Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 08:57:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779006.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_SRR1779006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779006_1.fastq.gz SRR1779006_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 08:57:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,585,450
Mapped reads	15,906,117 / 95.9%
Unmapped reads	679,333 / 4.1%
Mapped paired reads	15,906,117 / 95.9%
Mapped reads, first in pair	8,062,860 / 48.61%
Mapped reads, second in pair	7,843,257 / 47.29%
Mapped reads, both in pair	15,627,472 / 94.22%
Mapped reads, singletons	278,645 / 1.68%
Secondary alignments	0
Supplementary alignments	84,175 / 0.51%
Read min/max/mean length	30 / 101 / 101.2
Duplicated reads (estimated)	281,599 / 1.7%
Duplication rate	1.49%
Clipped reads	874,672 / 5.27%

2.2. ACGT Content

Number/percentage of A's	486,575,638 / 30.62%
Number/percentage of C's	305,941,094 / 19.25%
Number/percentage of T's	485,547,485 / 30.55%
Number/percentage of G's	310,564,639 / 19.54%
Number/percentage of N's	529,308 / 0.03%

GC Percentage	38.79%

2.3. Coverage

Mean	0.5135
Standard Deviation	1.3307

2.4. Mapping Quality

Mean Mapping Quality	53.61

2.5. Insert size

Mean	75,199.02
Standard Deviation	2,632,642.83
P25/Median/P75	207 / 270 / 343

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	7,899,288
Insertions	140,019
Mapped reads with at least one insertion	0.87%
Deletions	171,419
Mapped reads with at least one deletion	1.06%
Homopolymer indels	47.13%

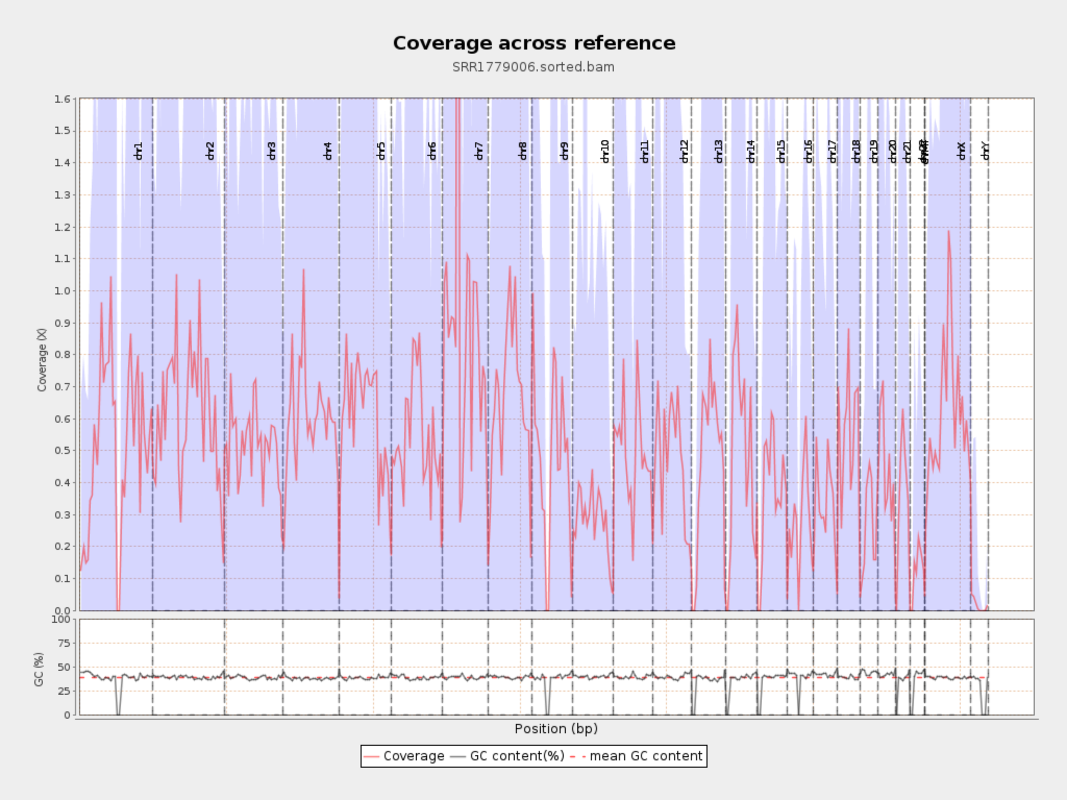
2.7. Chromosome stats

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

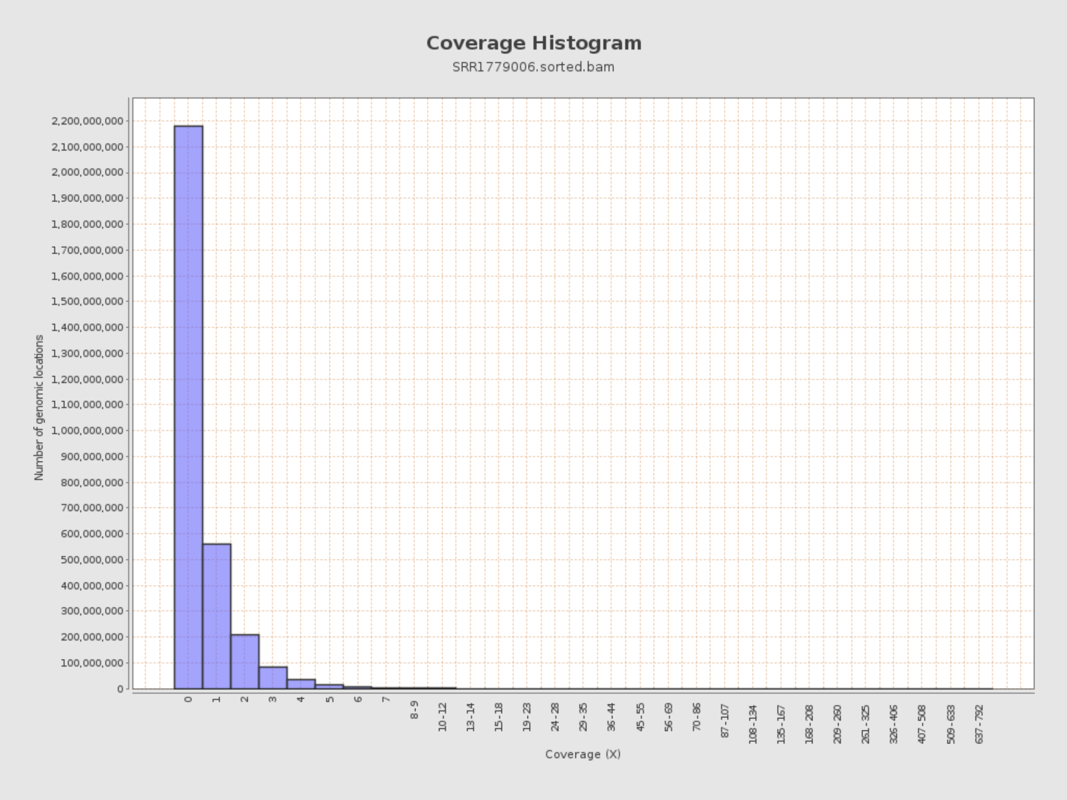
		bases	coverage	deviation
chr1	249250621	130276396	0.5227	1.324
chr2	243199373	150232005	0.6177	1.2803
chr3	198022430	102535176	0.5178	0.9803
chr4	191154276	116687753	0.6104	1.0877
chr5	180915260	108481944	0.5996	1.0802
chr6	171115067	94705598	0.5535	1.0512
chr7	159138663	149580636	0.9399	3.4698
chr8	146364022	99082705	0.677	1.18
chr9	141213431	65134059	0.4612	1.0358
chr10	135534747	38502226	0.2841	1.473
chr11	135006516	66549756	0.4929	0.9966
chr12	133851895	63173587	0.472	1.0153
chr13	115169878	54813328	0.4759	0.9655
chr14	107349540	52574145	0.4897	1.0456
chr15	102531392	37693830	0.3676	0.9331
chr16	90354753	24021468	0.2659	0.7221
chr17	81195210	26628959	0.328	0.8837
chr18	78077248	44172058	0.5657	1.0642
chr19	59128983	14917135	0.2523	0.8394
chr20	63025520	27523283	0.4367	0.9924
chr21	48129895	18095086	0.376	0.9198
chr22	51304566	6253928	0.1219	0.496
chrMT	16571	798	0.0482	0.2227
chrX	155270560	96940052	0.6243	1.2161

chrY	59373566	965698	0.0163	0.2813

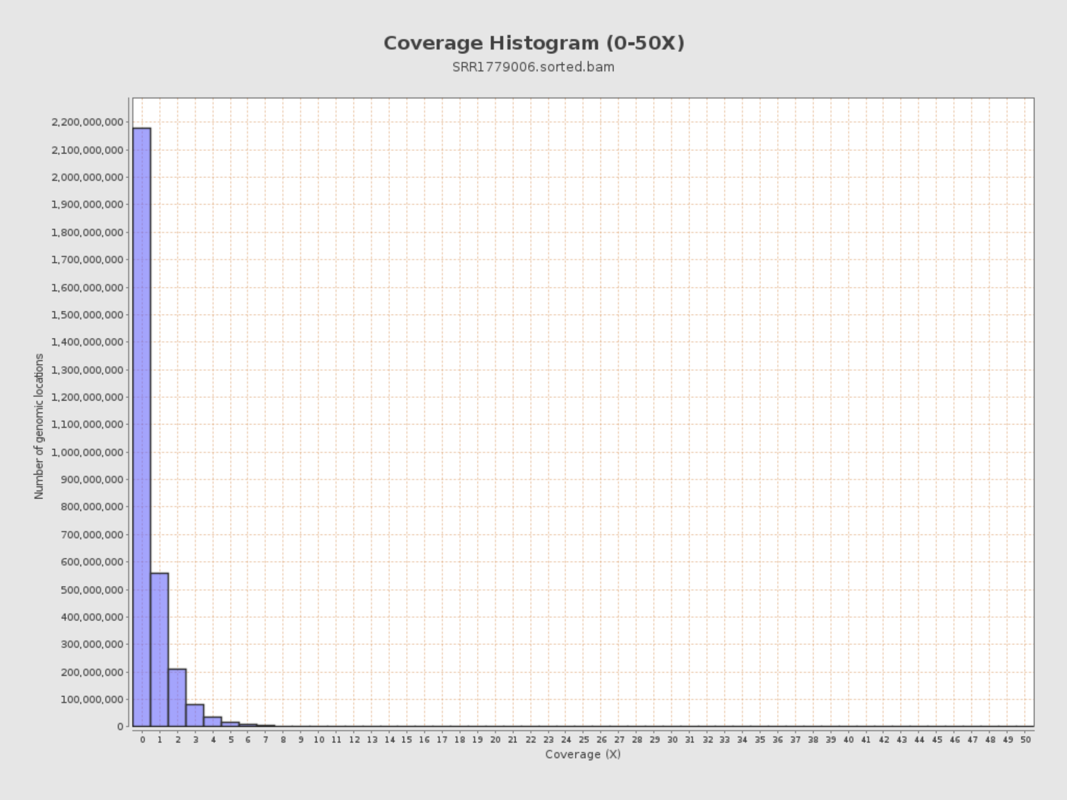
3. Results : Coverage across reference



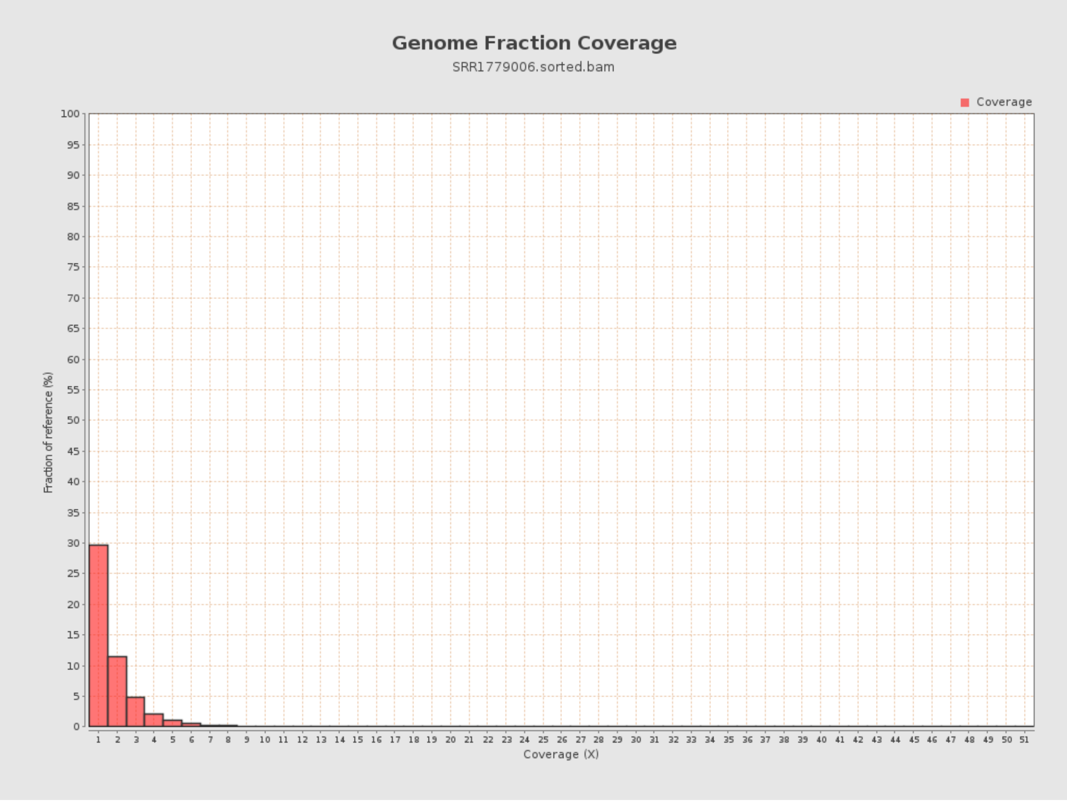
4. Results : Coverage Histogram



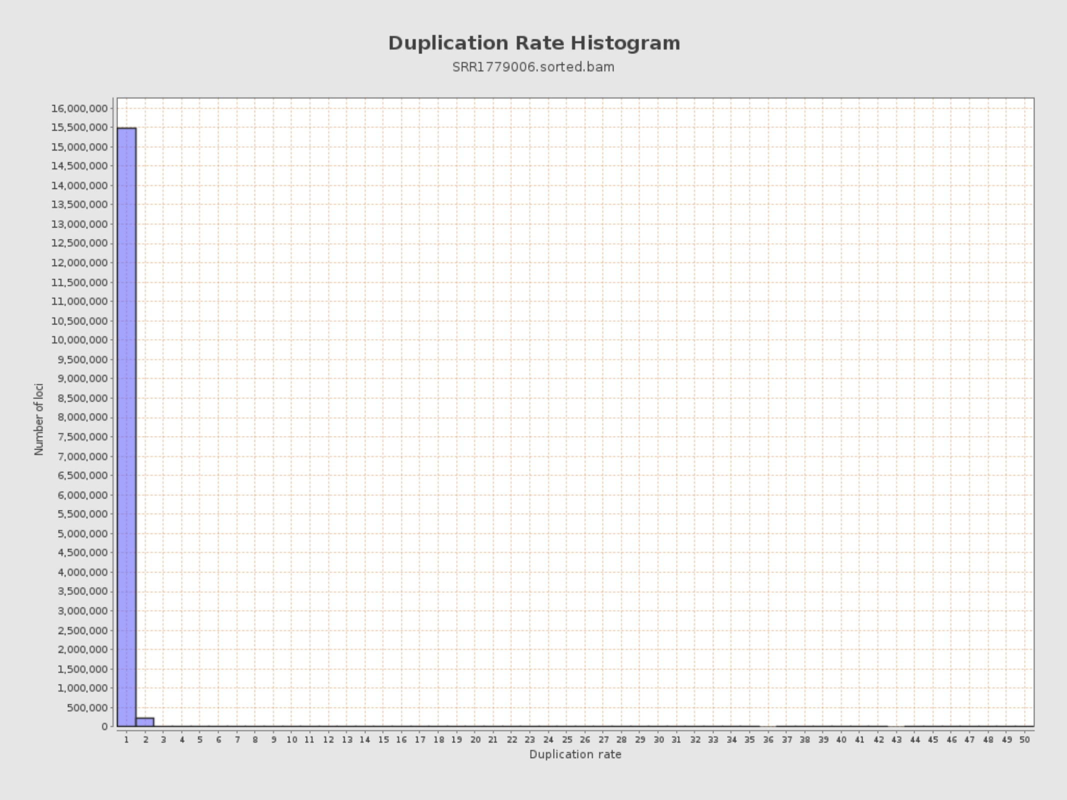
5. Results : Coverage Histogram (0-50X)



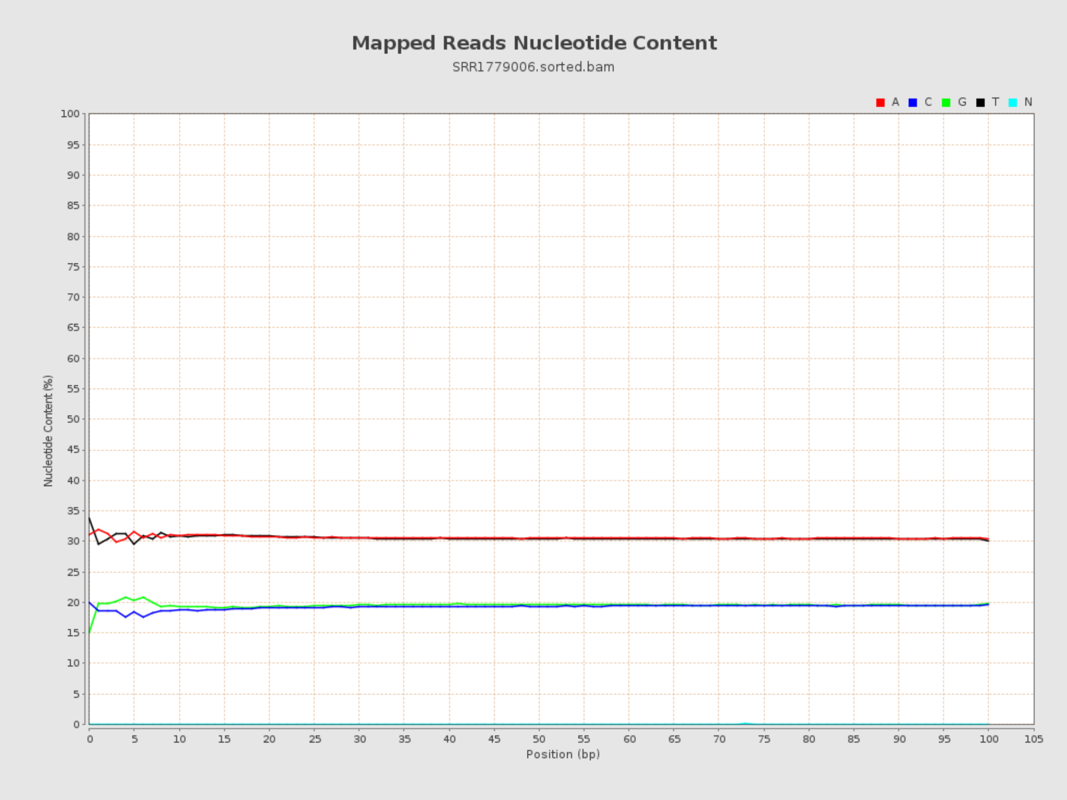
6. Results : Genome Fraction Coverage



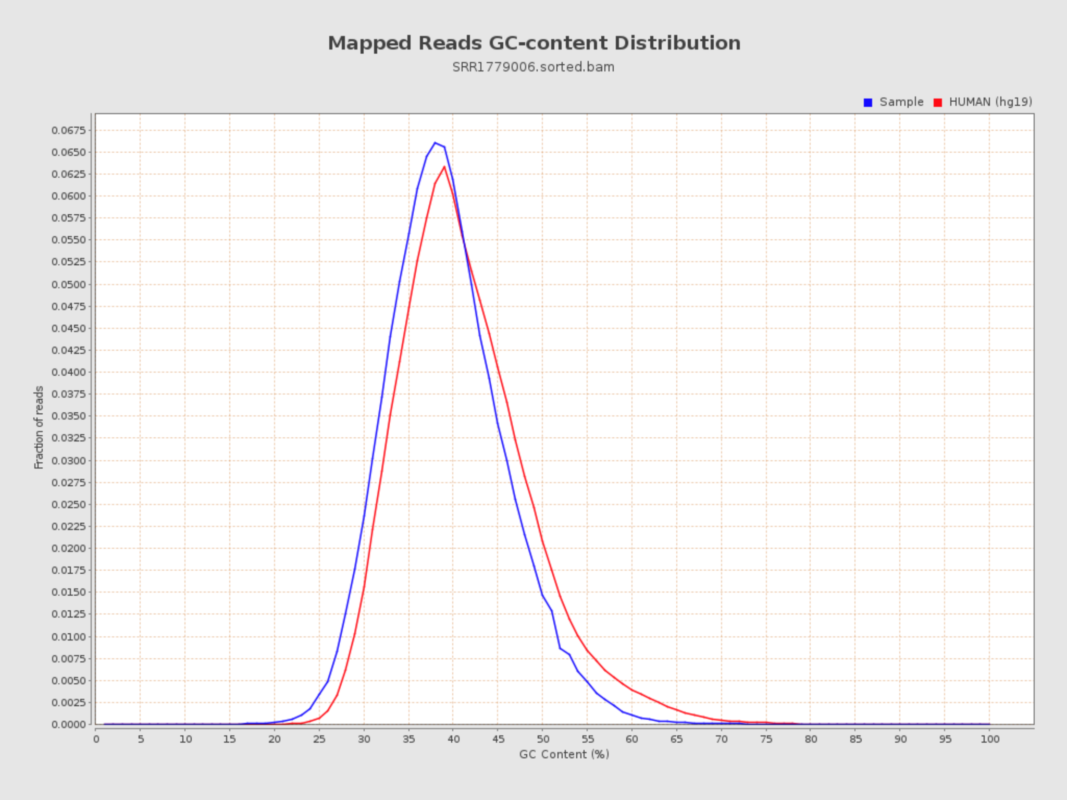
7. Results : Duplication Rate Histogram



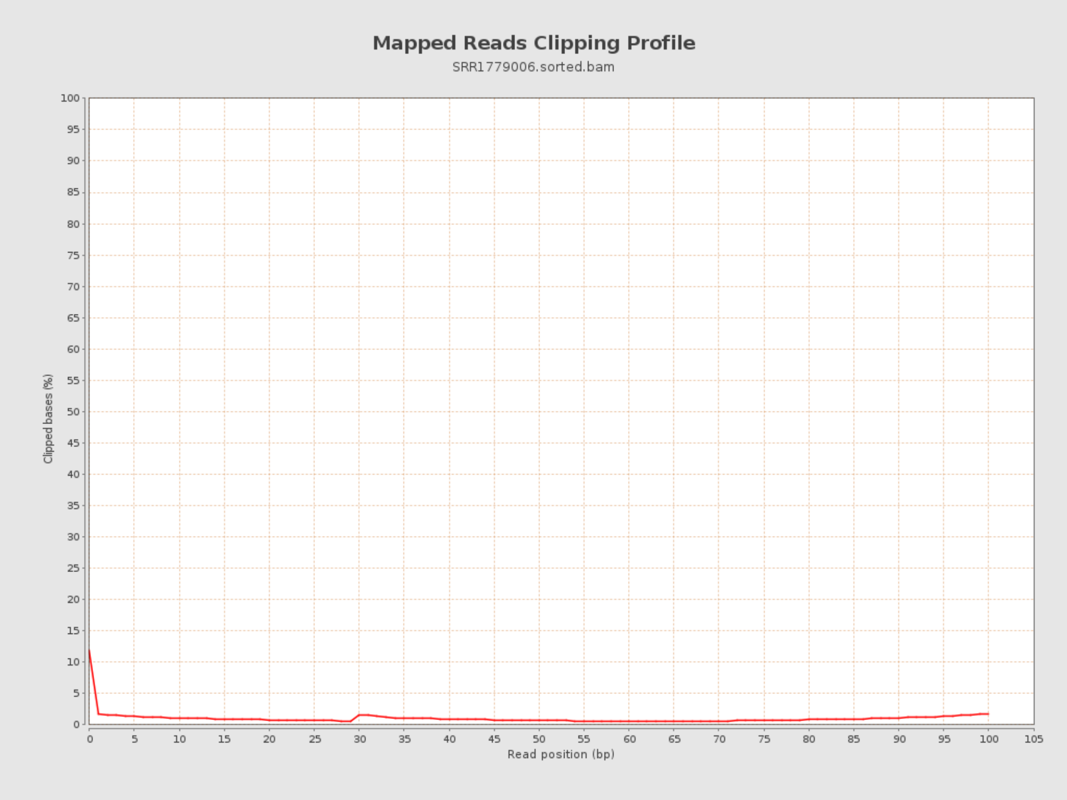
8. Results : Mapped Reads Nucleotide Content



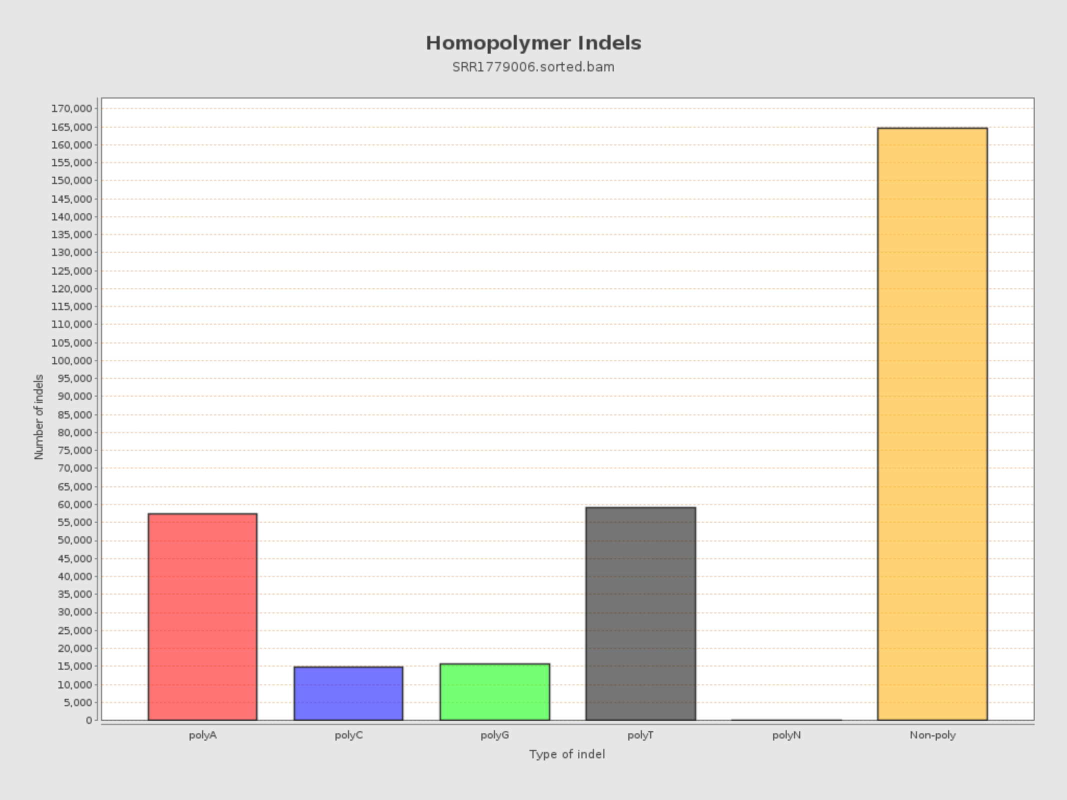
9. Results : Mapped Reads GC-content Distribution



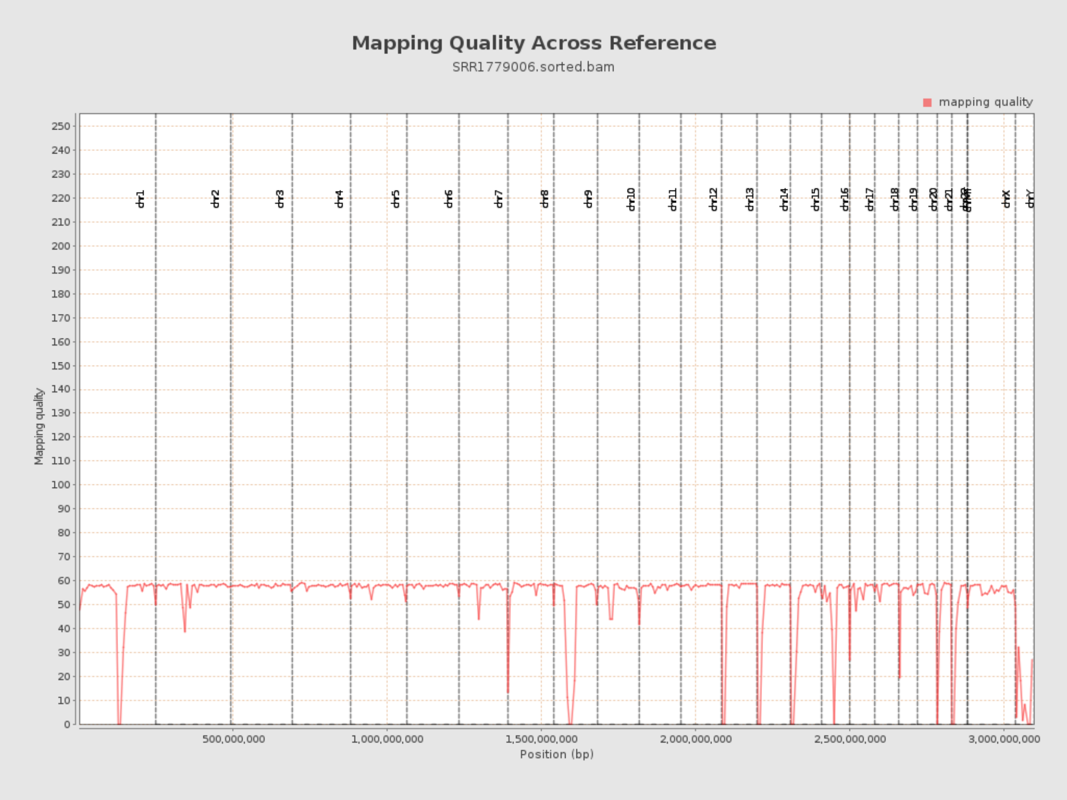
10. Results : Mapped Reads Clipping Profile



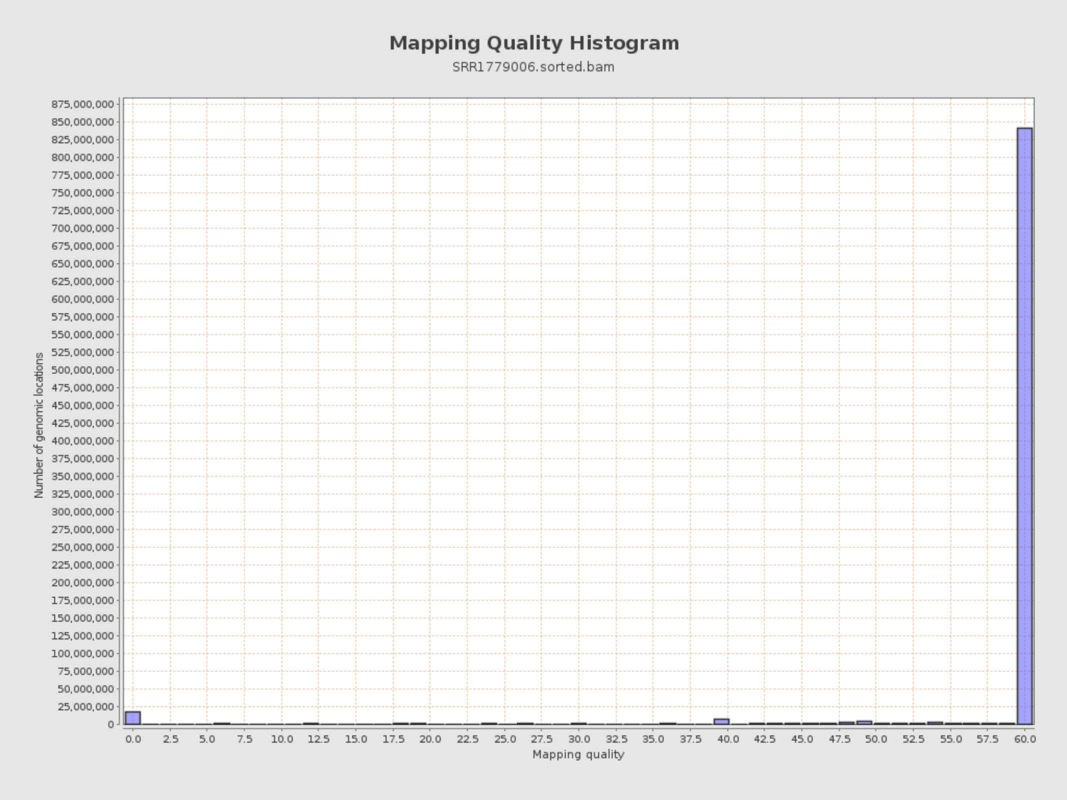
11. Results : Homopolymer Indels



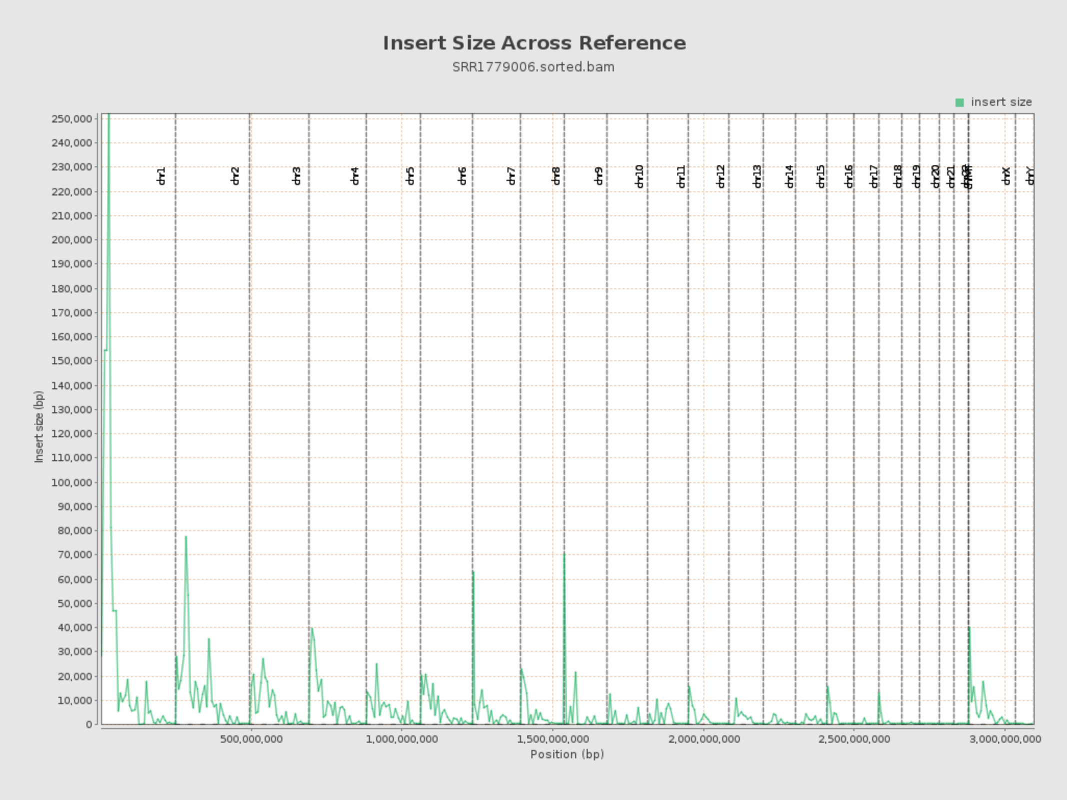
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram