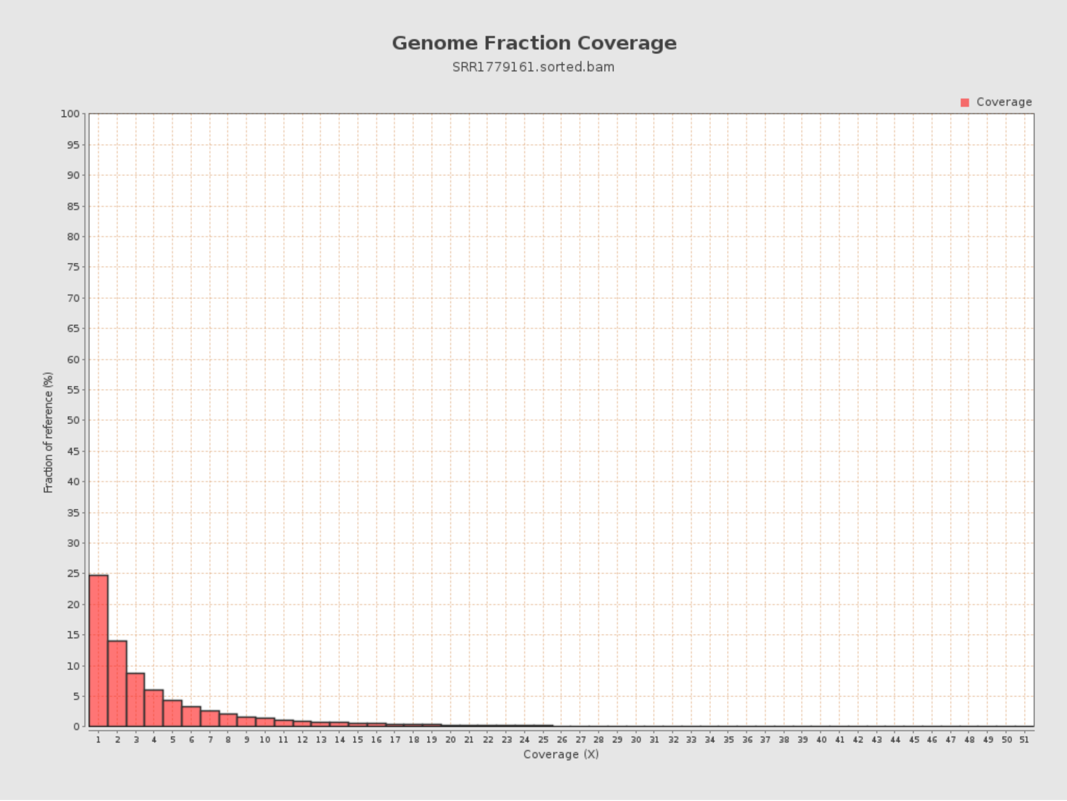
4. Results : Coverage Histogram



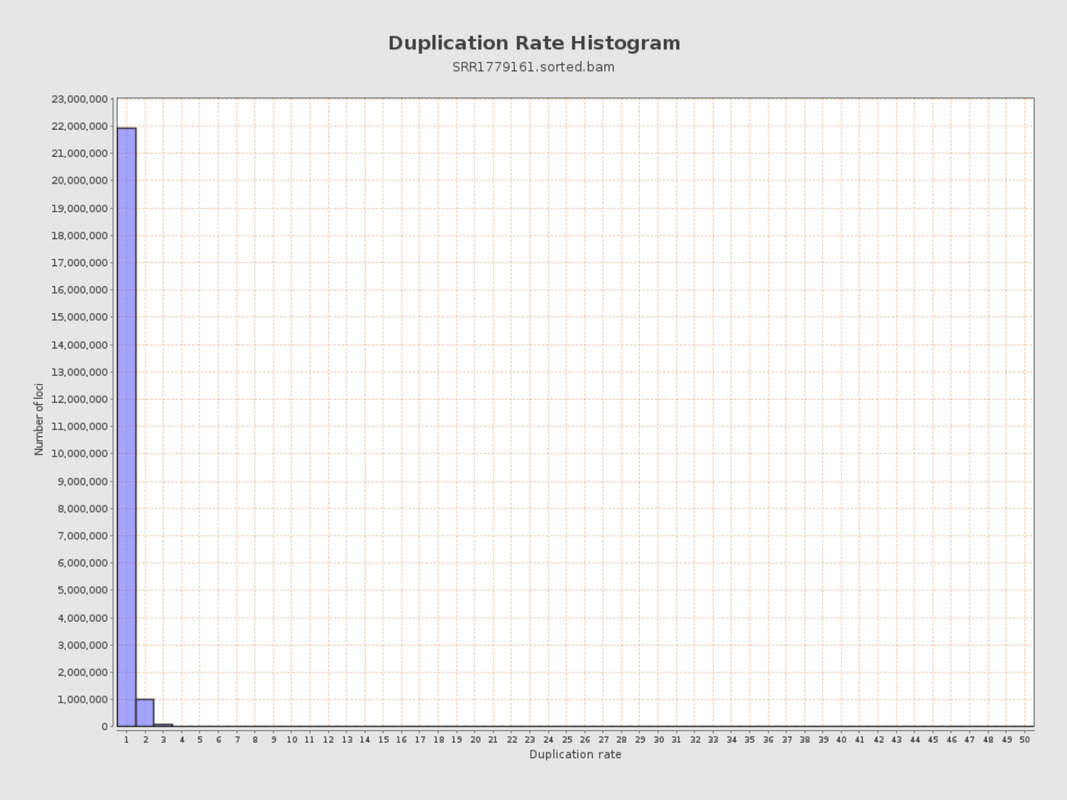
5. Results : Coverage Histogram (0-50X)



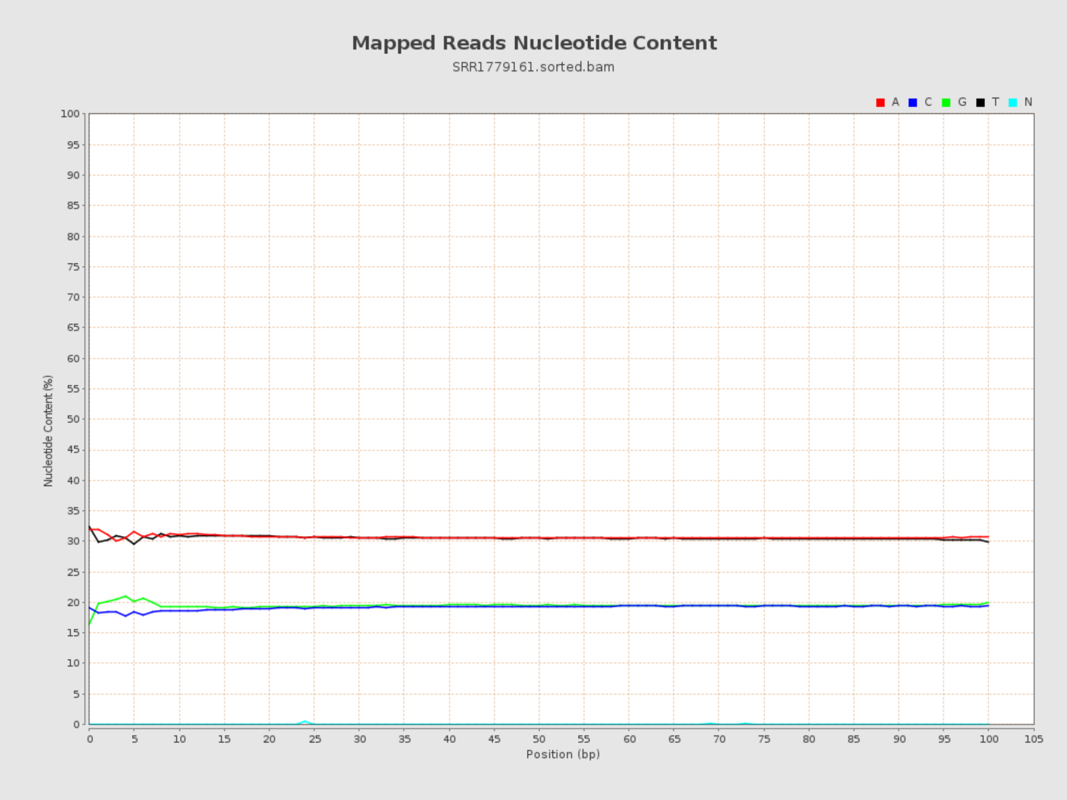
6. Results : Genome Fraction Coverage



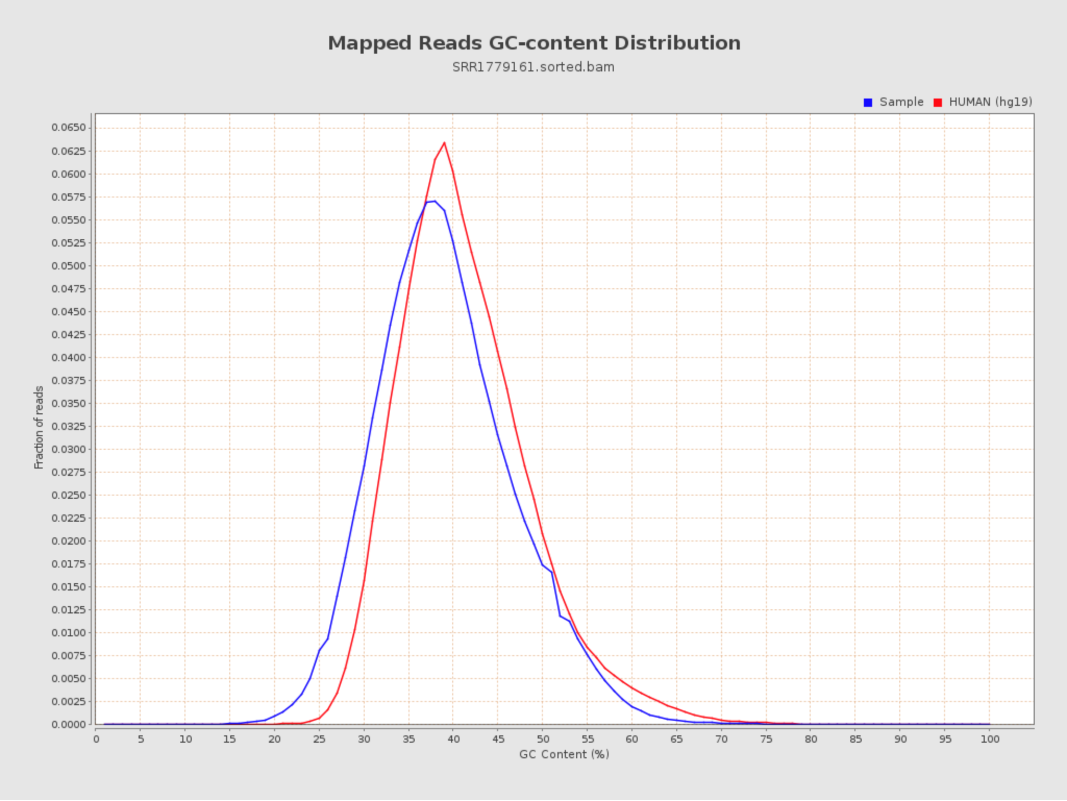
7. Results : Duplication Rate Histogram



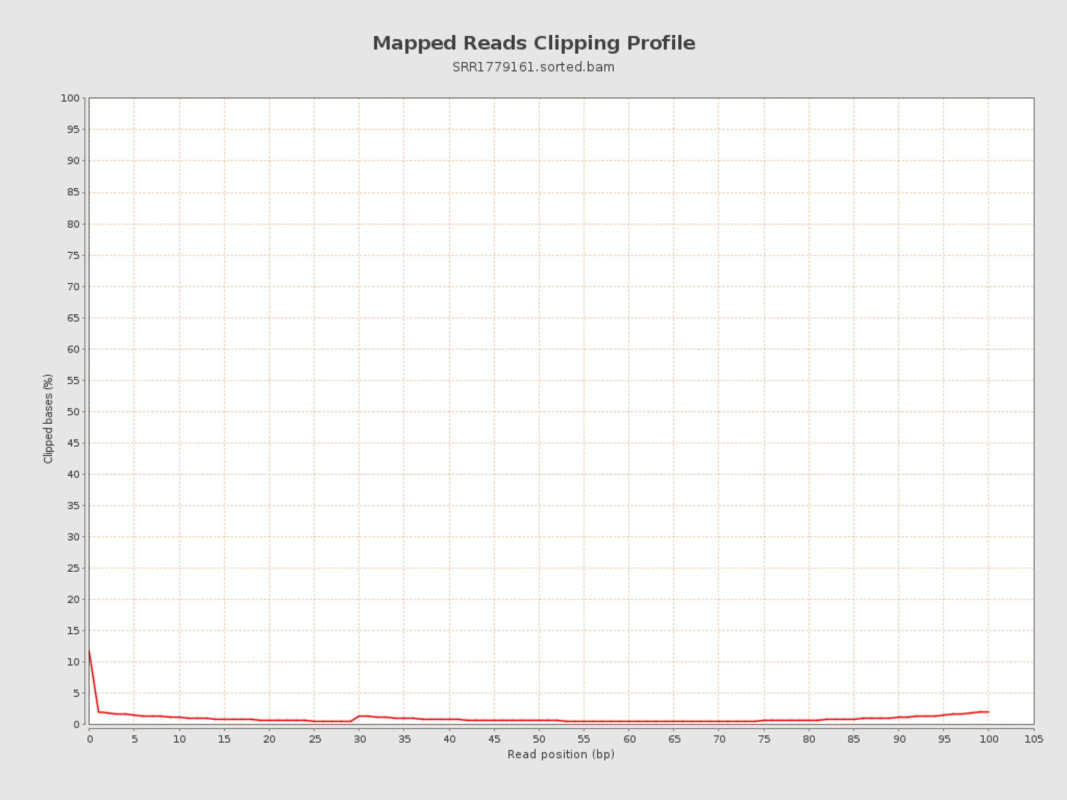
8. Results : Mapped Reads Nucleotide Content



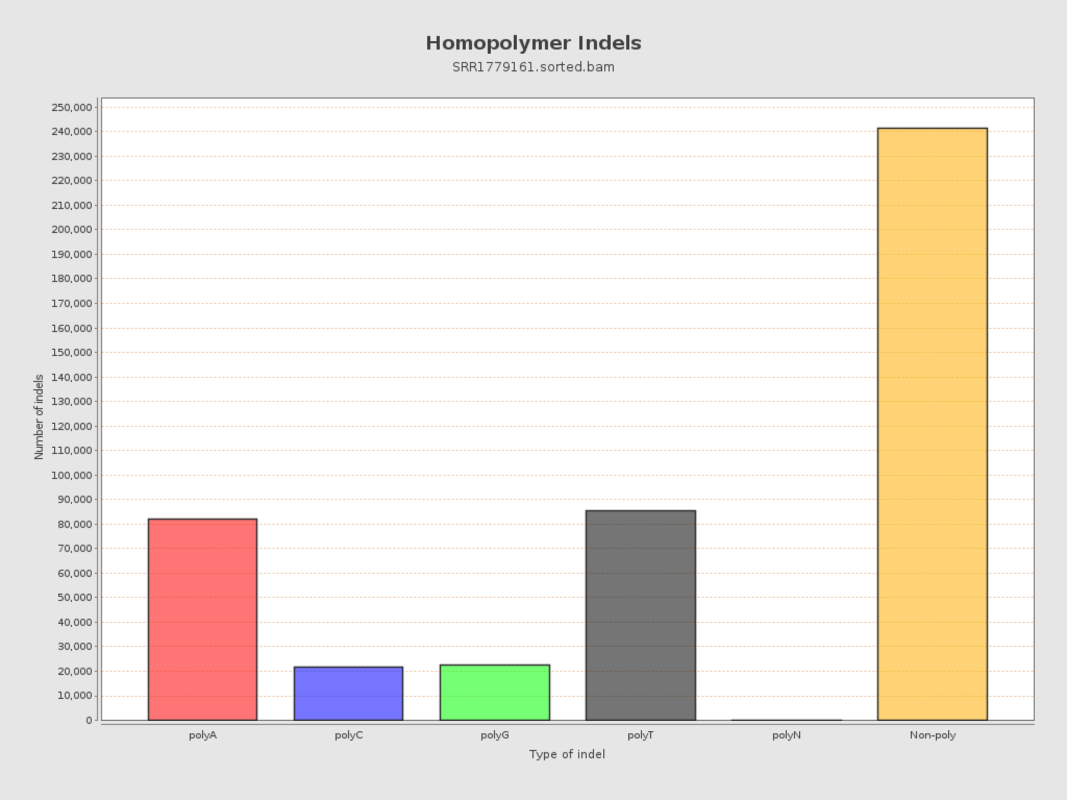
9. Results : Mapped Reads GC-content Distribution



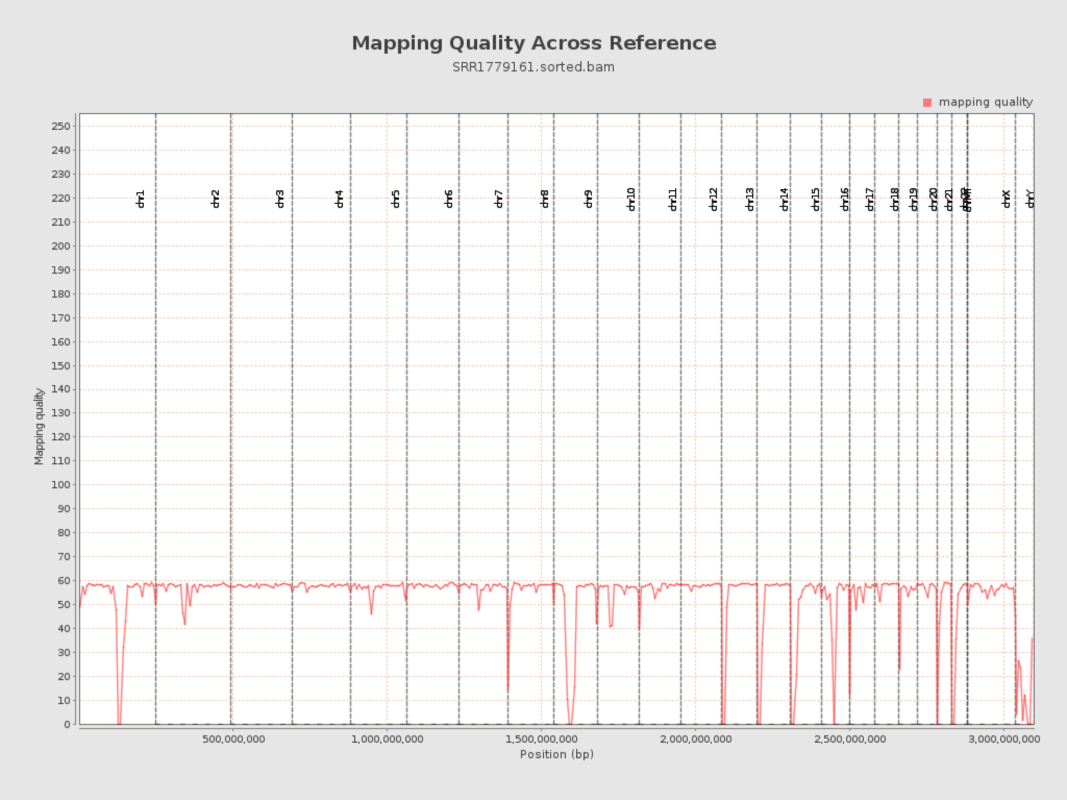
10. Results : Mapped Reads Clipping Profile



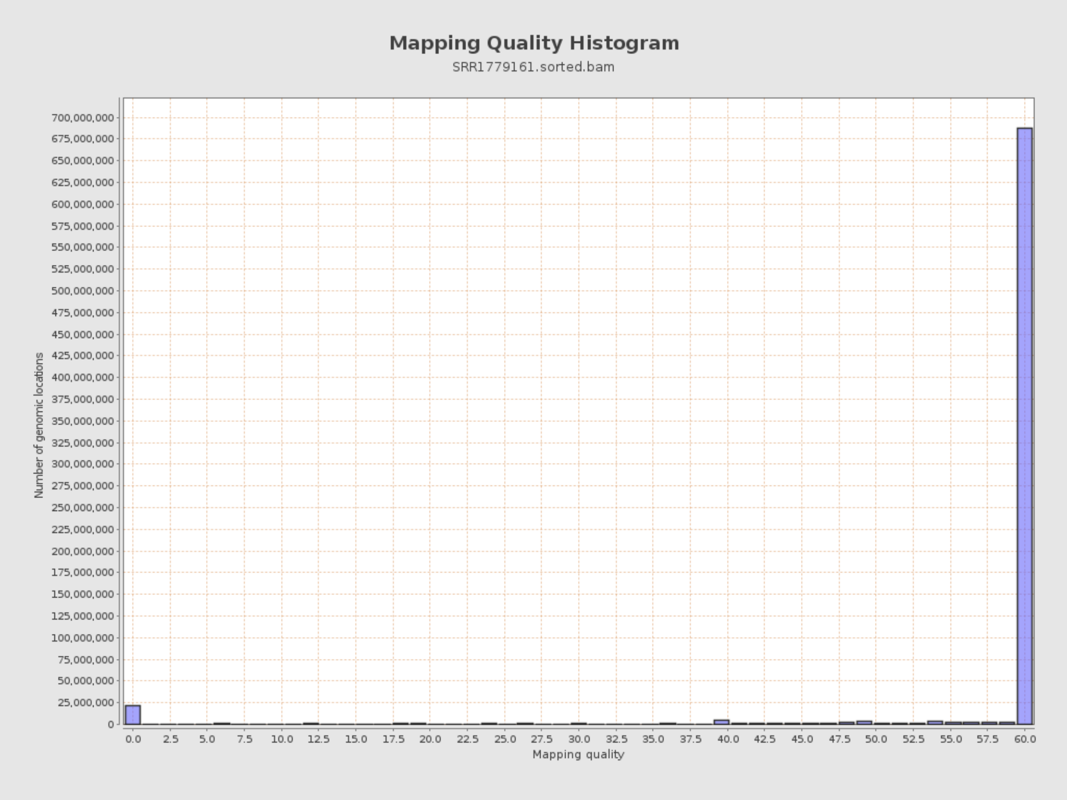
11. Results : Homopolymer Indels



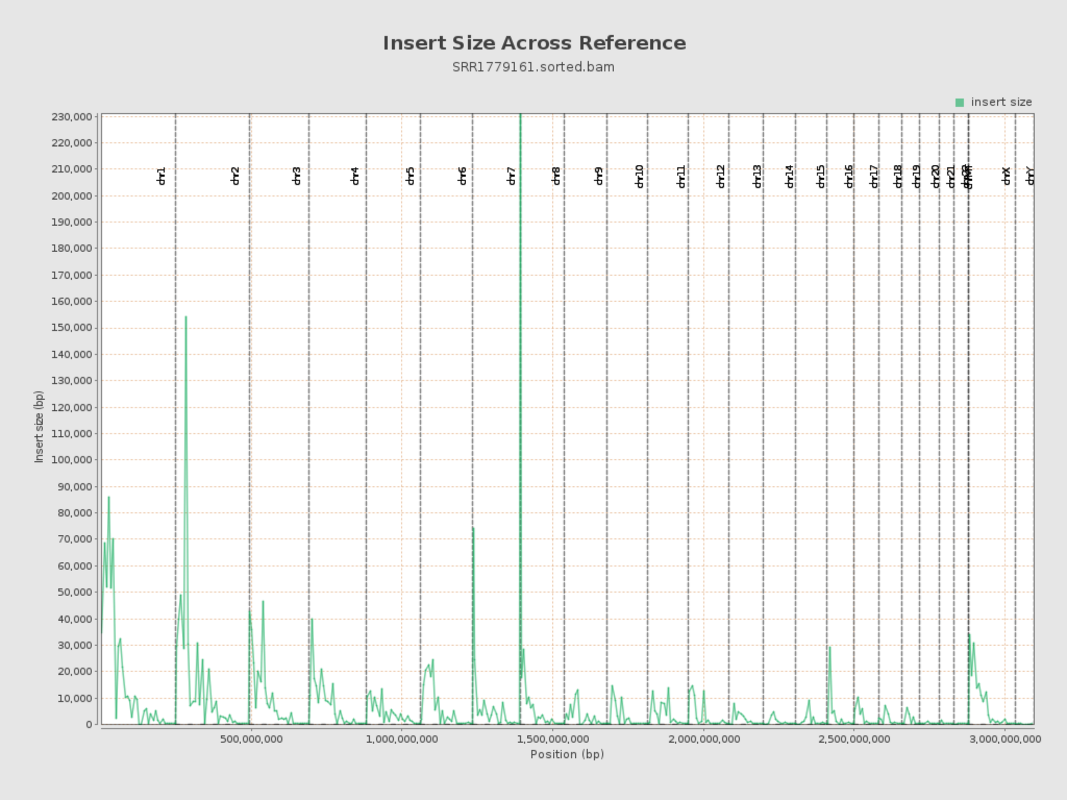
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram