Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 22:29:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779095.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_SRR1779095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779095_1.fastq.gz SRR1779095_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 22:29:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,261,318
Mapped reads	26,505,398 / 97.23%
Unmapped reads	755,920 / 2.77%
Mapped paired reads	26,505,398 / 97.23%
Mapped reads, first in pair	13,321,640 / 48.87%
Mapped reads, second in pair	13,183,758 / 48.36%
Mapped reads, both in pair	26,276,006 / 96.39%
Mapped reads, singletons	229,392 / 0.84%
Secondary alignments	0
Supplementary alignments	155,774 / 0.57%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	888,426 / 3.26%
Duplication rate	2.95%
Clipped reads	1,721,320 / 6.31%

2.2. ACGT Content

Number/percentage of A's	809,310,230 / 30.58%
Number/percentage of C's	512,322,184 / 19.36%
Number/percentage of T's	804,351,629 / 30.39%
Number/percentage of G's	519,771,823 / 19.64%
Number/percentage of N's	1,080,198 / 0.04%

GC Percentage	38.99%

2.3. Coverage

Mean	0.8552
Standard Deviation	2.2944

2.4. Mapping Quality

Mean Mapping Quality	53.45

2.5. Insert size

Mean	62,157.04
Standard Deviation	2,359,257.66
P25/Median/P75	154 / 205 / 277

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	10,921,484
Insertions	220,016
Mapped reads with at least one insertion	0.82%
Deletions	268,013
Mapped reads with at least one deletion	0.99%
Homopolymer indels	46.59%

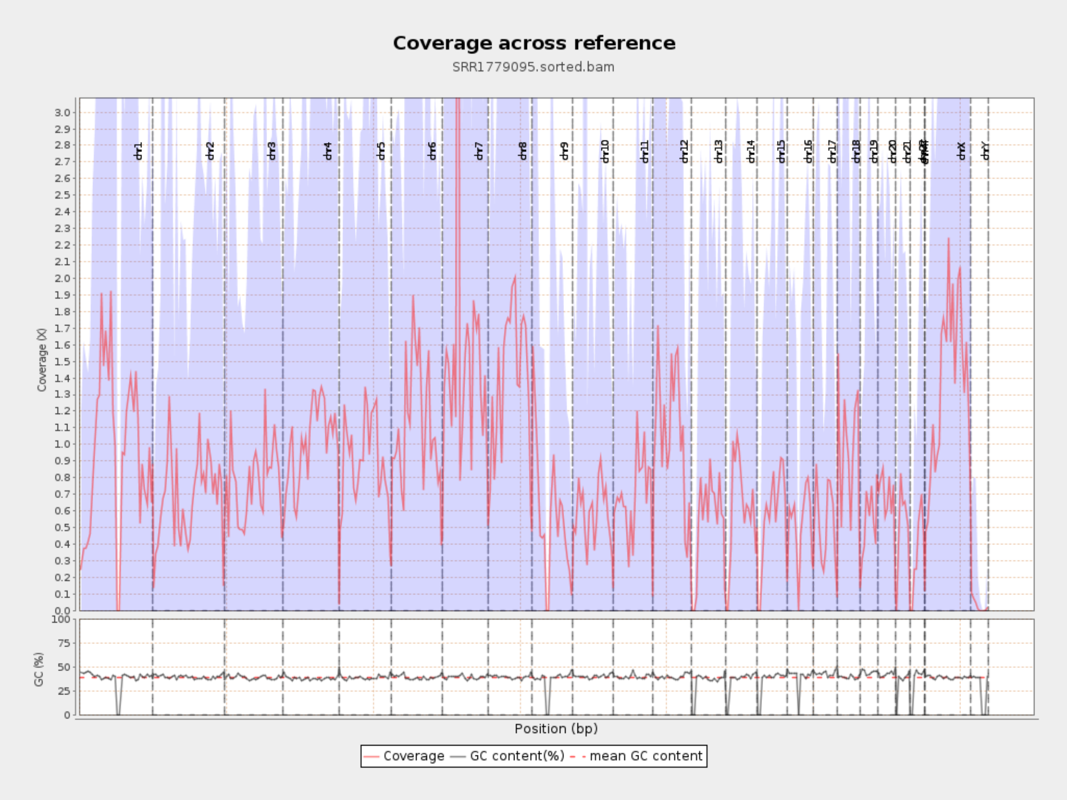
2.7. Chromosome stats

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

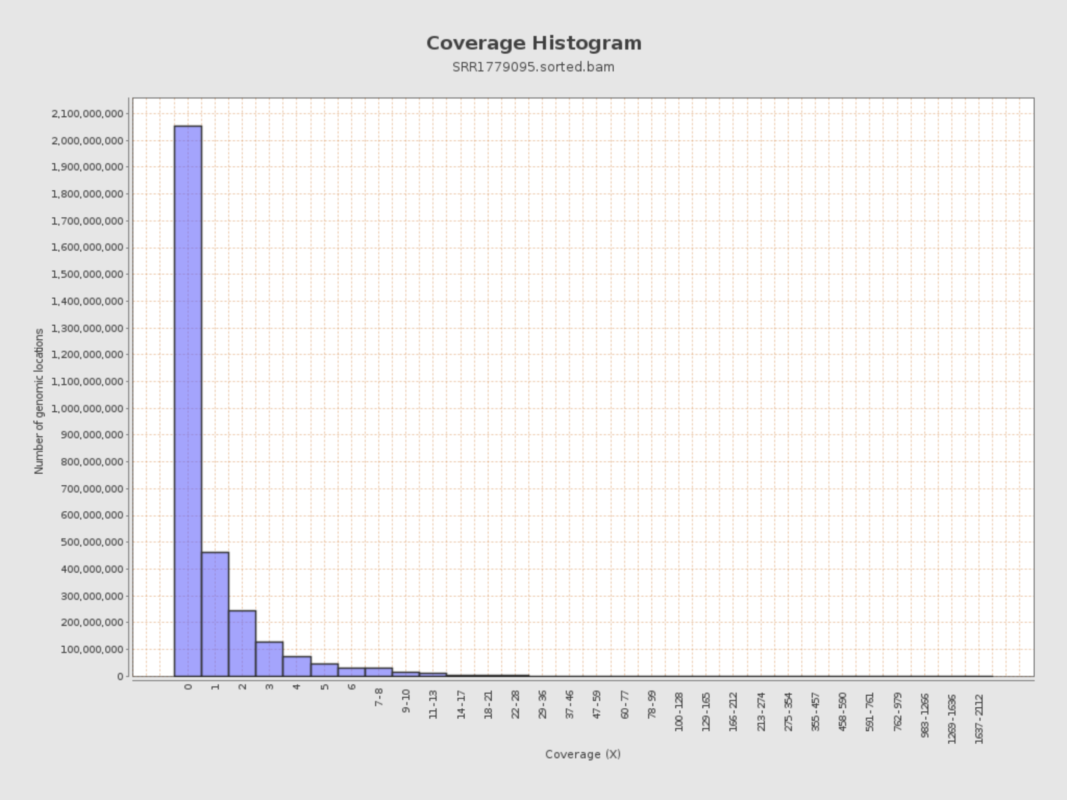
		bases	coverage	deviation
chr1	249250621	238882183	0.9584	2.6489
chr2	243199373	166522165	0.6847	1.8586
chr3	198022430	153415009	0.7747	1.6804
chr4	191154276	193593023	1.0128	1.9342
chr5	180915260	161374581	0.892	1.7414
chr6	171115067	195253615	1.1411	2.082
chr7	159138663	254179961	1.5972	5.1199
chr8	146364022	207622165	1.4185	2.3981
chr9	141213431	79694524	0.5644	1.5065
chr10	135534747	79902325	0.5895	3.5363
chr11	135006516	94017874	0.6964	1.5944
chr12	133851895	141740457	1.0589	2.0911
chr13	115169878	63077109	0.5477	1.3934
chr14	107349540	66012996	0.6149	1.4528
chr15	102531392	57514308	0.5609	1.5053
chr16	90354753	45663910	0.5054	1.243
chr17	81195210	41152012	0.5068	1.5551
chr18	78077248	75967556	0.973	1.9439
chr19	59128983	30510935	0.516	1.5478
chr20	63025520	42626947	0.6763	1.5444
chr21	48129895	24760651	0.5145	1.3361
chr22	51304566	17229511	0.3358	1.1152
chrMT	16571	1993	0.1203	0.5247
chrX	155270560	214976187	1.3845	2.6187

chrY	59373566	1740528	0.0293	0.4212

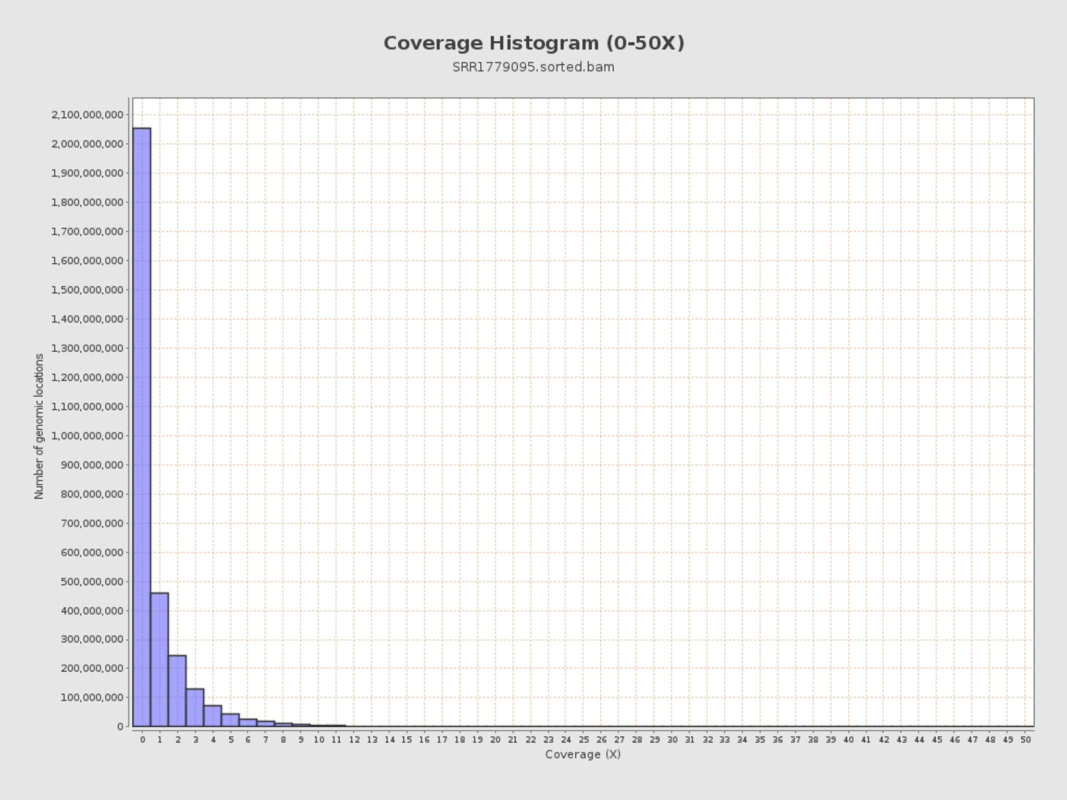
3. Results : Coverage across reference



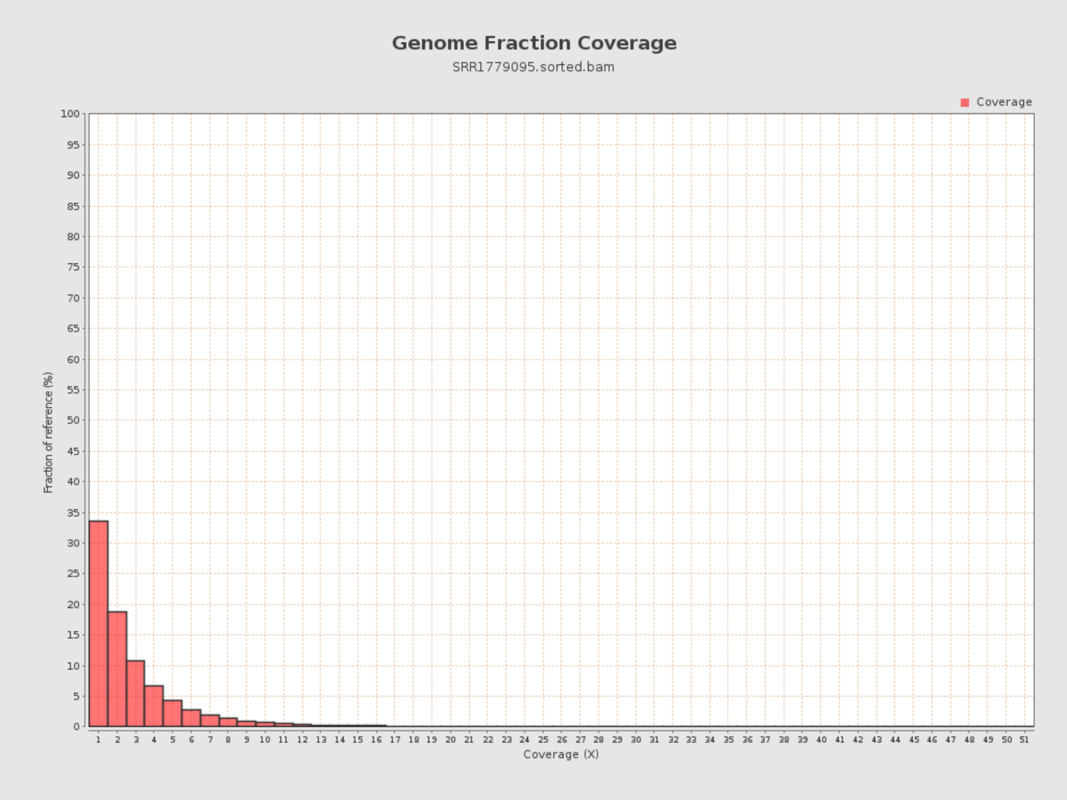
4. Results : Coverage Histogram



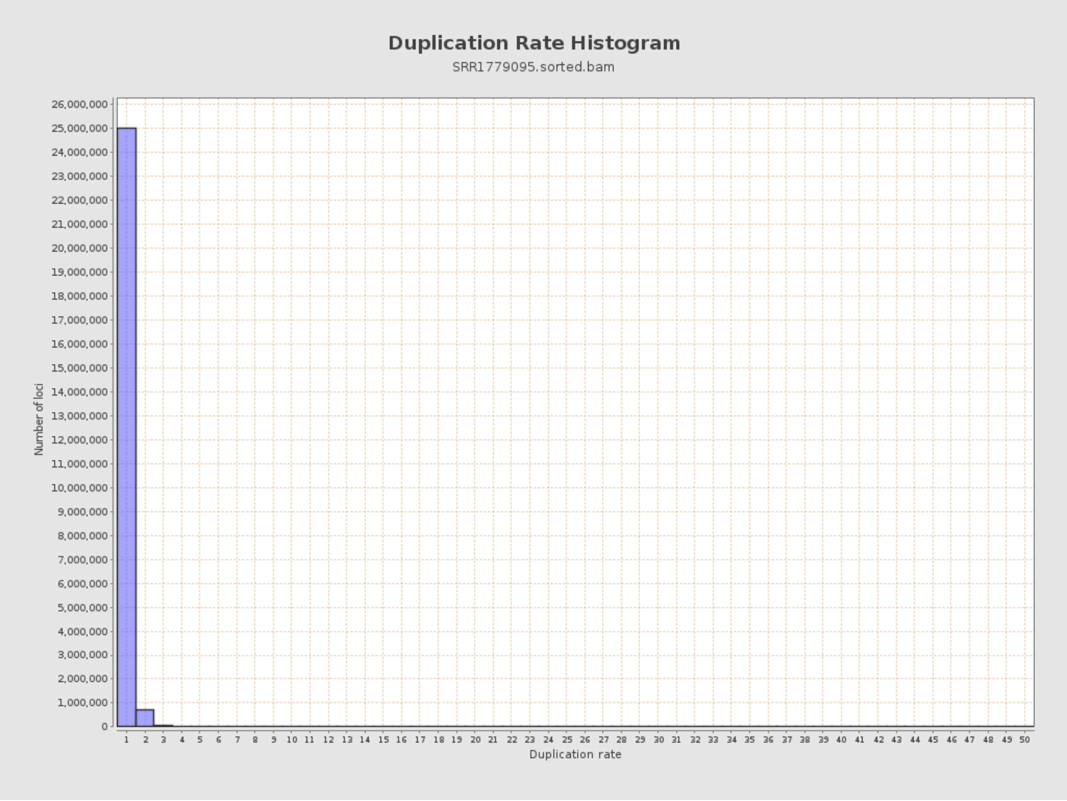
5. Results : Coverage Histogram (0-50X)



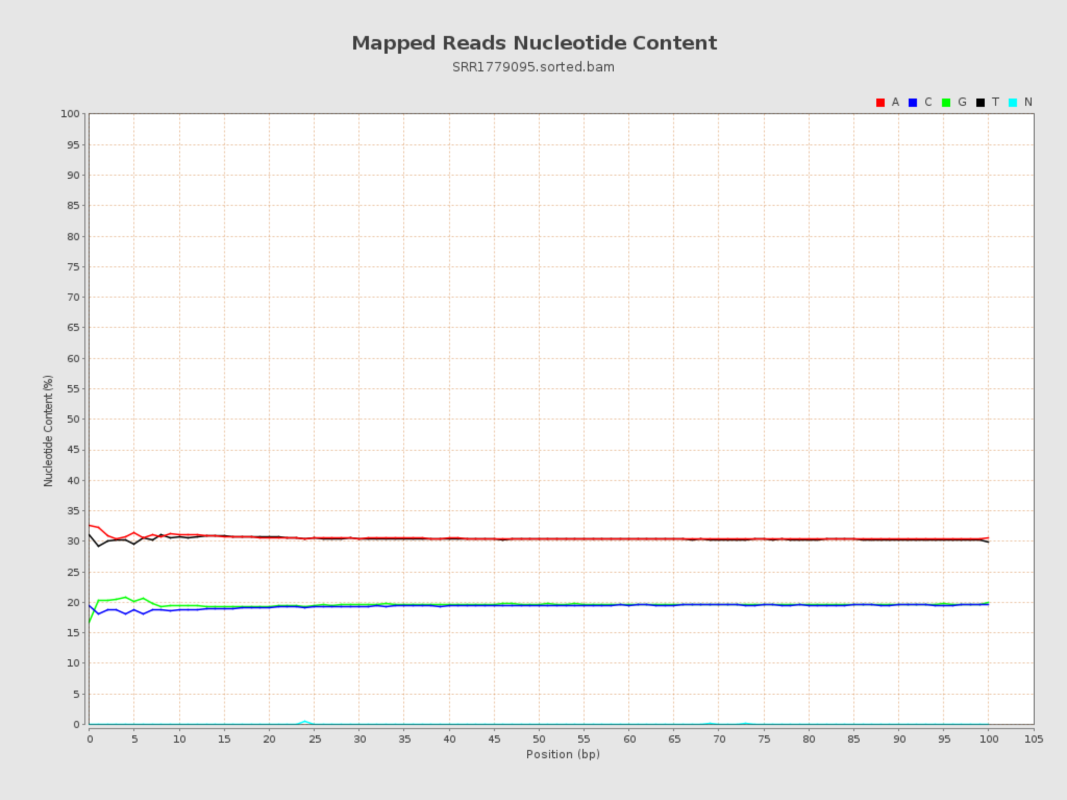
6. Results : Genome Fraction Coverage



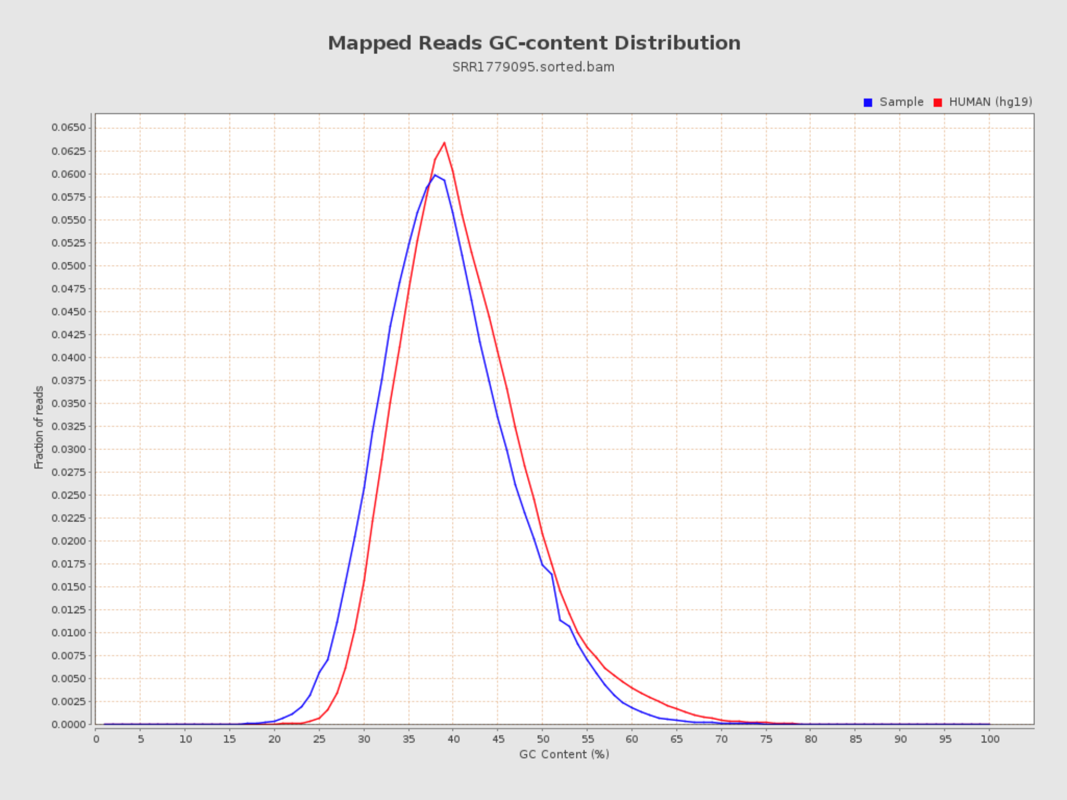
7. Results : Duplication Rate Histogram



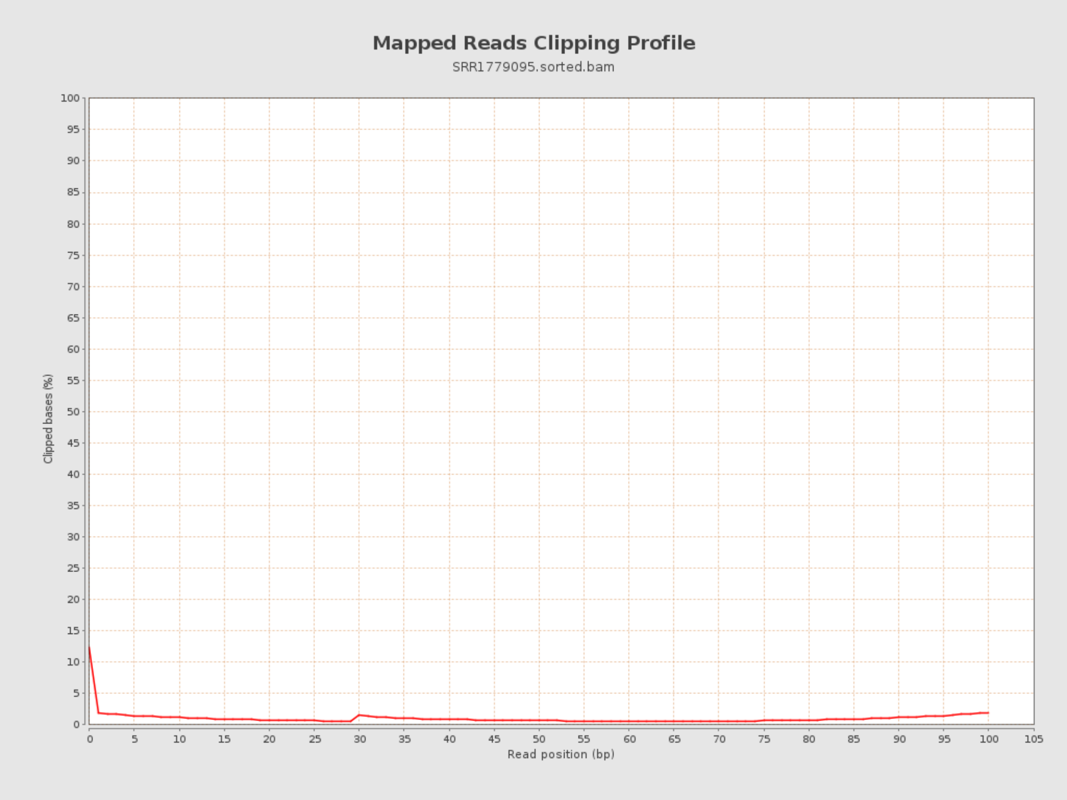
8. Results : Mapped Reads Nucleotide Content



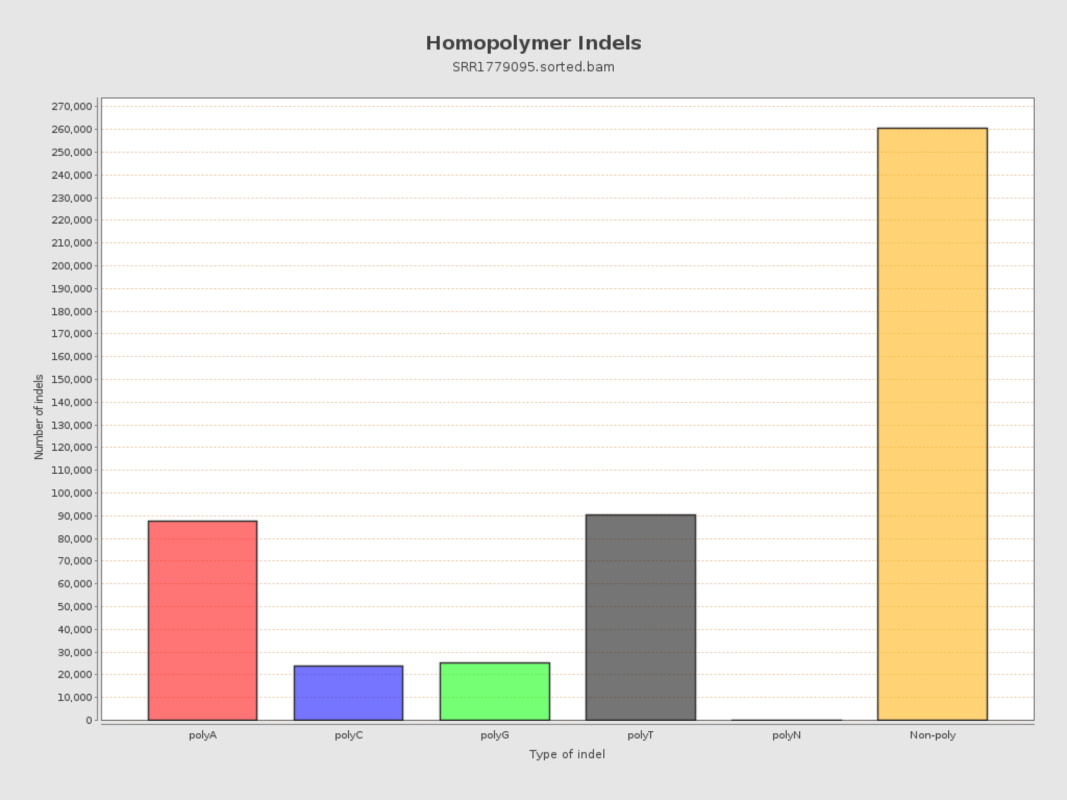
9. Results : Mapped Reads GC-content Distribution



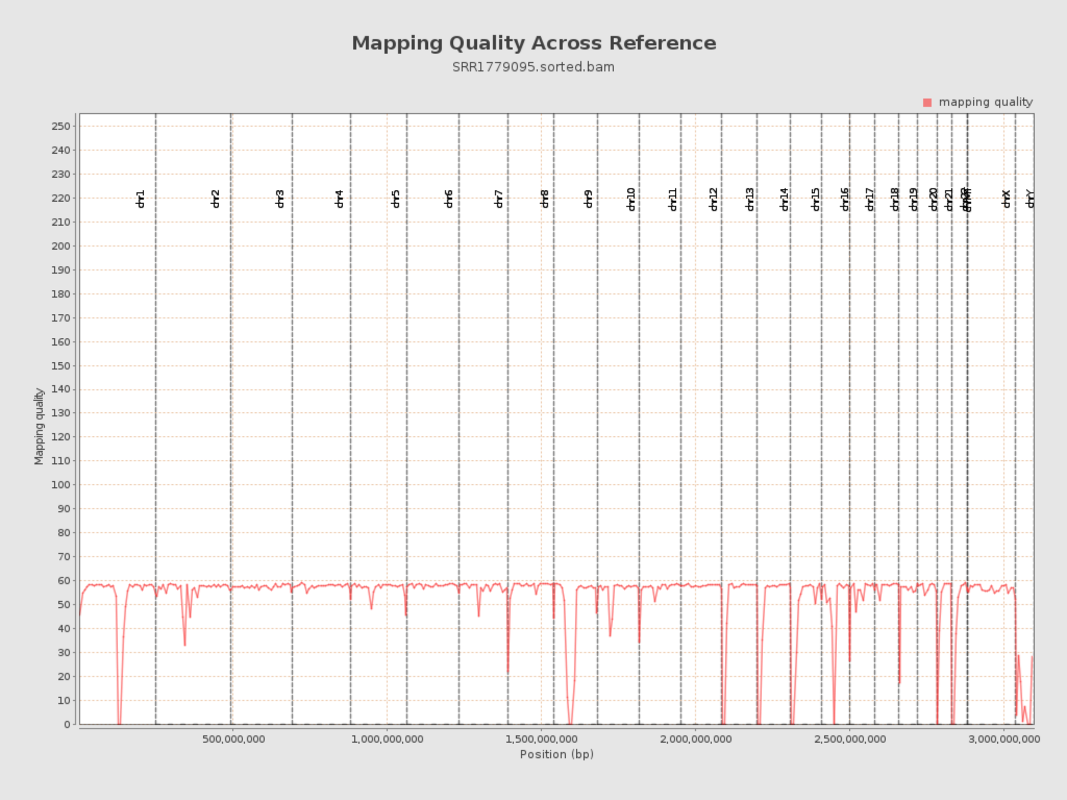
10. Results : Mapped Reads Clipping Profile



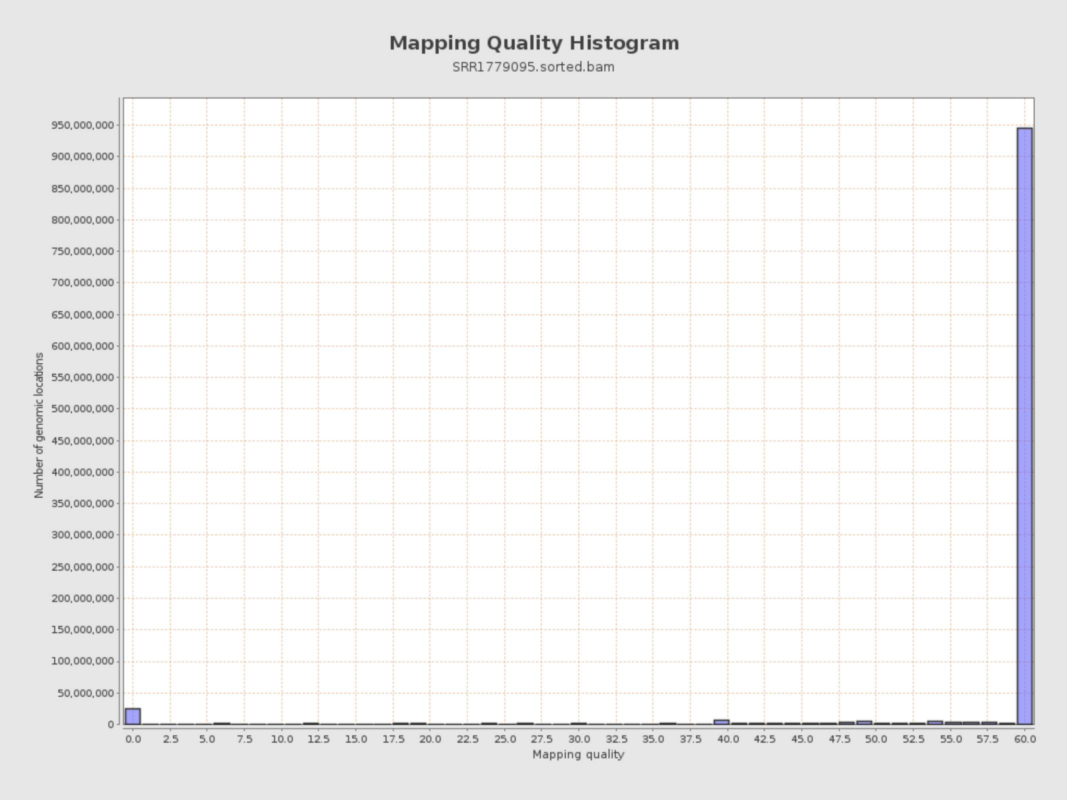
11. Results : Homopolymer Indels



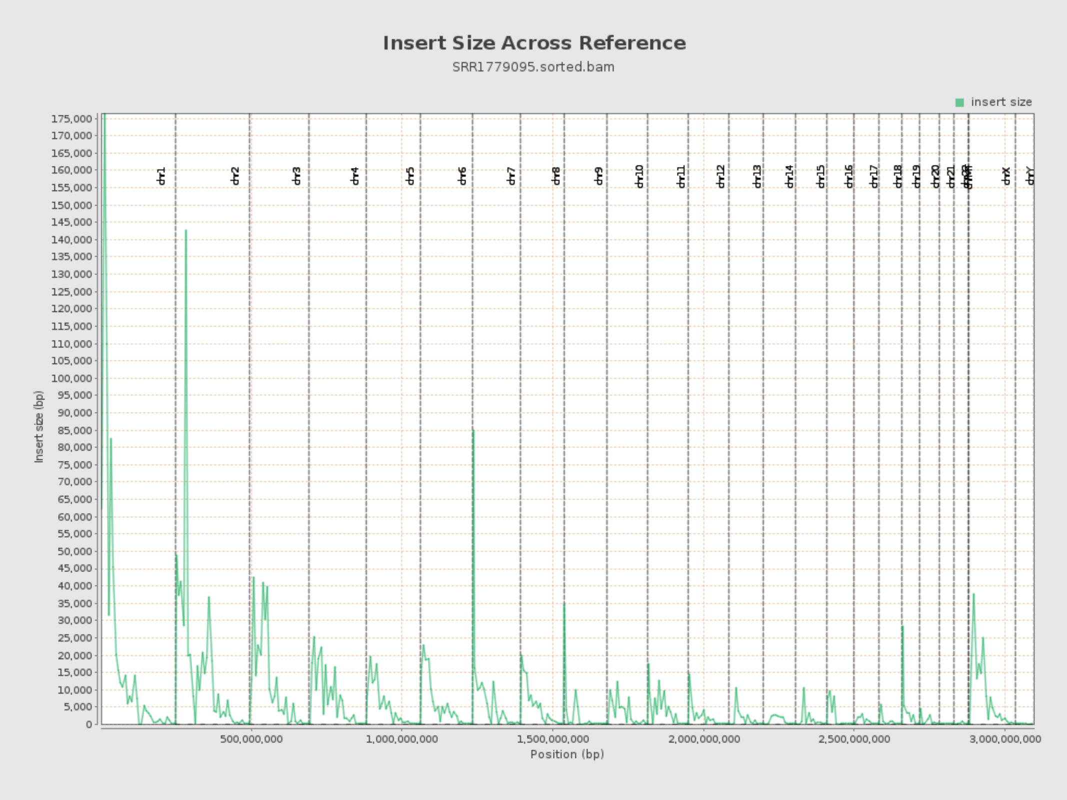
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram