Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 16:24:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779212.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_SRR1779212 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779212_1.fastq.gz SRR1779212_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 16:24:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779212.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,303,602
Mapped reads	13,986,131 / 97.78%
Unmapped reads	317,471 / 2.22%
Mapped paired reads	13,986,131 / 97.78%
Mapped reads, first in pair	7,032,924 / 49.17%
Mapped reads, second in pair	6,953,207 / 48.61%
Mapped reads, both in pair	13,889,898 / 97.11%
Mapped reads, singletons	96,233 / 0.67%
Secondary alignments	0
Supplementary alignments	33,986 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	173,845 / 1.22%
Duplication rate	1.15%
Clipped reads	450,862 / 3.15%

2.2. ACGT Content

Number/percentage of A's	341,239,930 / 30.66%
Number/percentage of C's	213,957,097 / 19.22%
Number/percentage of T's	340,498,035 / 30.59%
Number/percentage of G's	217,197,321 / 19.51%
Number/percentage of N's	212,641 / 0.02%

GC Percentage	38.73%

2.3. Coverage

Mean	0.3596
Standard Deviation	0.9376

2.4. Mapping Quality

Mean Mapping Quality	52.92

2.5. Insert size

Mean	46,054.47
Standard Deviation	2,006,656.98
P25/Median/P75	153 / 200 / 268

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	4,169,254
Insertions	79,522
Mapped reads with at least one insertion	0.56%
Deletions	99,433
Mapped reads with at least one deletion	0.7%
Homopolymer indels	46.92%

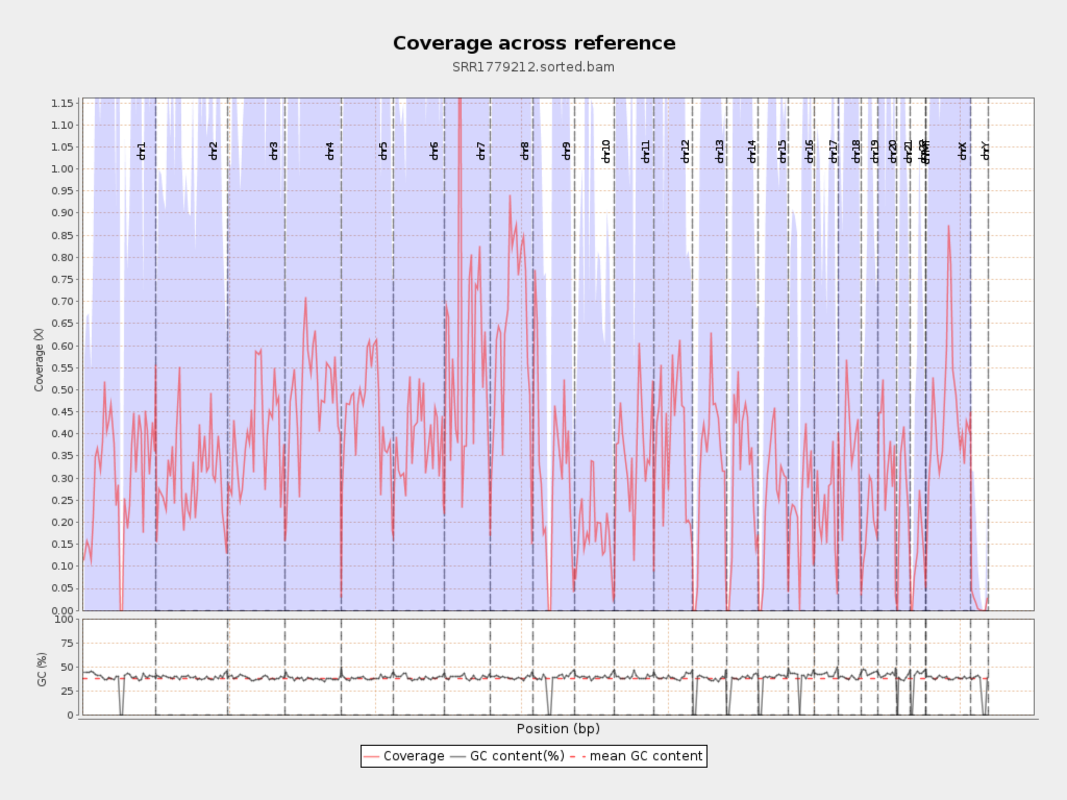
2.7. Chromosome stats

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

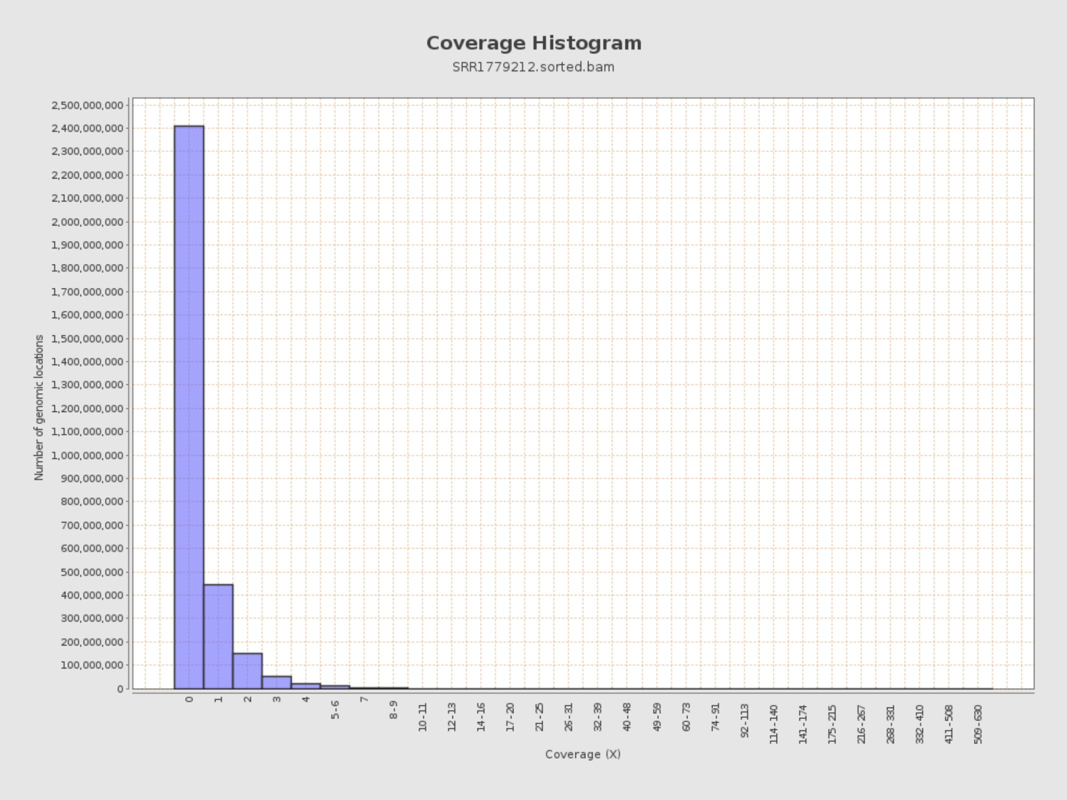
		bases	coverage	deviation
chr1	249250621	75783804	0.304	0.9702
chr2	243199373	72865986	0.2996	0.7435
chr3	198022430	77693737	0.3923	0.8585
chr4	191154276	94308257	0.4934	0.9739
chr5	180915260	80044233	0.4424	0.9182
chr6	171115067	66483557	0.3885	0.8663
chr7	159138663	93544039	0.5878	1.6875
chr8	146364022	94120023	0.6431	1.154
chr9	141213431	45041541	0.319	0.8282
chr10	135534747	24351379	0.1797	1.1324
chr11	135006516	48413394	0.3586	0.8518
chr12	133851895	52345741	0.3911	0.8699
chr13	115169878	38264814	0.3322	0.7813
chr14	107349540	33432691	0.3114	0.7965
chr15	102531392	25955183	0.2531	0.7106
chr16	90354753	20898092	0.2313	0.6502
chr17	81195210	18582694	0.2289	0.6724
chr18	78077248	28344813	0.363	0.8284
chr19	59128983	11670984	0.1974	0.7043
chr20	63025520	22316019	0.3541	0.8649
chr21	48129895	11702466	0.2431	0.6797
chr22	51304566	6420400	0.1251	0.4721
chrMT	16571	1209	0.073	0.3638
chrX	155270560	69839431	0.4498	0.9715

chrY	59373566	884575	0.0149	0.1756

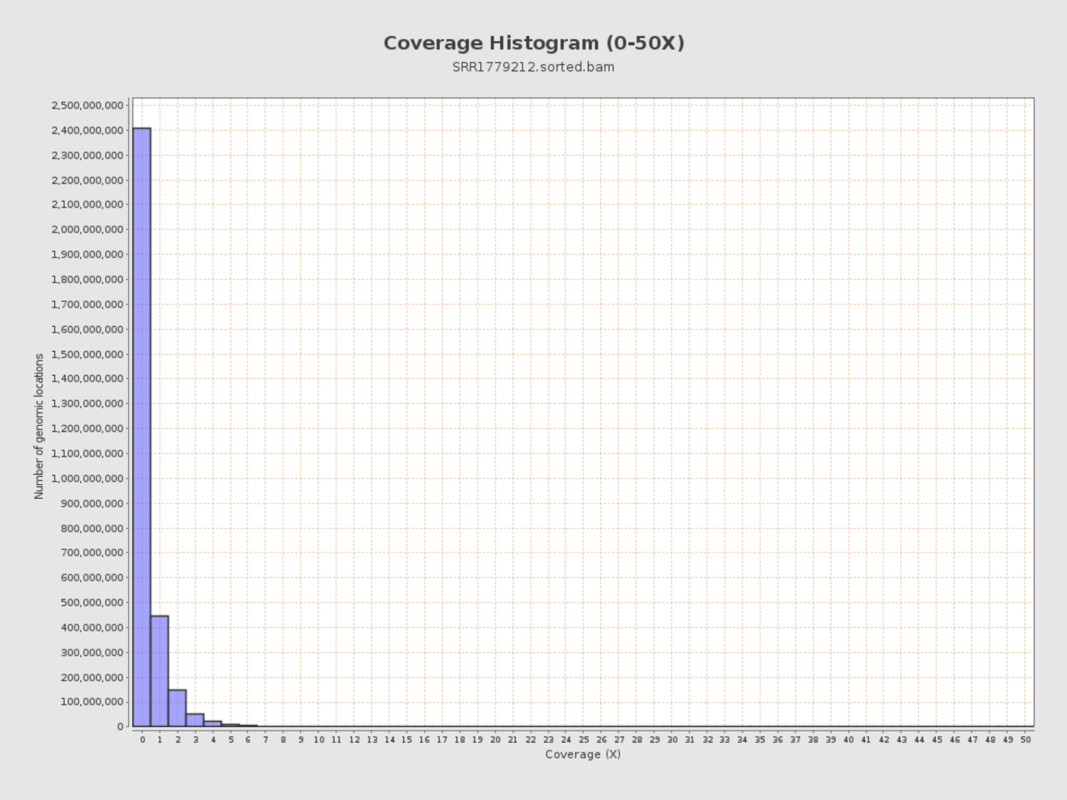
3. Results : Coverage across reference



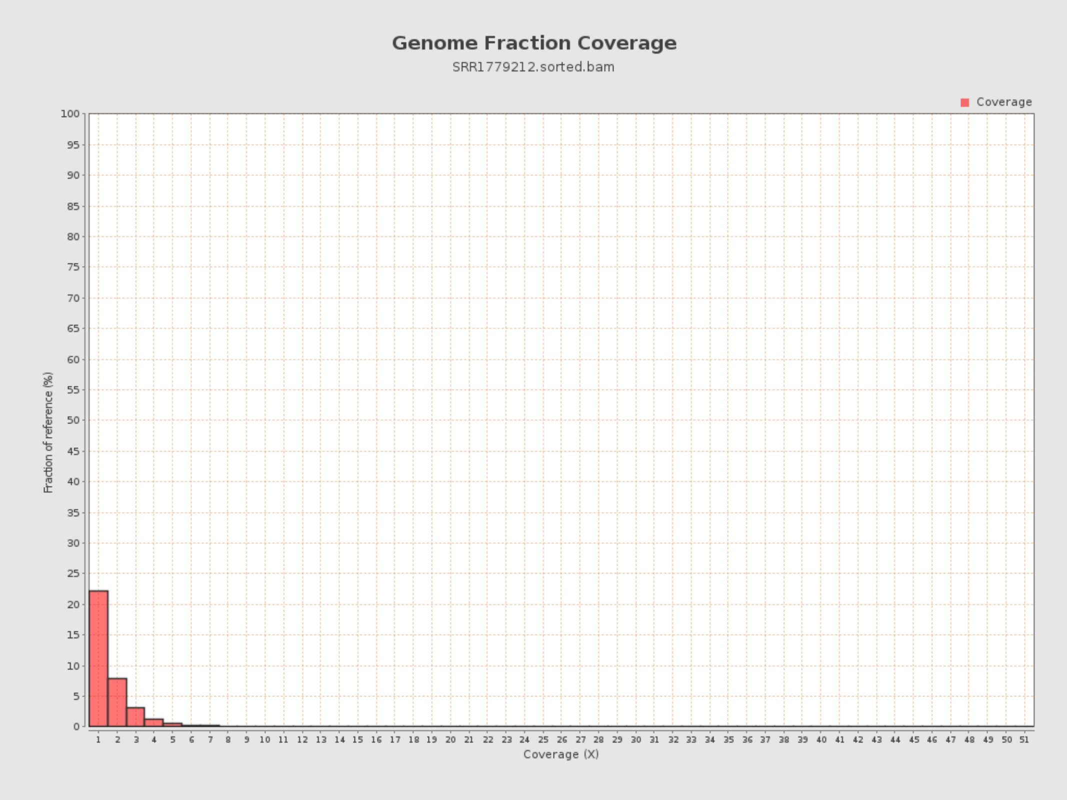
4. Results : Coverage Histogram



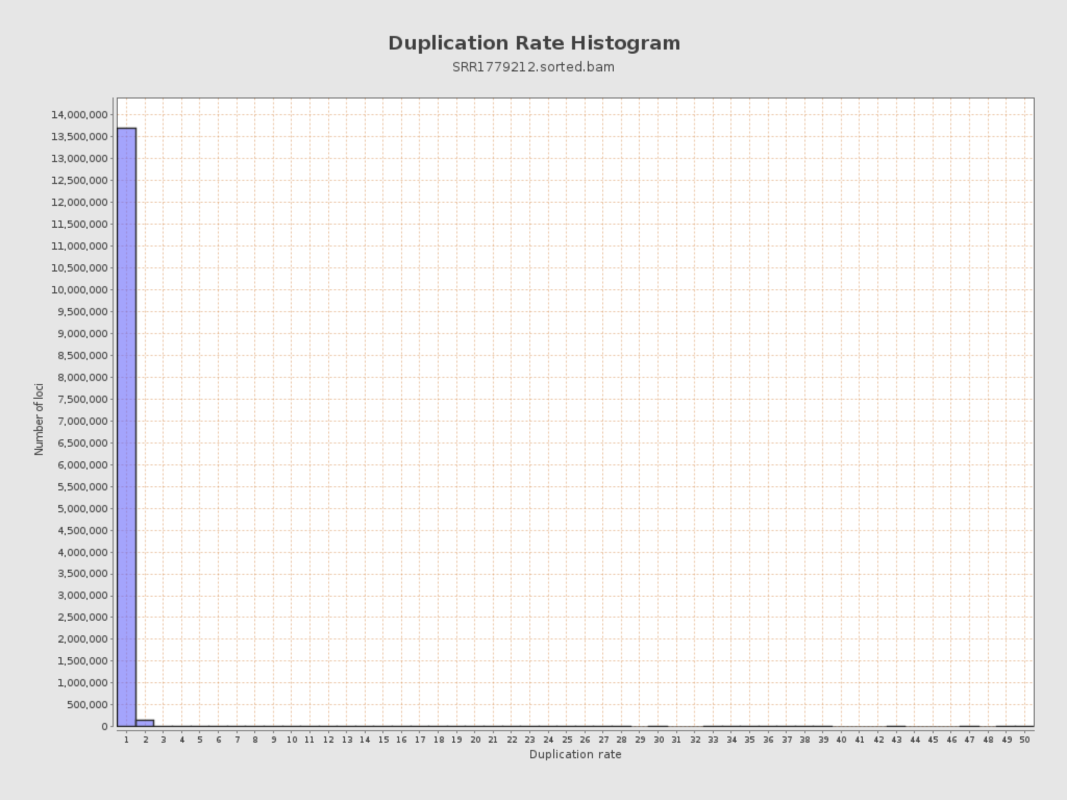
5. Results : Coverage Histogram (0-50X)



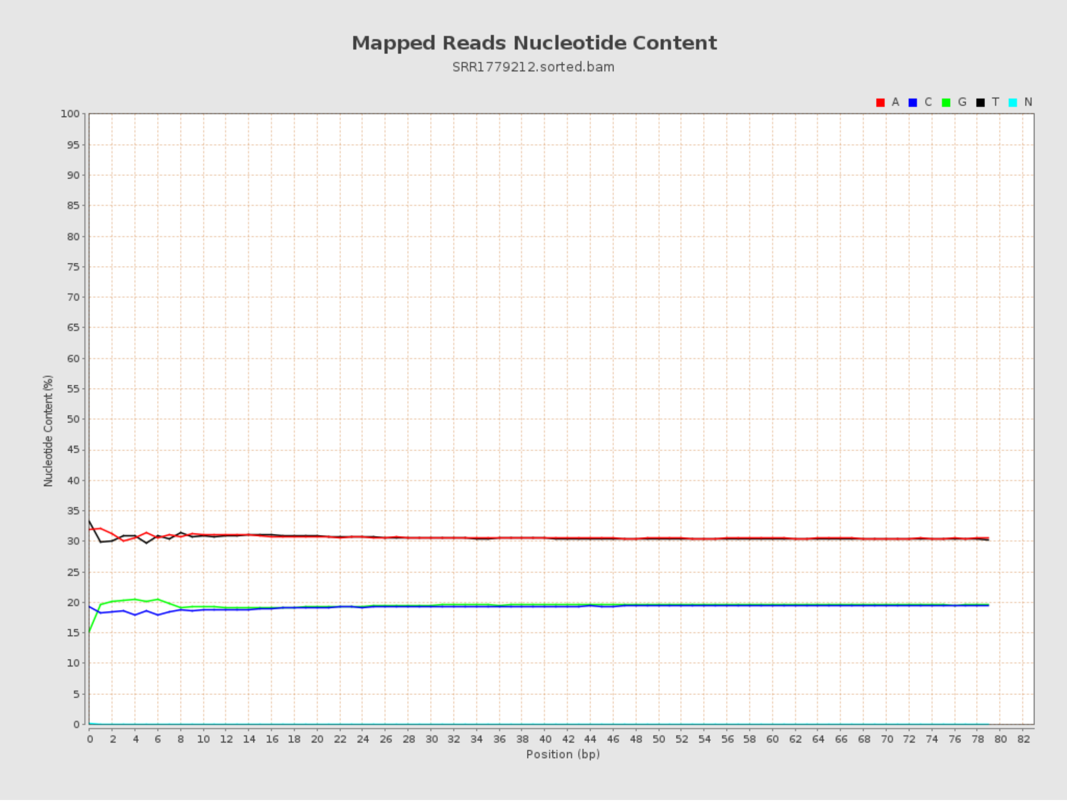
6. Results : Genome Fraction Coverage



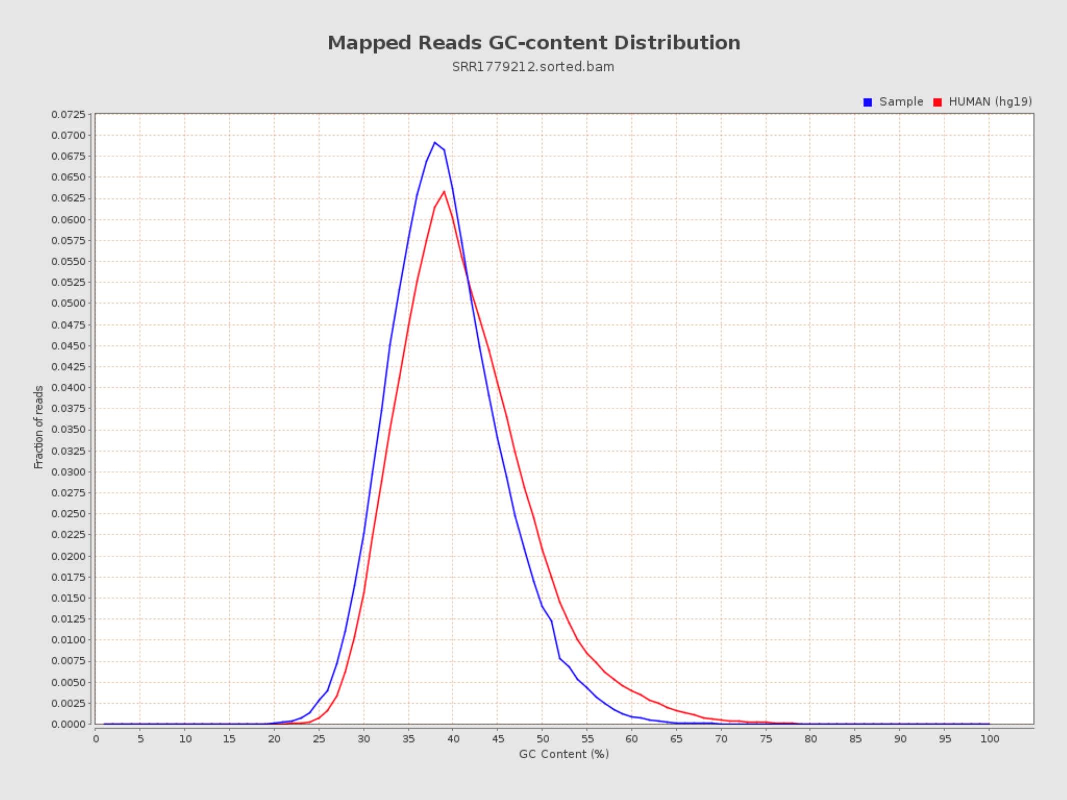
7. Results : Duplication Rate Histogram



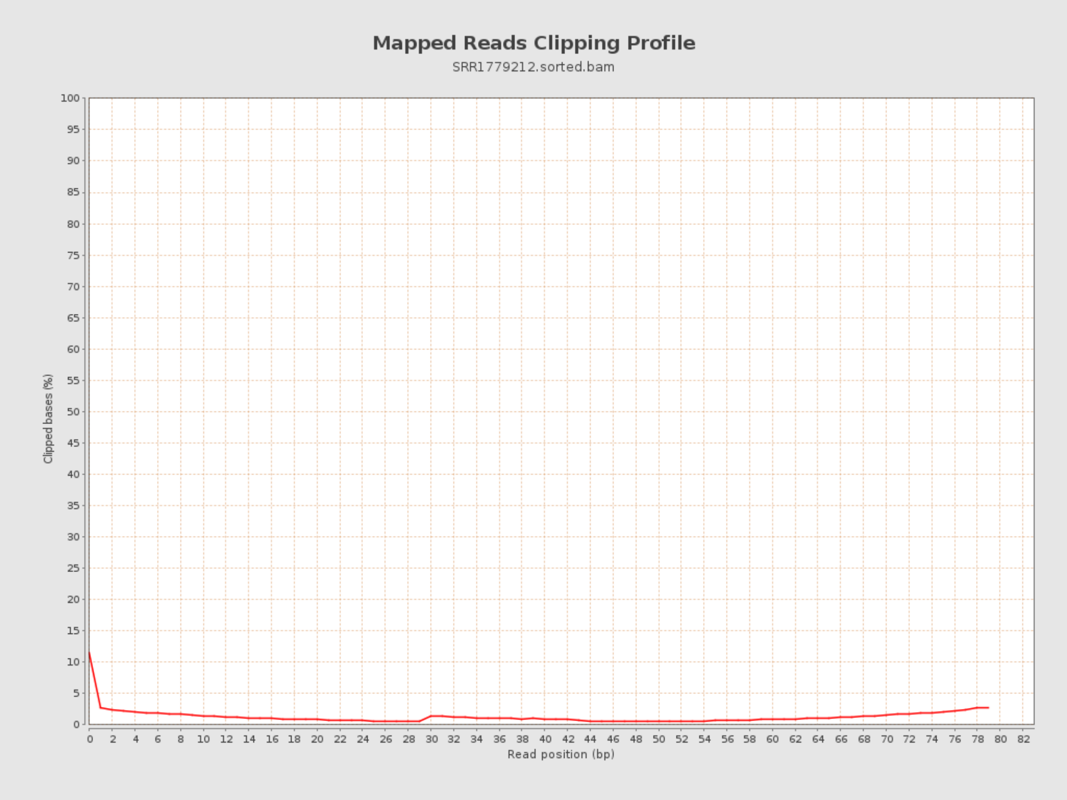
8. Results : Mapped Reads Nucleotide Content



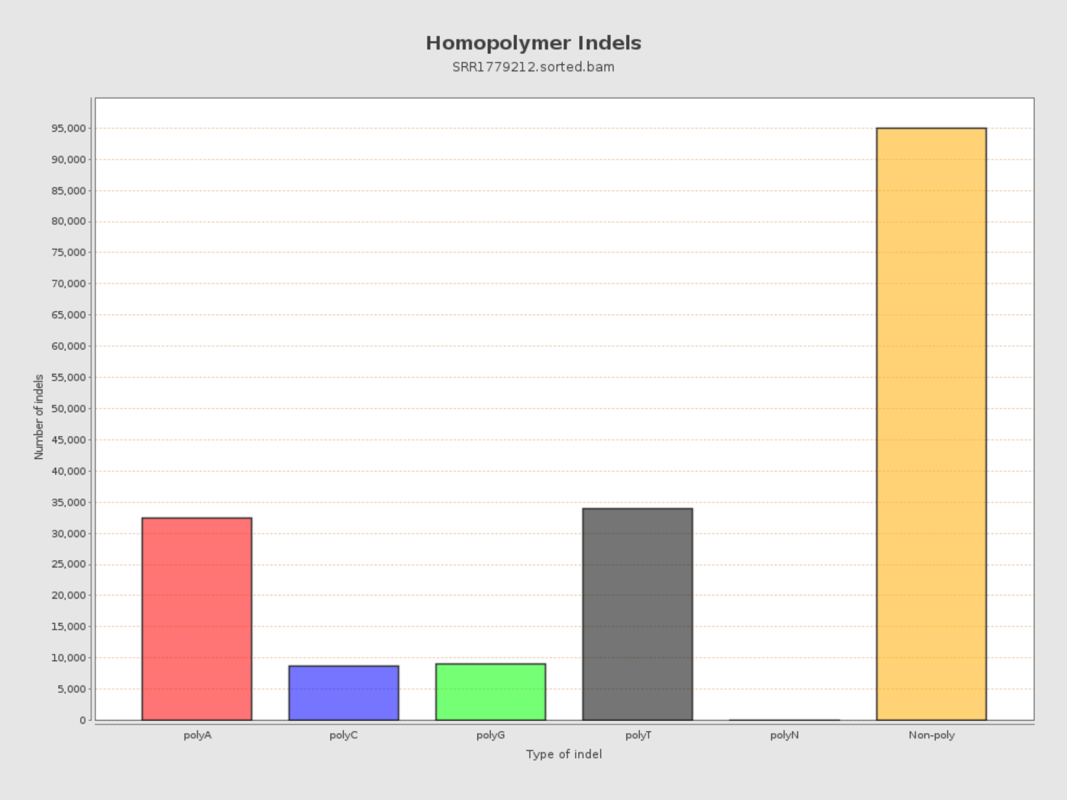
9. Results : Mapped Reads GC-content Distribution



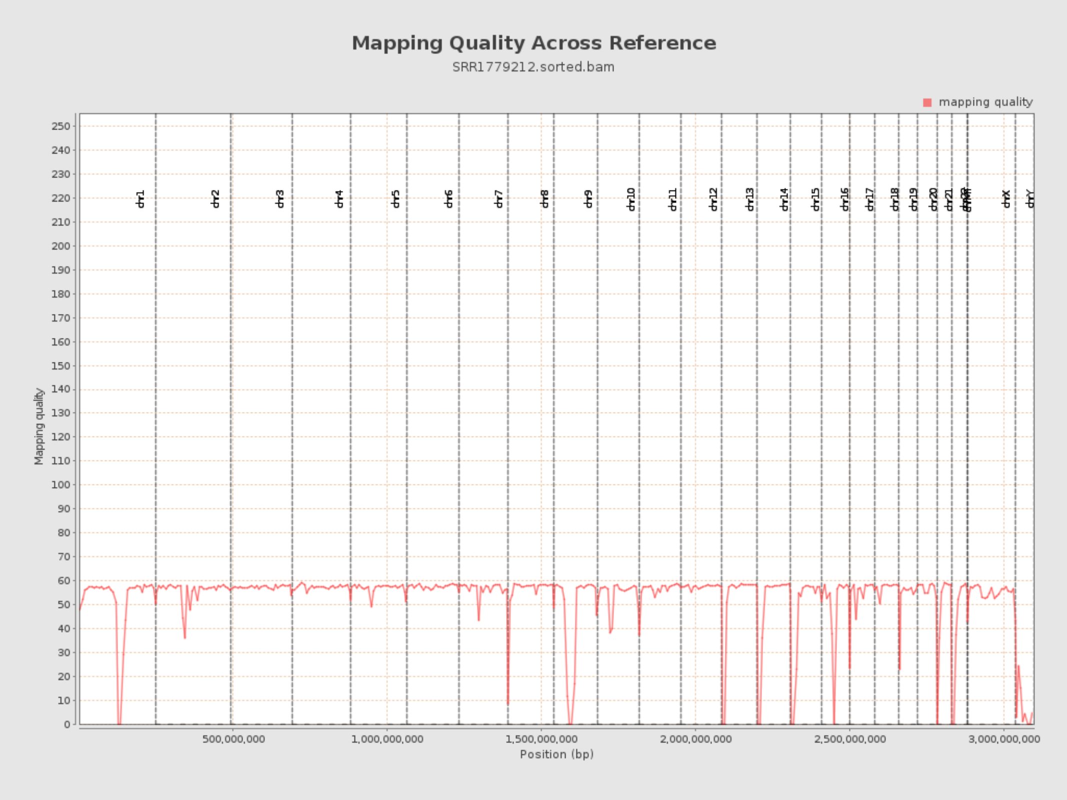
10. Results : Mapped Reads Clipping Profile



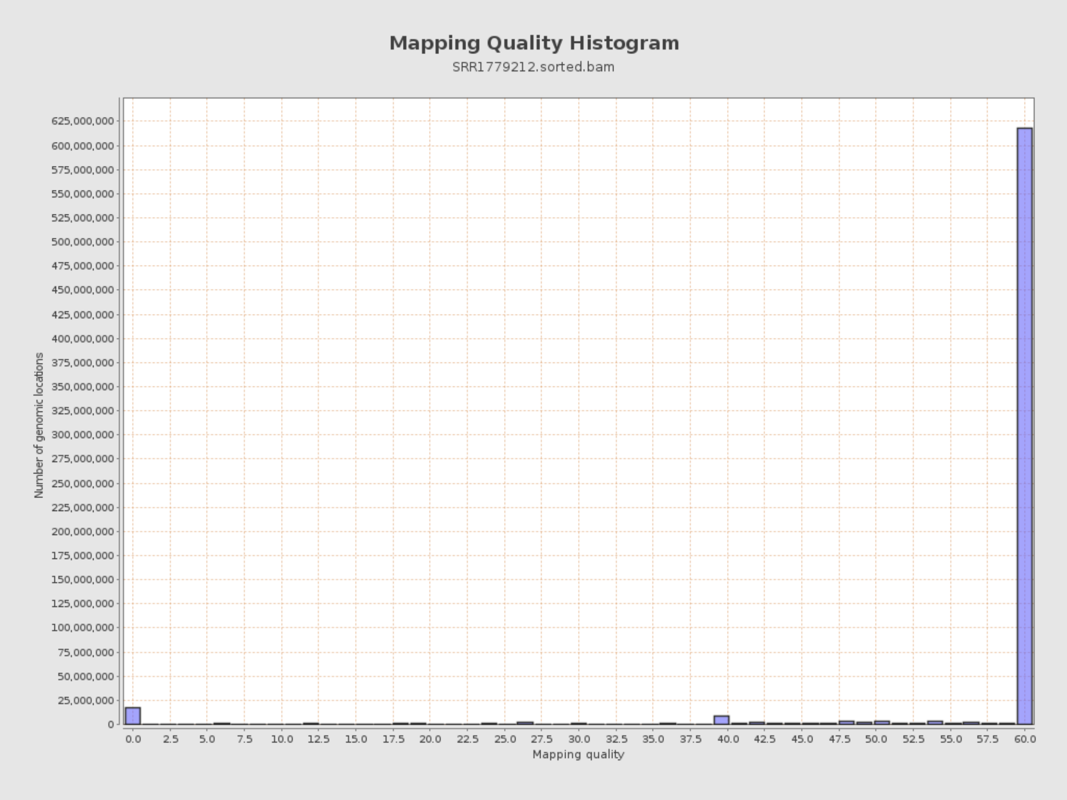
11. Results : Homopolymer Indels



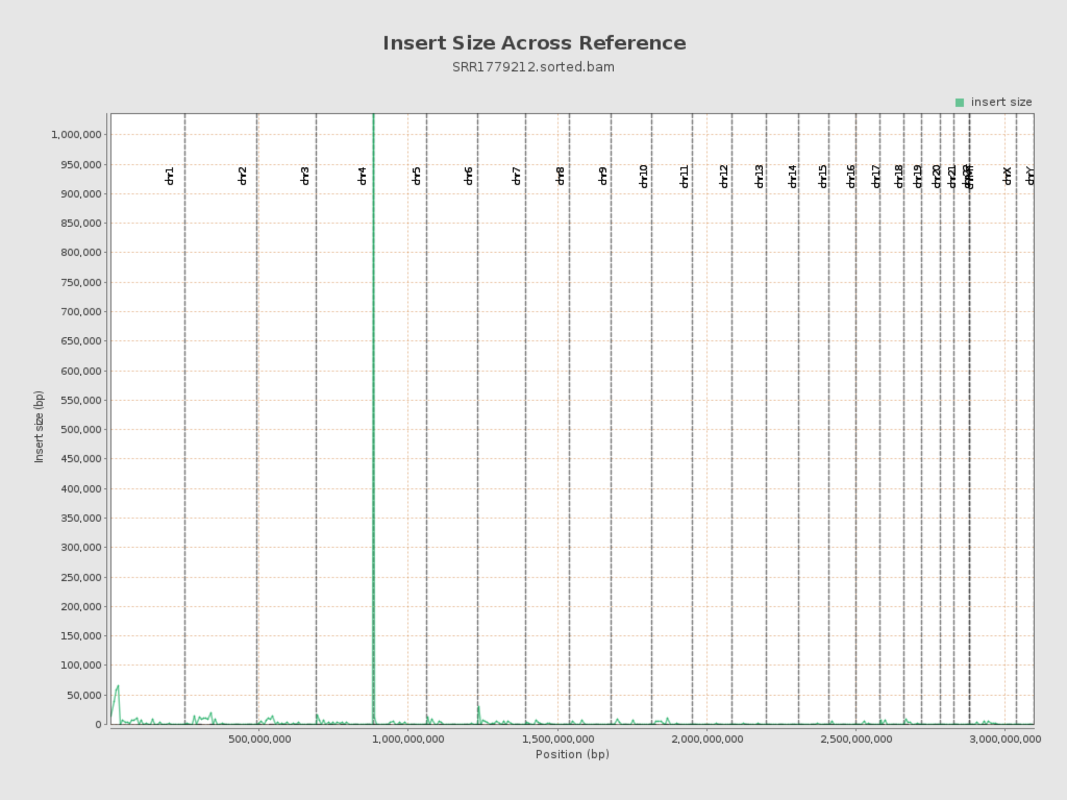
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram