Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 20:54:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779406.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_SRR1779406 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779406_1.fastq.gz SRR1779406_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 20:54:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779406.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,682,436
Mapped reads	15,178,312 / 96.79%
Unmapped reads	504,124 / 3.21%
Mapped paired reads	15,178,312 / 96.79%
Mapped reads, first in pair	7,663,797 / 48.87%
Mapped reads, second in pair	7,514,515 / 47.92%
Mapped reads, both in pair	14,999,056 / 95.64%
Mapped reads, singletons	179,256 / 1.14%
Secondary alignments	0
Supplementary alignments	55,732 / 0.36%
Read min/max/mean length	30 / 80 / 80.13
Duplicated reads (estimated)	470,555 / 3%
Duplication rate	2.72%
Clipped reads	608,596 / 3.88%

2.2. ACGT Content

Number/percentage of A's	365,569,853 / 30.3%
Number/percentage of C's	237,788,089 / 19.71%
Number/percentage of T's	358,785,011 / 29.74%
Number/percentage of G's	244,135,827 / 20.23%
Number/percentage of N's	266,937 / 0.02%

GC Percentage	39.94%

2.3. Coverage

Mean	0.3898
Standard Deviation	1.4546

2.4. Mapping Quality

Mean Mapping Quality	53.28

2.5. Insert size

Mean	131,328.07
Standard Deviation	3,483,991.91
P25/Median/P75	152 / 195 / 248

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	4,041,014
Insertions	106,616
Mapped reads with at least one insertion	0.7%
Deletions	122,861
Mapped reads with at least one deletion	0.8%
Homopolymer indels	47.3%

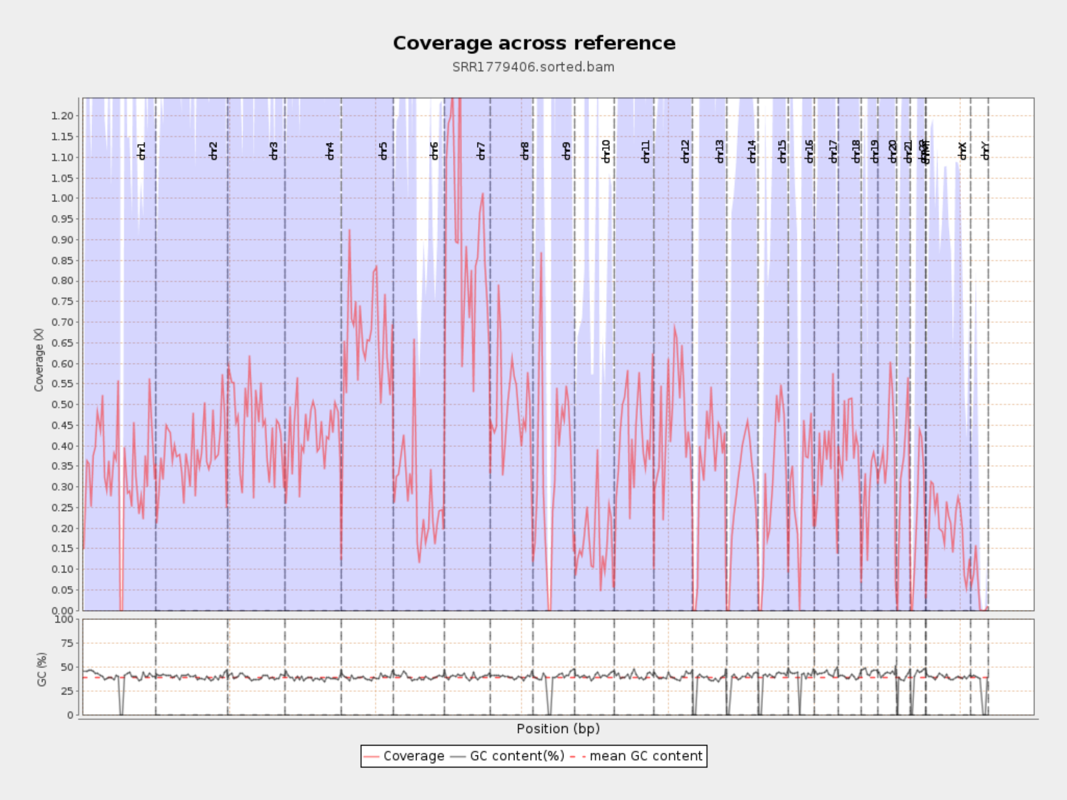
2.7. Chromosome stats

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

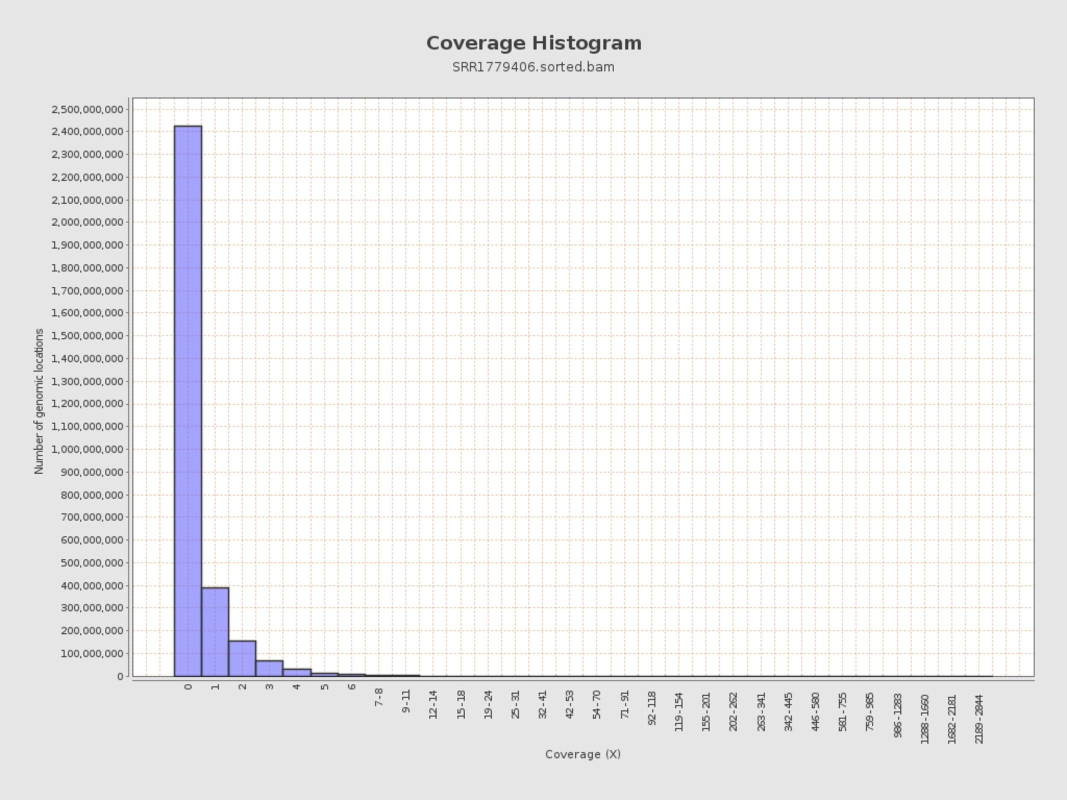
		bases	coverage	deviation
chr1	249250621	82680580	0.3317	3.0803
chr2	243199373	92334802	0.3797	0.9949
chr3	198022430	88641774	0.4476	0.9865
chr4	191154276	81307465	0.4253	0.9732
chr5	180915260	117745874	0.6508	1.2138
chr6	171115067	46887687	0.274	0.849
chr7	159138663	142487666	0.8954	2.1695
chr8	146364022	72952427	0.4984	1.098
chr9	141213431	50251260	0.3559	1.1871
chr10	135534747	22315245	0.1646	2.1303
chr11	135006516	56136132	0.4158	1.0506
chr12	133851895	61807928	0.4618	1.0331
chr13	115169878	39255986	0.3409	0.8589
chr14	107349540	31159123	0.2903	0.8088
chr15	102531392	30281232	0.2953	0.8567
chr16	90354753	25717231	0.2846	0.8186
chr17	81195210	29004187	0.3572	1.3063
chr18	78077248	31915665	0.4088	1.3219
chr19	59128983	16867693	0.2853	2.2088
chr20	63025520	25153645	0.3991	0.9824
chr21	48129895	15061311	0.3129	0.8747
chr22	51304566	12314963	0.24	0.8181
chrMT	16571	483	0.0291	0.2617
chrX	155270560	31609100	0.2036	0.6808

chrY	59373566	2910233	0.049	0.3267

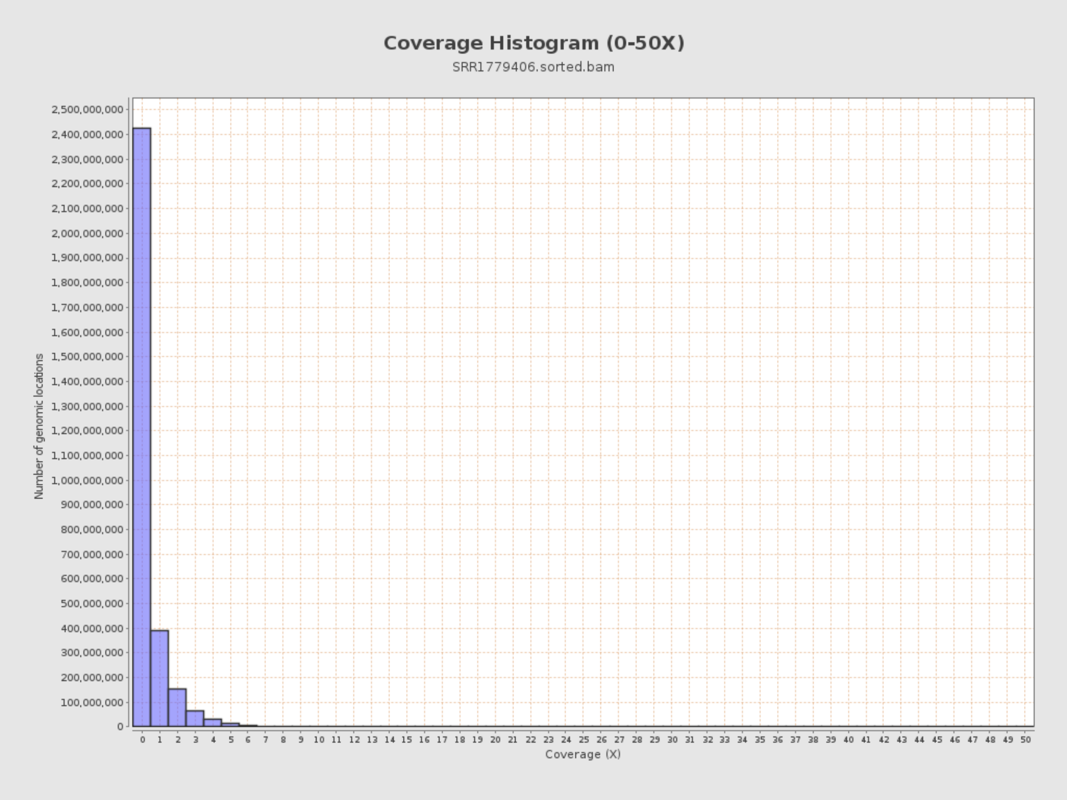
3. Results : Coverage across reference



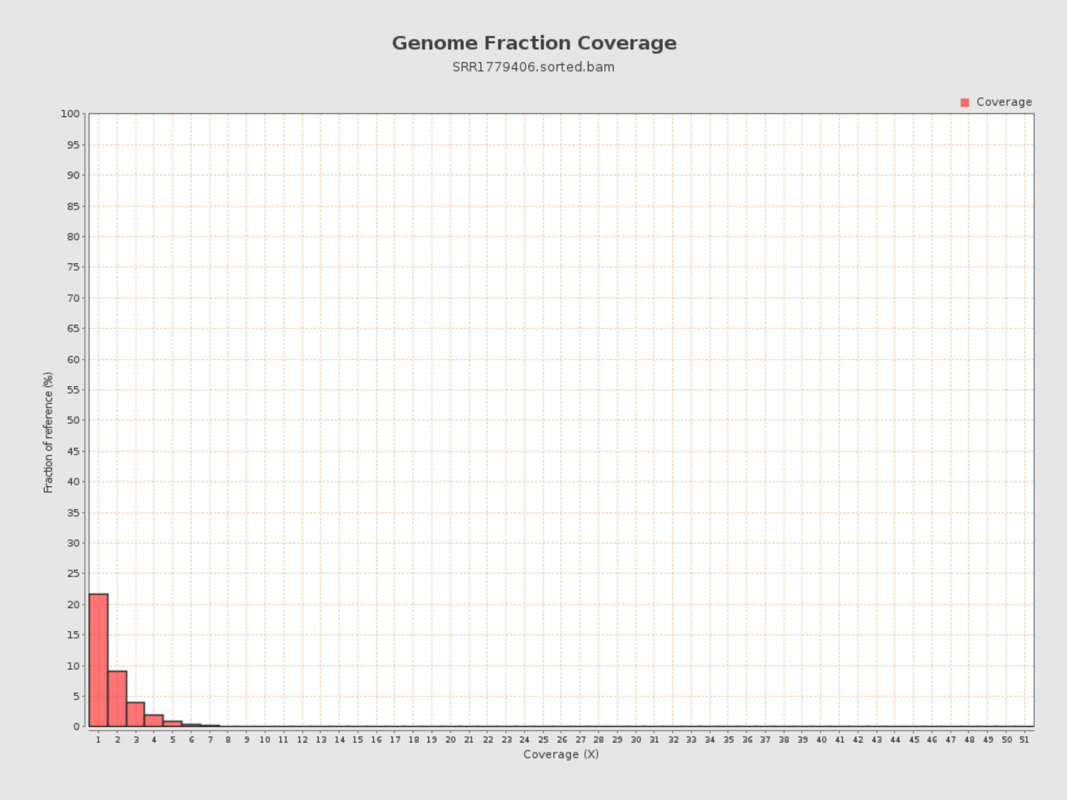
4. Results : Coverage Histogram



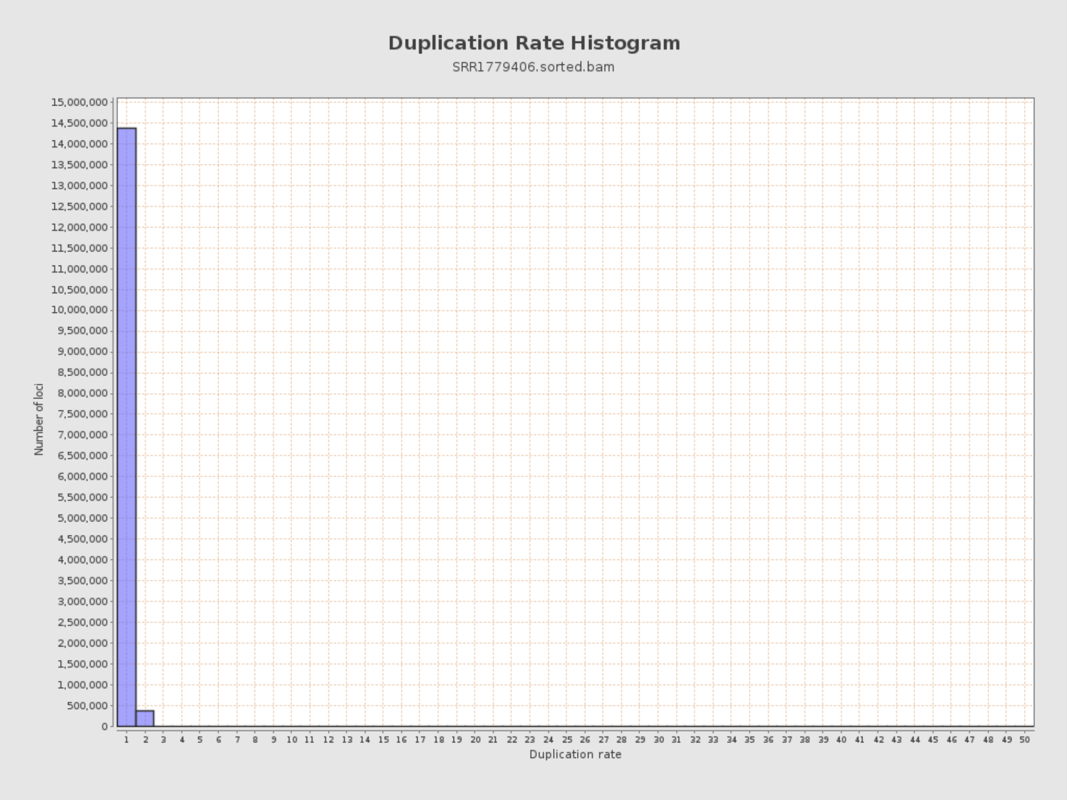
5. Results : Coverage Histogram (0-50X)



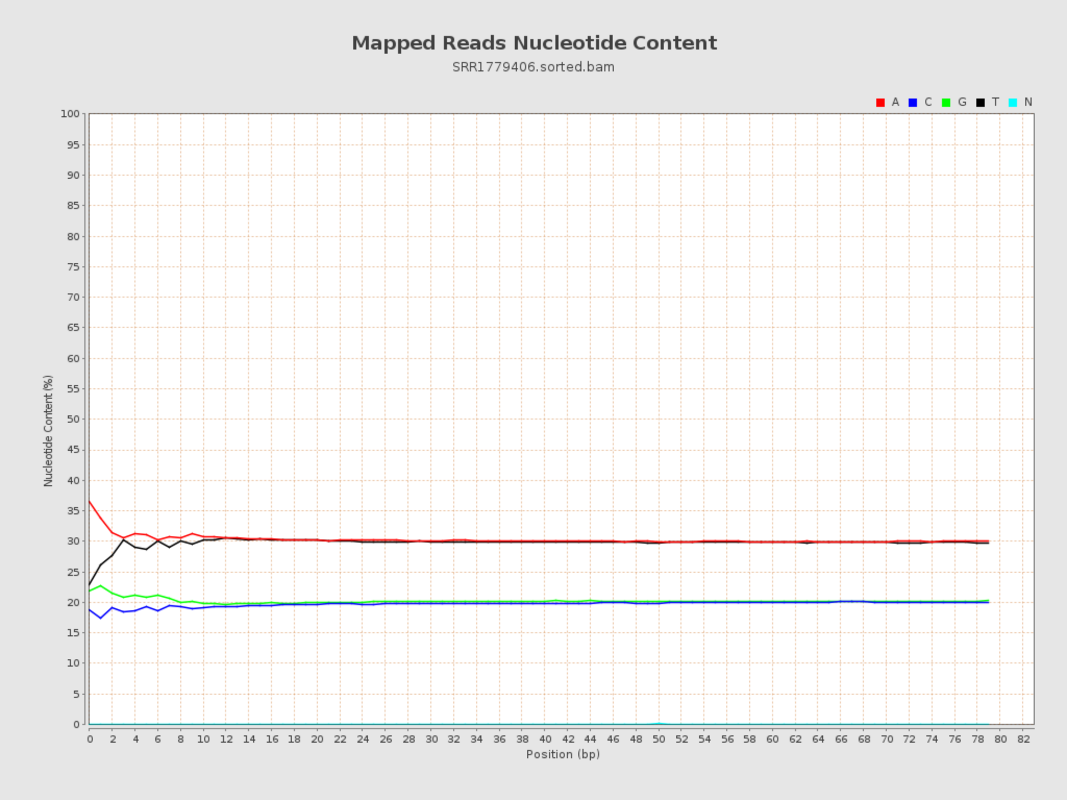
6. Results : Genome Fraction Coverage



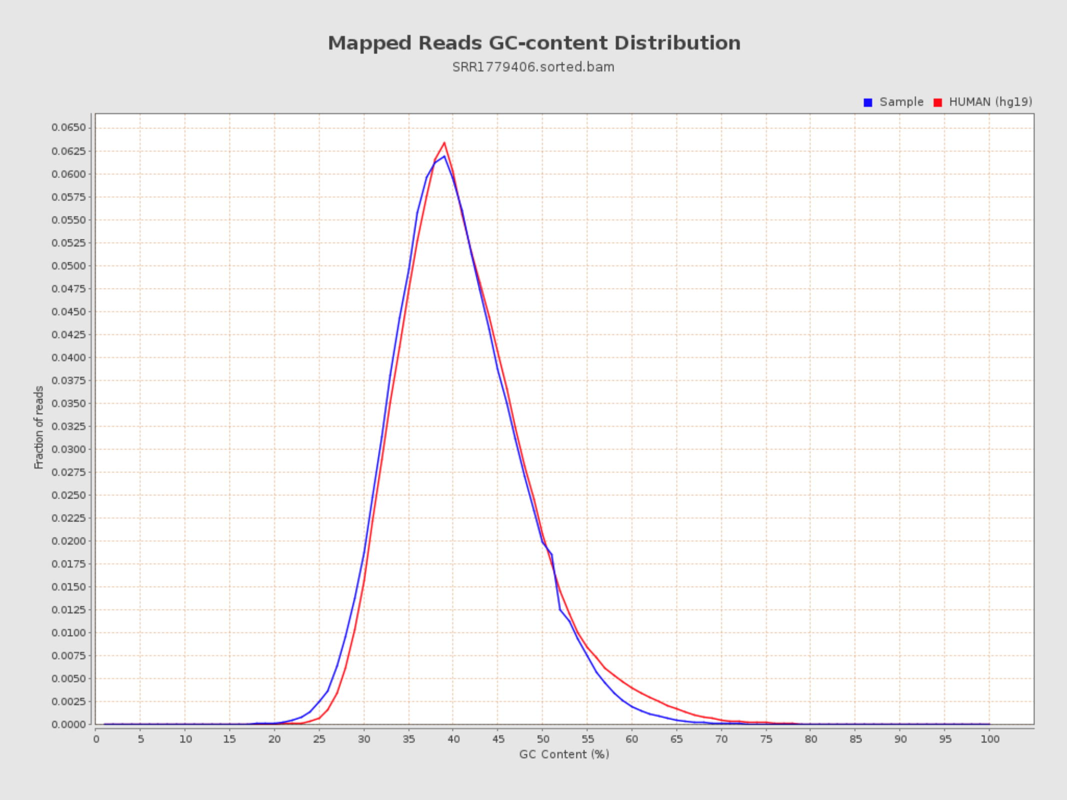
7. Results : Duplication Rate Histogram



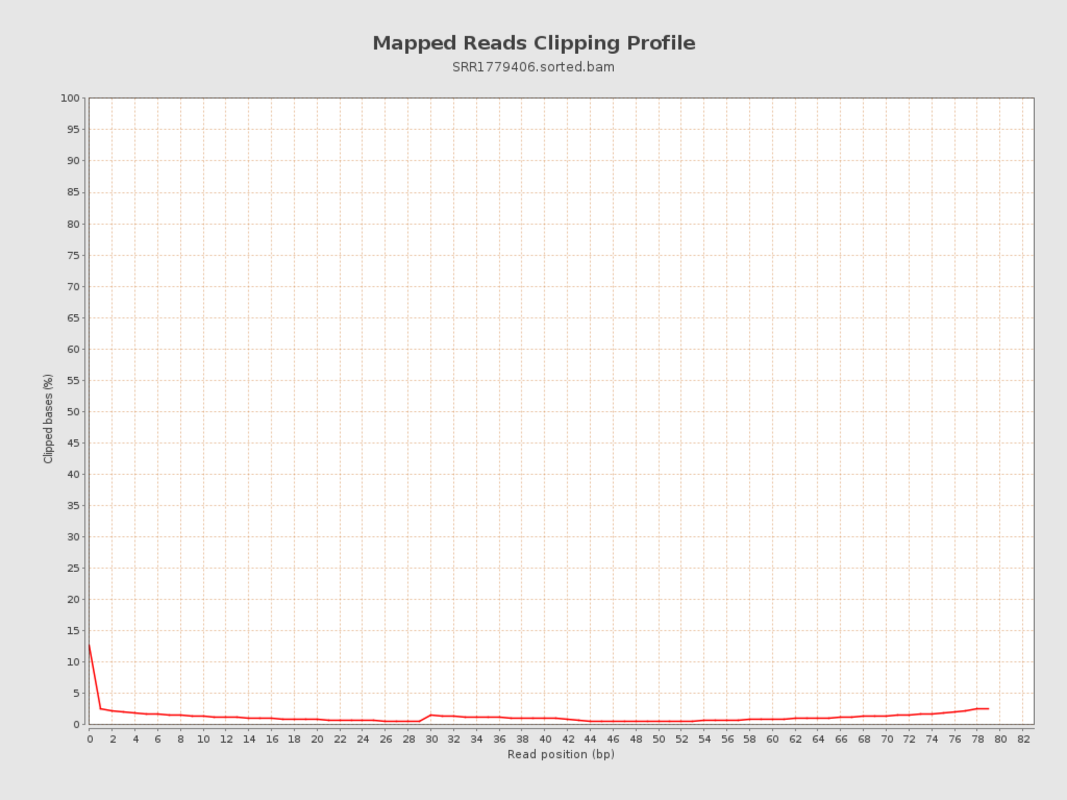
8. Results : Mapped Reads Nucleotide Content



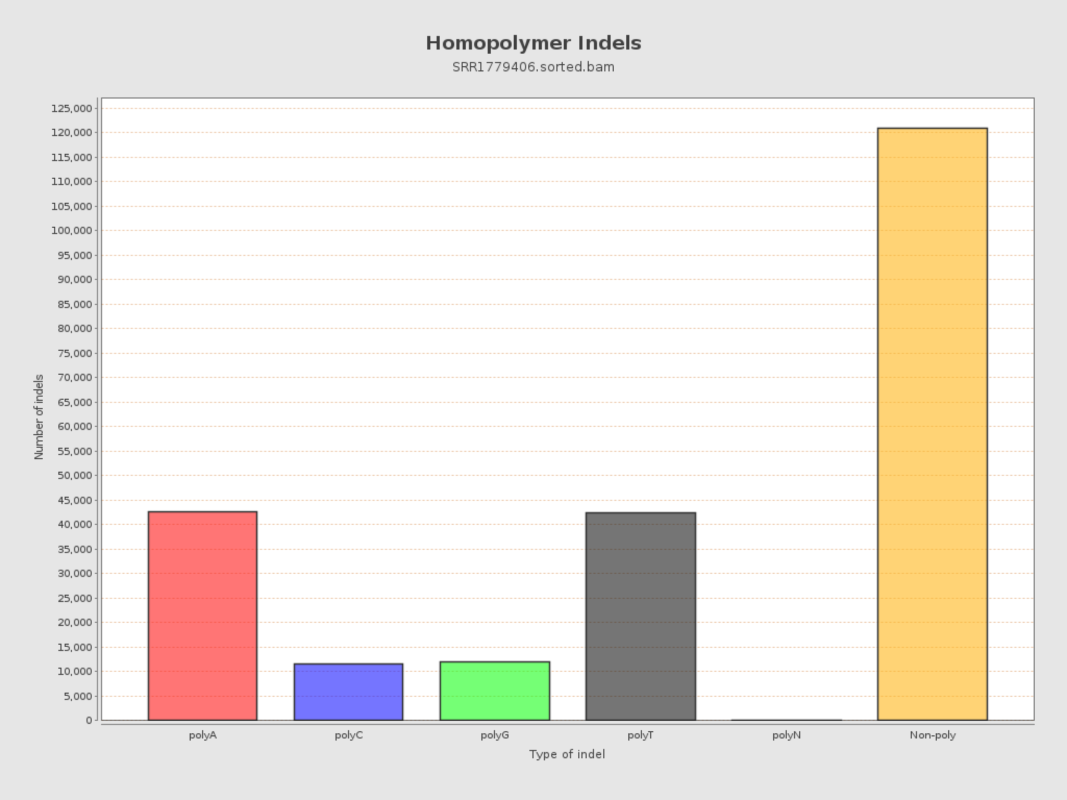
9. Results : Mapped Reads GC-content Distribution



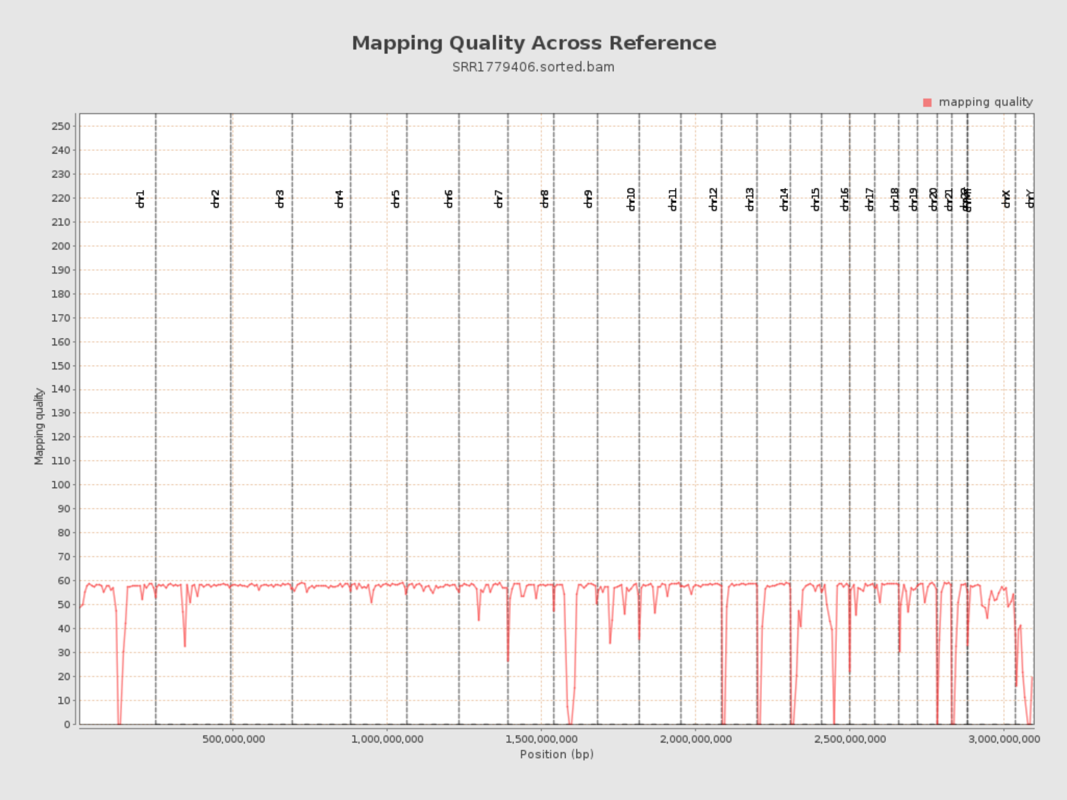
10. Results : Mapped Reads Clipping Profile



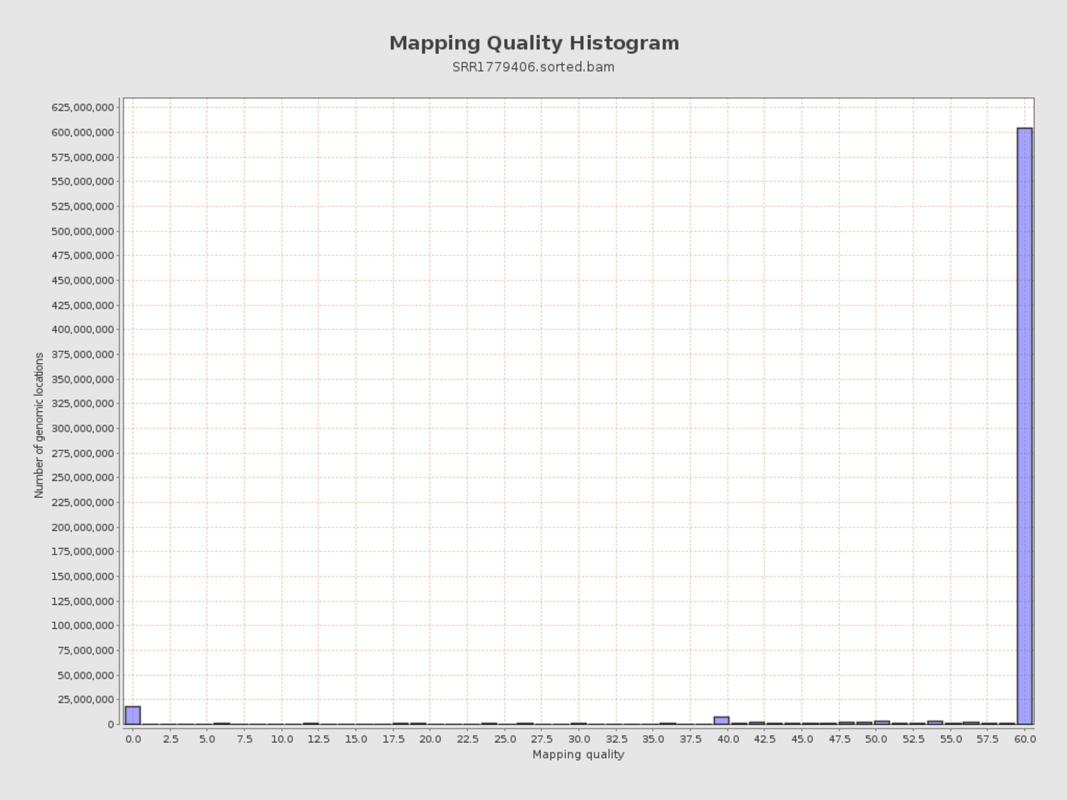
11. Results : Homopolymer Indels



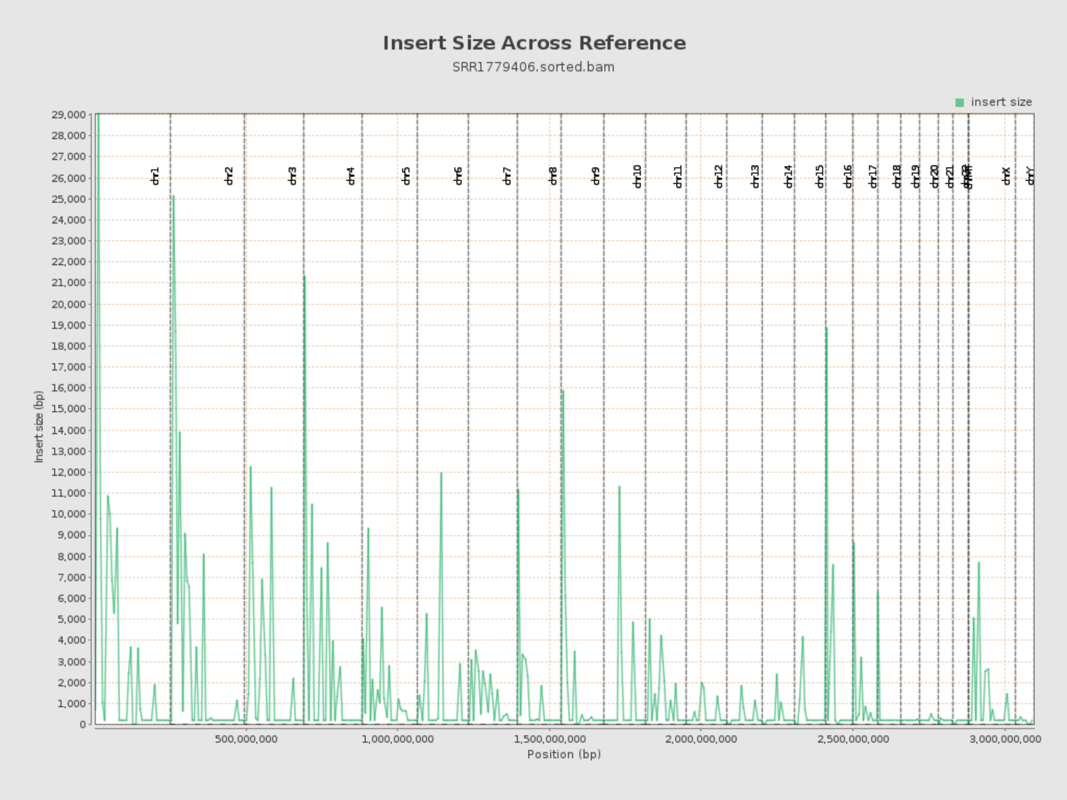
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram