Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 10:30:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617706.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_SRR8617706 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617706_1.fastq.gz SRR8617706_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 10:30:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617706.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,006,370
Mapped reads	58,237,631 / 98.7%
Unmapped reads	768,739 / 1.3%
Mapped paired reads	58,237,631 / 98.7%
Mapped reads, first in pair	29,316,954 / 49.68%
Mapped reads, second in pair	28,920,677 / 49.01%
Mapped reads, both in pair	57,735,984 / 97.85%
Mapped reads, singletons	501,647 / 0.85%
Secondary alignments	0
Supplementary alignments	1,772,560 / 3%
Read min/max/mean length	30 / 150 / 151.47
Duplicated reads (estimated)	19,167,045 / 32.48%
Duplication rate	24.56%
Clipped reads	32,860,719 / 55.69%

2.2. ACGT Content

Number/percentage of A's	2,281,071,819 / 29.46%
Number/percentage of C's	1,427,141,116 / 18.43%
Number/percentage of T's	2,372,079,703 / 30.63%
Number/percentage of G's	1,663,103,918 / 21.48%
Number/percentage of N's	308,049 / 0%

GC Percentage	39.91%

2.3. Coverage

Mean	2.5034
Standard Deviation	31.4929

2.4. Mapping Quality

Mean Mapping Quality	53.3

2.5. Insert size

Mean	179,463.12
Standard Deviation	4,003,530.33
P25/Median/P75	209 / 262 / 330

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	84,793,132
Insertions	1,420,639
Mapped reads with at least one insertion	2.28%
Deletions	2,955,224
Mapped reads with at least one deletion	4.86%
Homopolymer indels	45.52%

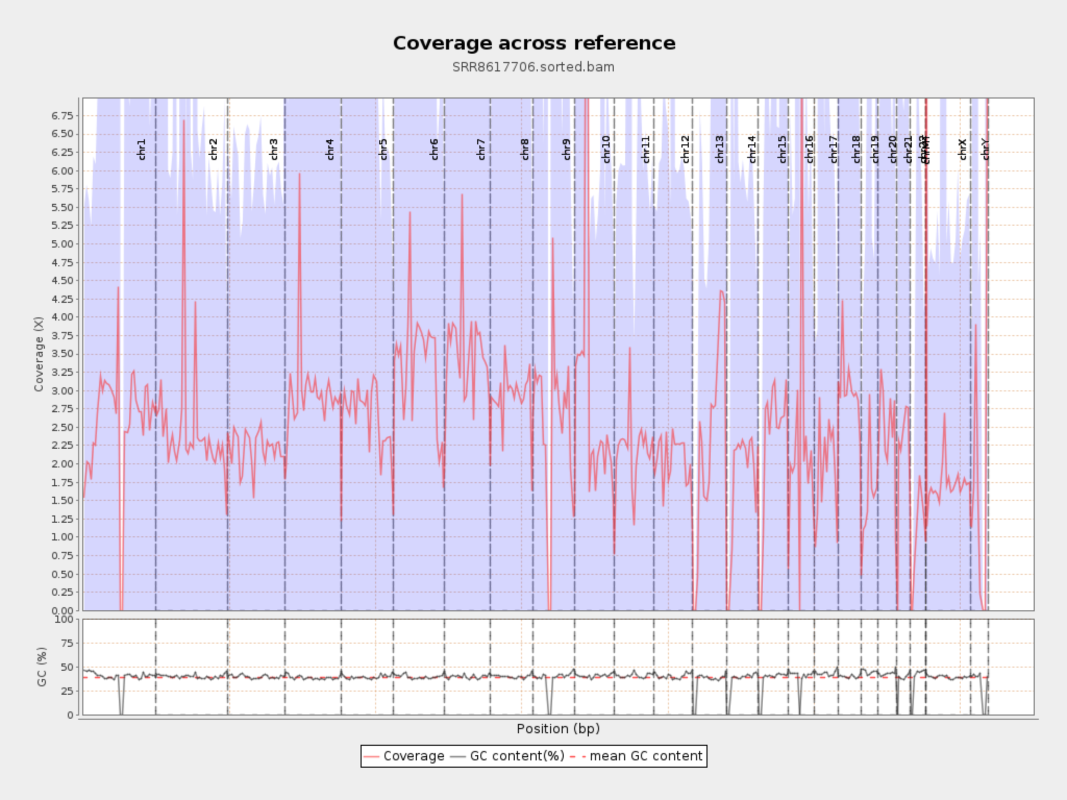
2.7. Chromosome stats

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

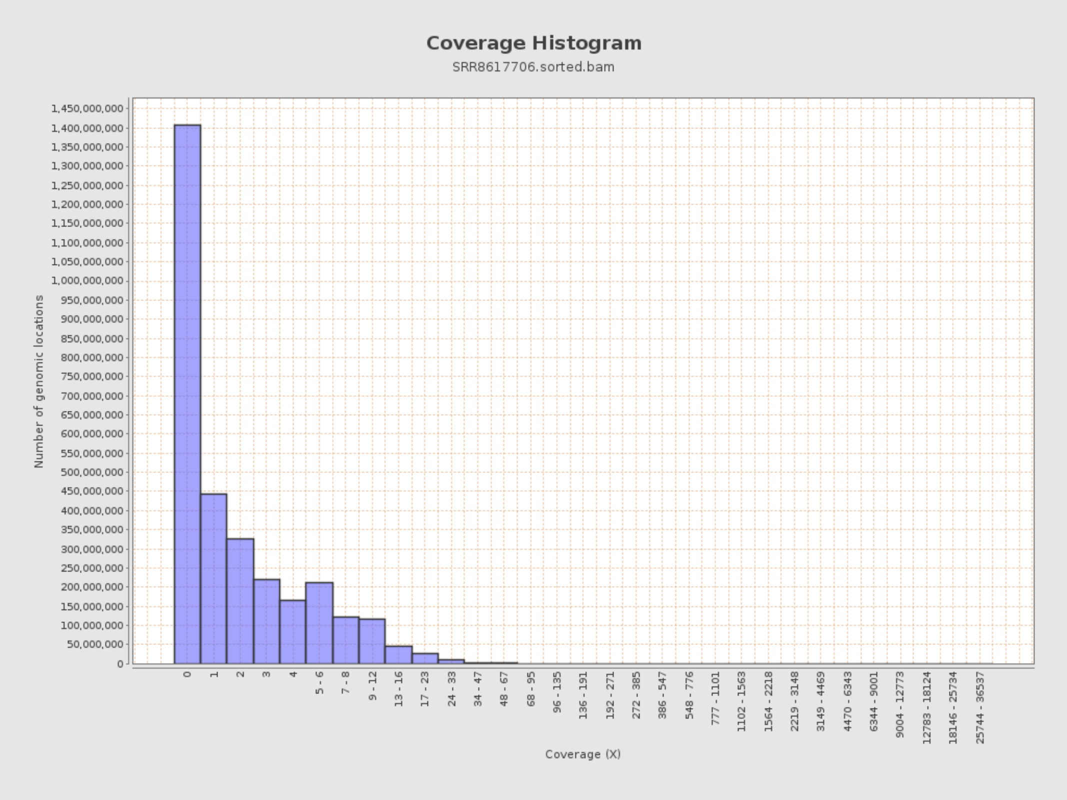
		bases	coverage	deviation
chr1	249250621	638132510	2.5602	30.0064
chr2	243199373	605504325	2.4897	34.5046
chr3	198022430	438076857	2.2123	4.1483
chr4	191154276	575459938	3.0104	25.2195
chr5	180915260	477755603	2.6408	4.901
chr6	171115067	582100092	3.4018	21.4363
chr7	159138663	559988933	3.5189	50.3543
chr8	146364022	426801765	2.916	9.0711
chr9	141213431	360850468	2.5554	52.1425
chr10	135534747	412416415	3.0429	81.7531
chr11	135006516	297558778	2.204	28.9921
chr12	133851895	276604274	2.0665	10.7746
chr13	115169878	275735155	2.3942	4.3007
chr14	107349540	189206064	1.7625	4.6417
chr15	102531392	229117350	2.2346	6.0951
chr16	90354753	206618393	2.2867	41.4299
chr17	81195210	158894550	1.9569	22.78
chr18	78077248	239017403	3.0613	42.7442
chr19	59128983	94066485	1.5909	15.6474
chr20	63025520	160402194	2.545	8.4259
chr21	48129895	104431368	2.1698	11.9168
chr22	51304566	53556480	1.0439	3.8997
chrMT	16571	1044290	63.0191	35.8162
chrX	155270560	266140352	1.714	9.0237

chrY	59373566	120155366	2.0237	46.0202

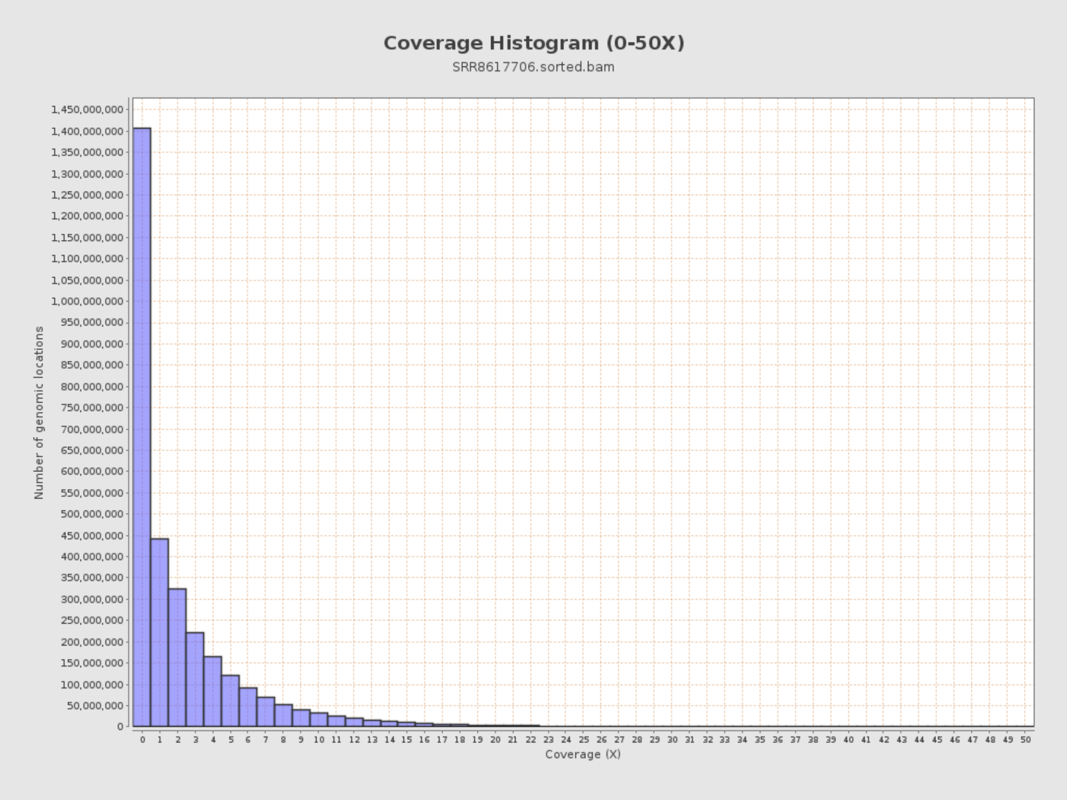
3. Results : Coverage across reference



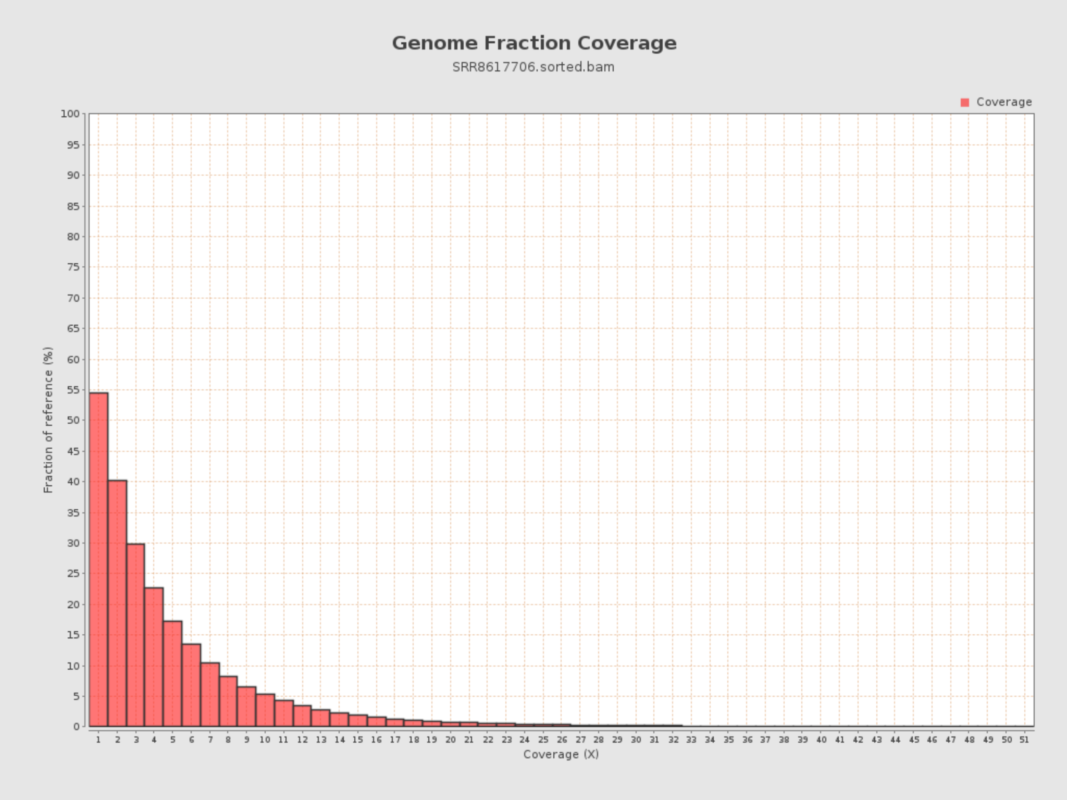
4. Results : Coverage Histogram



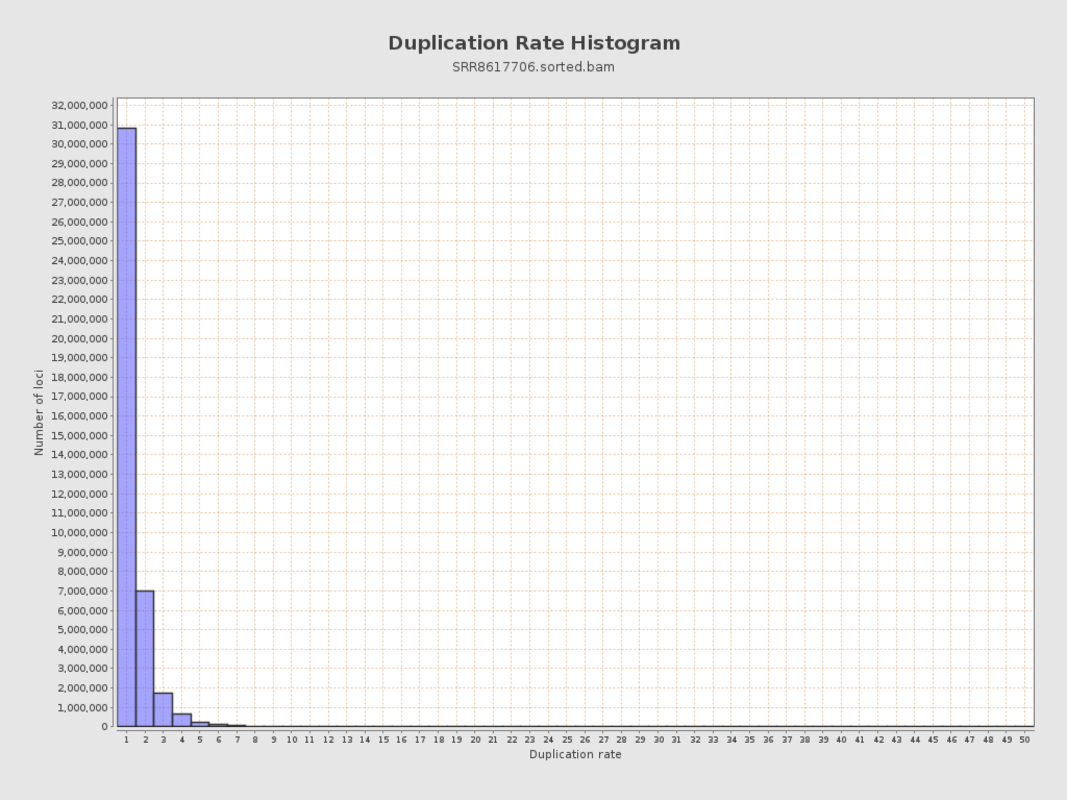
5. Results : Coverage Histogram (0-50X)



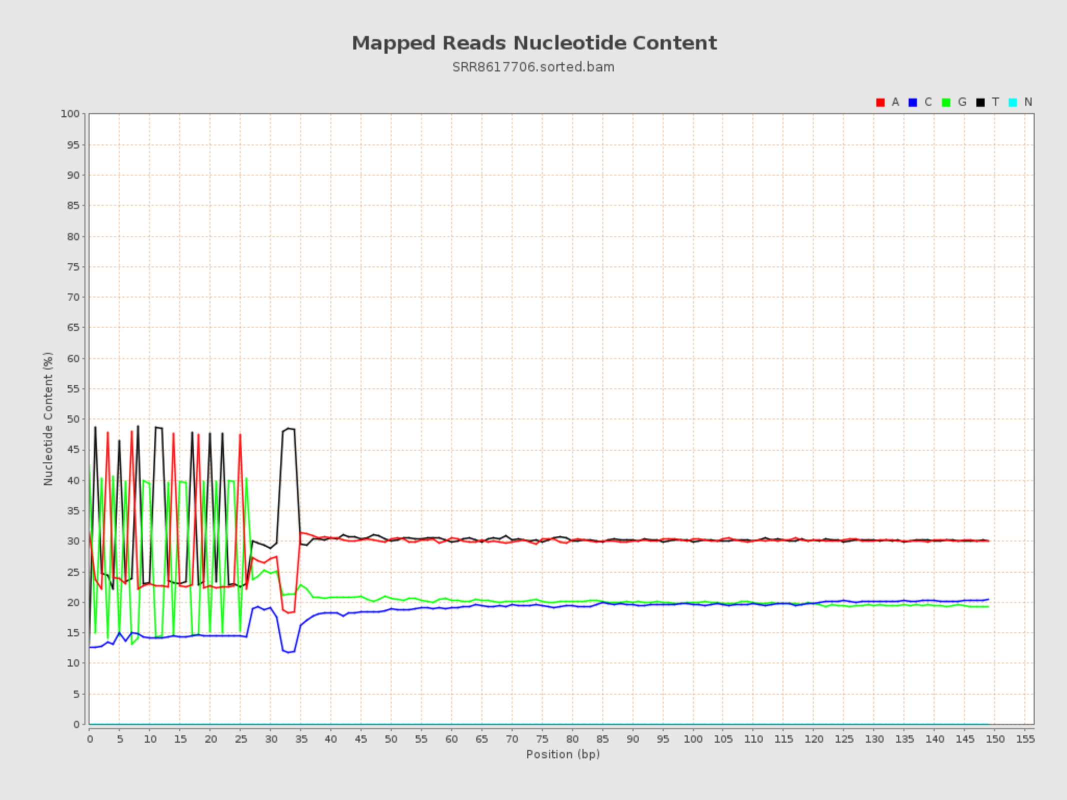
6. Results : Genome Fraction Coverage



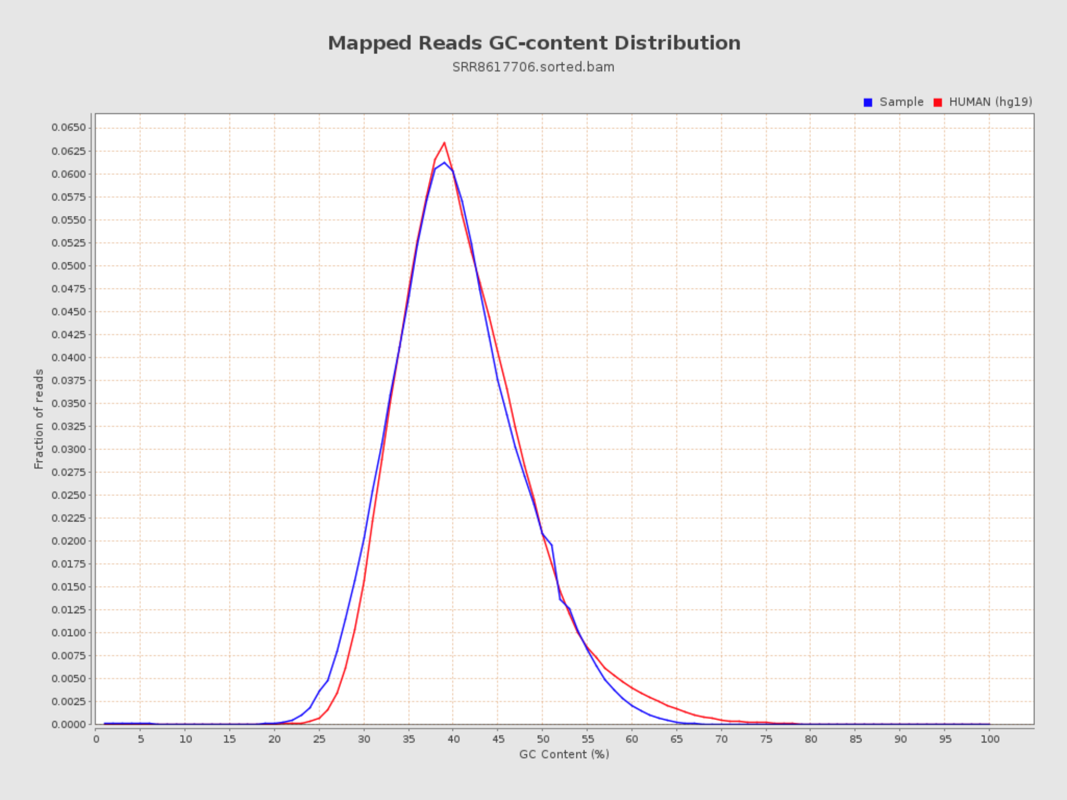
7. Results : Duplication Rate Histogram



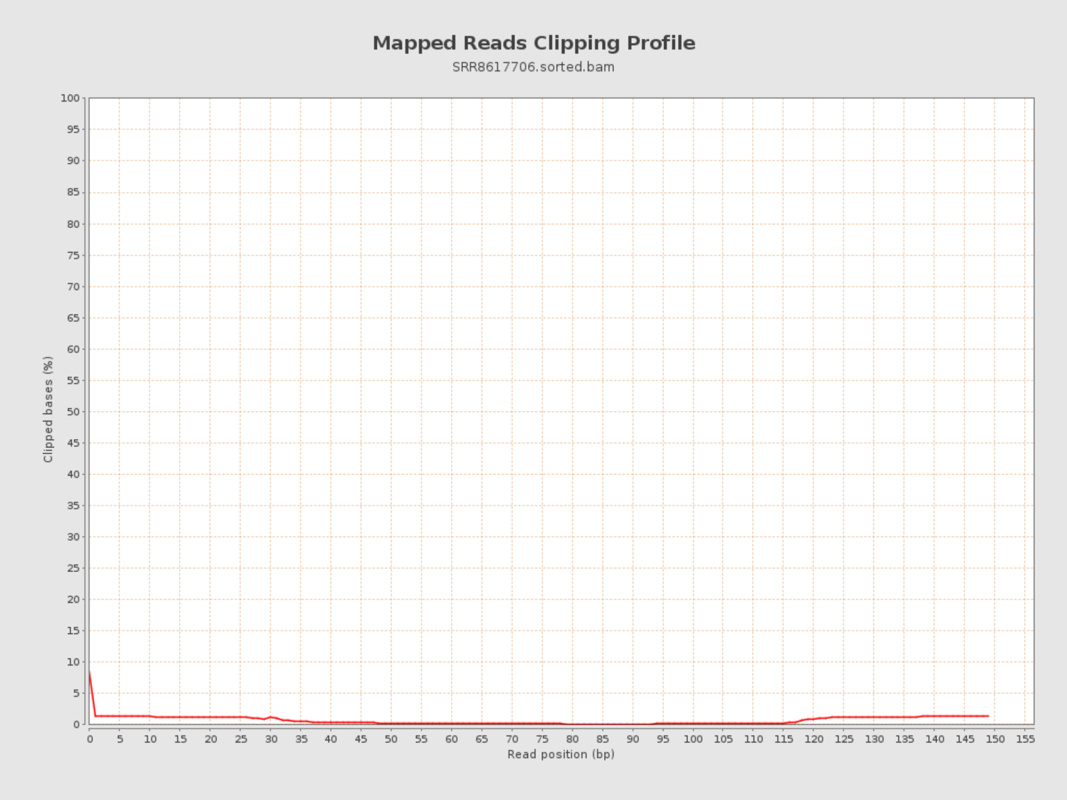
8. Results : Mapped Reads Nucleotide Content



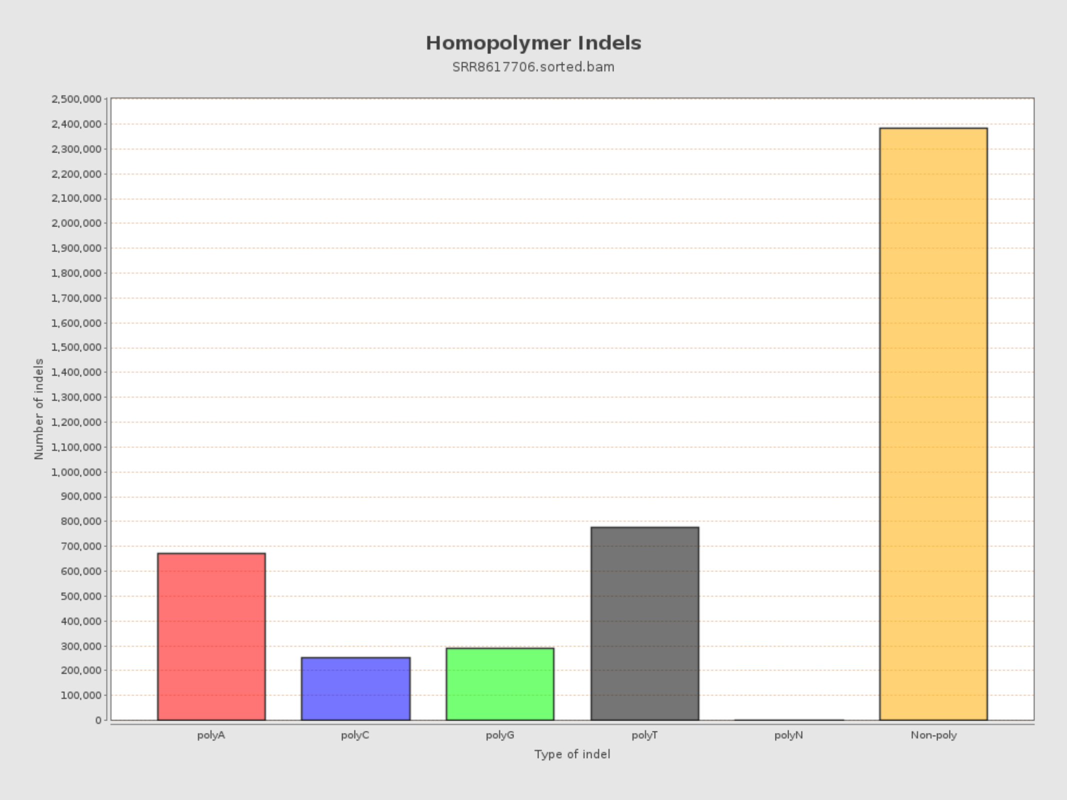
9. Results : Mapped Reads GC-content Distribution



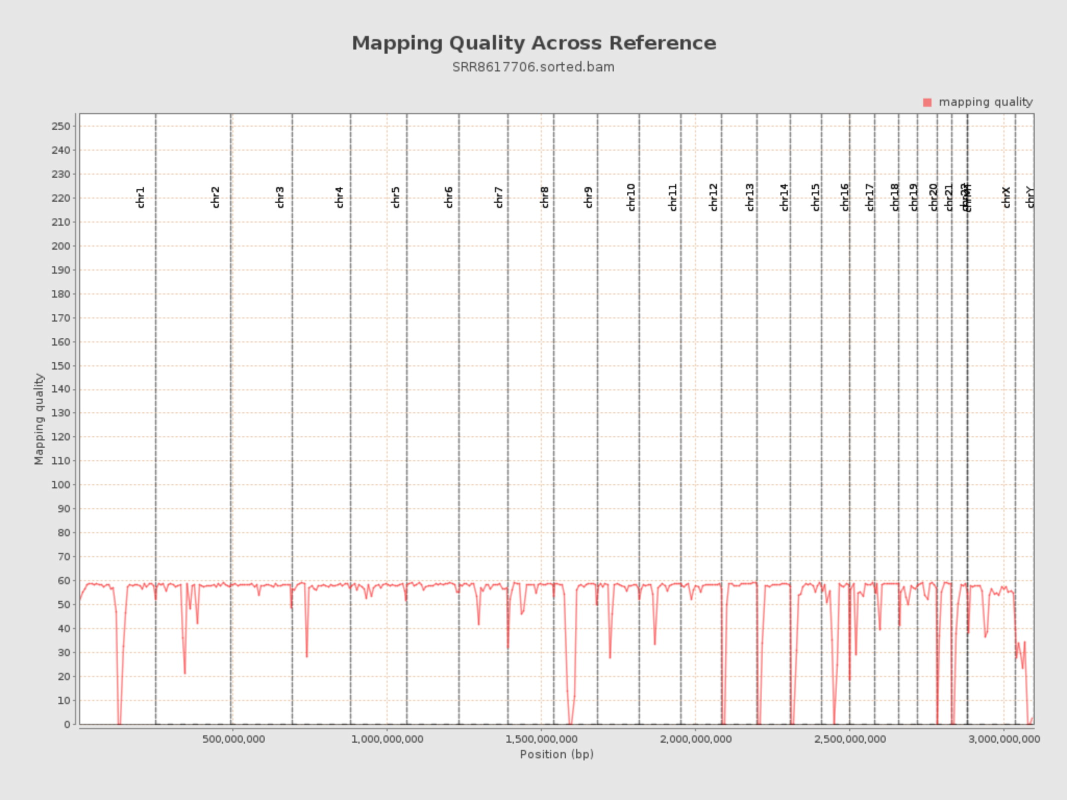
10. Results : Mapped Reads Clipping Profile



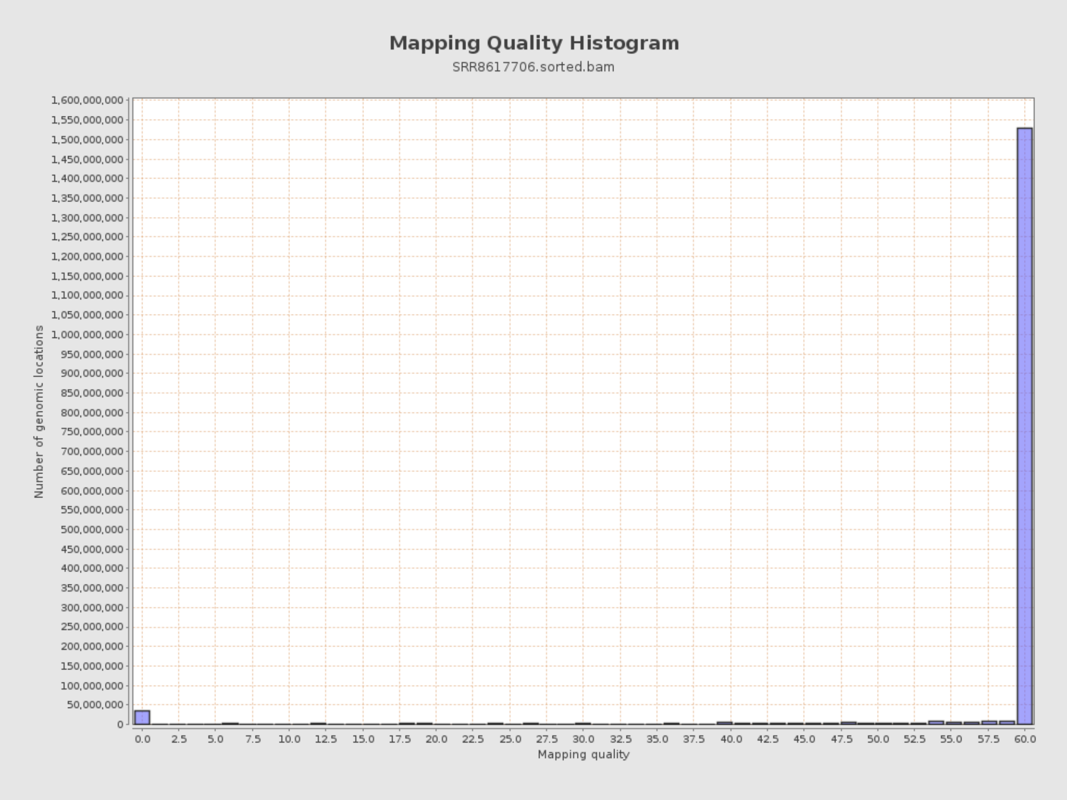
11. Results : Homopolymer Indels



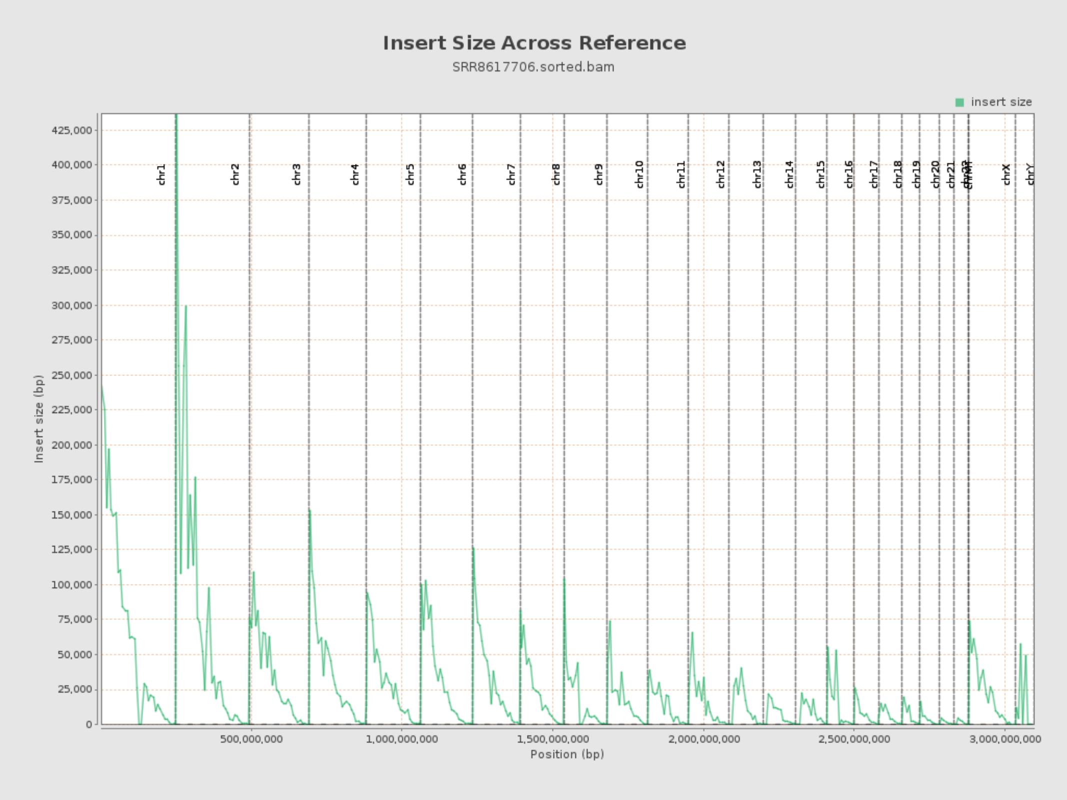
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram