Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 01:20:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617724.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_SRR8617724 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617724_1.fastq.gz SRR8617724_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 01:20:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617724.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,378,006
Mapped reads	41,494,481 / 97.92%
Unmapped reads	883,525 / 2.08%
Mapped paired reads	41,494,481 / 97.92%
Mapped reads, first in pair	20,959,340 / 49.46%
Mapped reads, second in pair	20,535,141 / 48.46%
Mapped reads, both in pair	40,931,792 / 96.59%
Mapped reads, singletons	562,689 / 1.33%
Secondary alignments	0
Supplementary alignments	1,518,404 / 3.58%
Read min/max/mean length	30 / 150 / 151.77
Duplicated reads (estimated)	14,418,748 / 34.02%
Duplication rate	24.77%
Clipped reads	24,680,569 / 58.24%

2.2. ACGT Content

Number/percentage of A's	1,569,770,456 / 28.6%
Number/percentage of C's	1,053,183,658 / 19.19%
Number/percentage of T's	1,620,264,566 / 29.52%
Number/percentage of G's	1,246,158,519 / 22.7%
Number/percentage of N's	212,166 / 0%

GC Percentage	41.89%

2.3. Coverage

Mean	1.7747
Standard Deviation	15.3215

2.4. Mapping Quality

Mean Mapping Quality	53.11

2.5. Insert size

Mean	269,359.83
Standard Deviation	5,169,050.62
P25/Median/P75	215 / 273 / 343

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	64,482,872
Insertions	1,033,127
Mapped reads with at least one insertion	2.33%
Deletions	2,276,676
Mapped reads with at least one deletion	5.25%
Homopolymer indels	45.38%

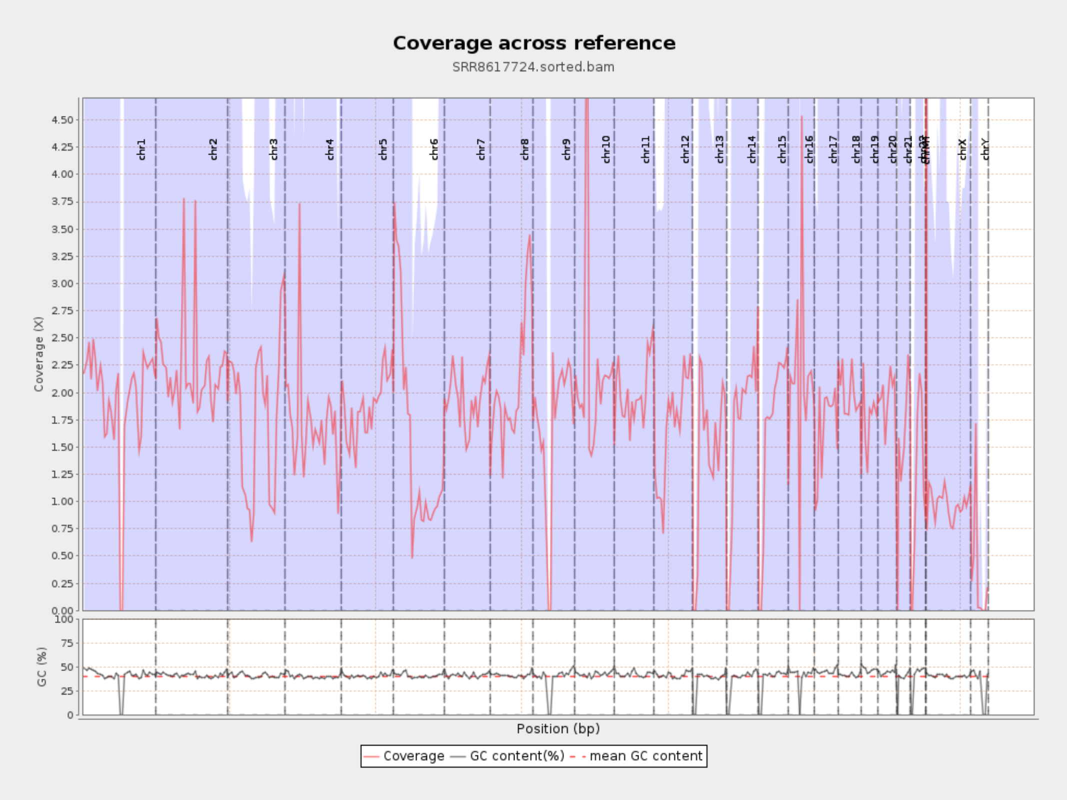
2.7. Chromosome stats

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

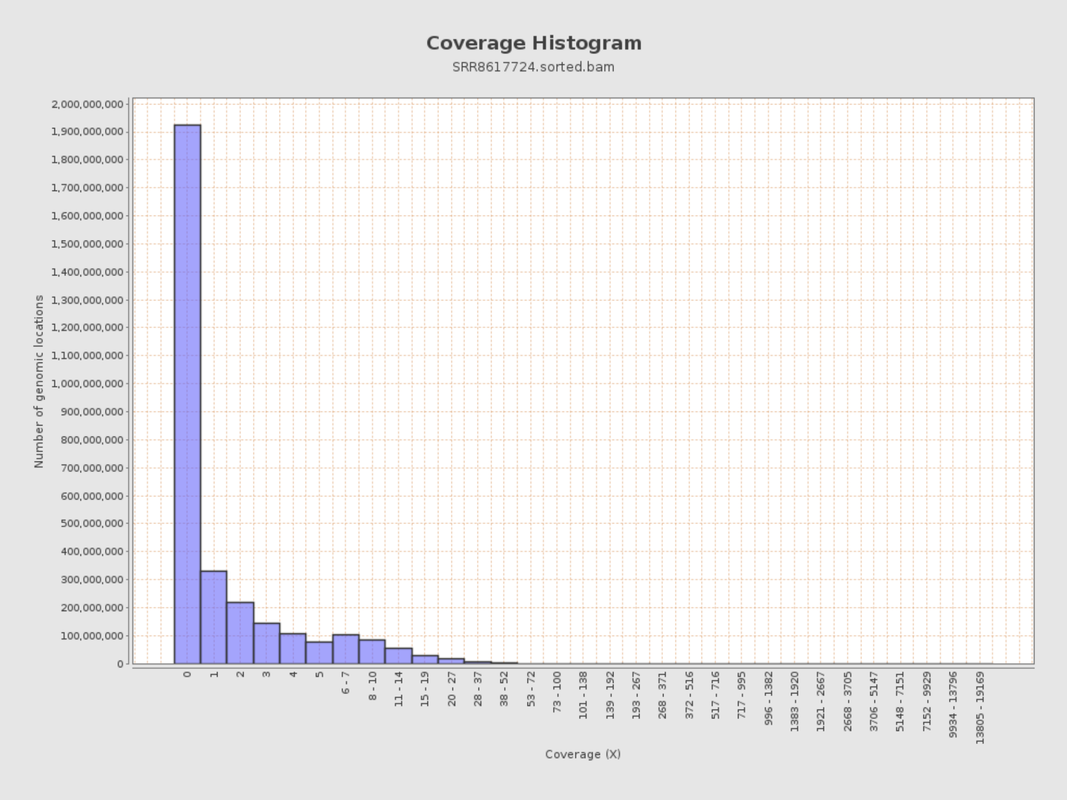
		bases	coverage	deviation
chr1	249250621	480230730	1.9267	9.689
chr2	243199373	543575622	2.2351	20.2774
chr3	198022430	353404260	1.7847	4.0984
chr4	191154276	327574193	1.7137	16.211
chr5	180915260	340538931	1.8823	4.3038
chr6	171115067	259042597	1.5139	6.2164
chr7	159138663	311566274	1.9578	17.2779
chr8	146364022	310647699	2.1224	5.496
chr9	141213431	237677118	1.6831	22.3762
chr10	135534747	297364591	2.194	41.2304
chr11	135006516	269479541	1.996	9.3411
chr12	133851895	226314368	1.6908	9.0251
chr13	115169878	166527616	1.4459	3.5205
chr14	107349540	182146277	1.6968	4.39
chr15	102531392	168525511	1.6436	5.2191
chr16	90354753	190241425	2.1055	24.3839
chr17	81195210	135718107	1.6715	14.5387
chr18	78077248	155074100	1.9862	20.1942
chr19	59128983	103797706	1.7554	6.1208
chr20	63025520	123014537	1.9518	6.3715
chr21	48129895	75394085	1.5665	9.1995
chr22	51304566	60604693	1.1813	4.0532
chrMT	16571	3369849	203.3582	110.225
chrX	155270560	151611250	0.9764	4.0474

chrY	59373566	20607272	0.3471	26.4543

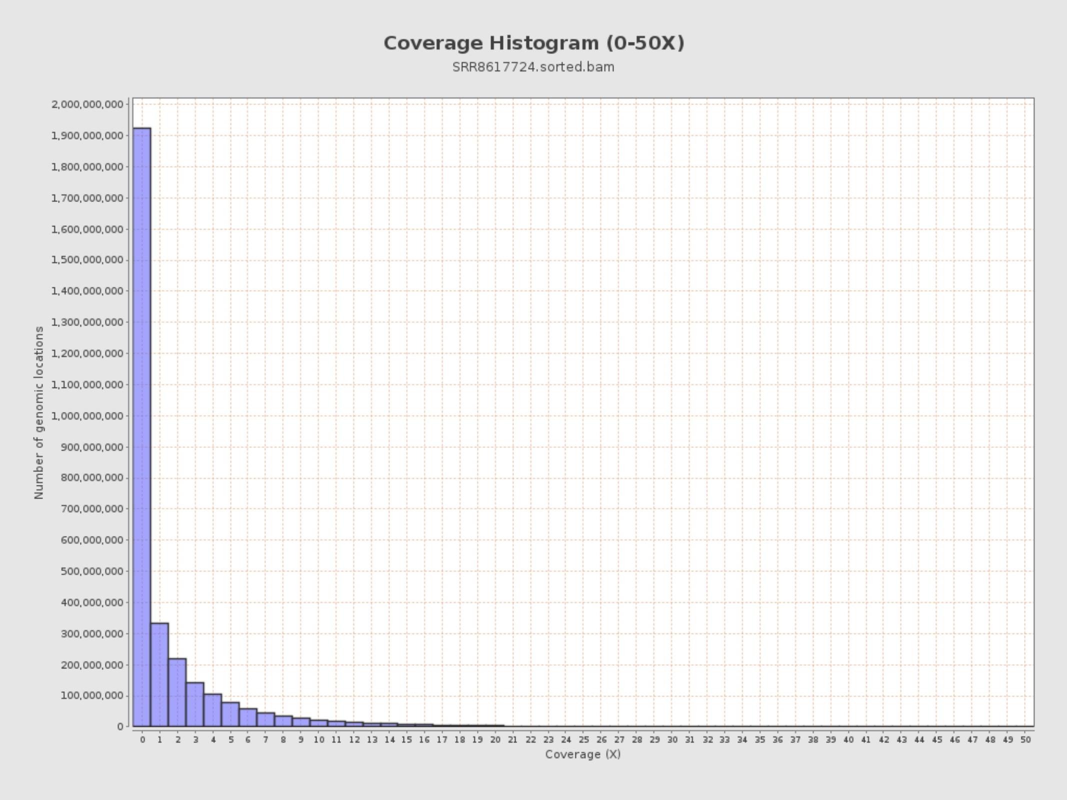
3. Results : Coverage across reference



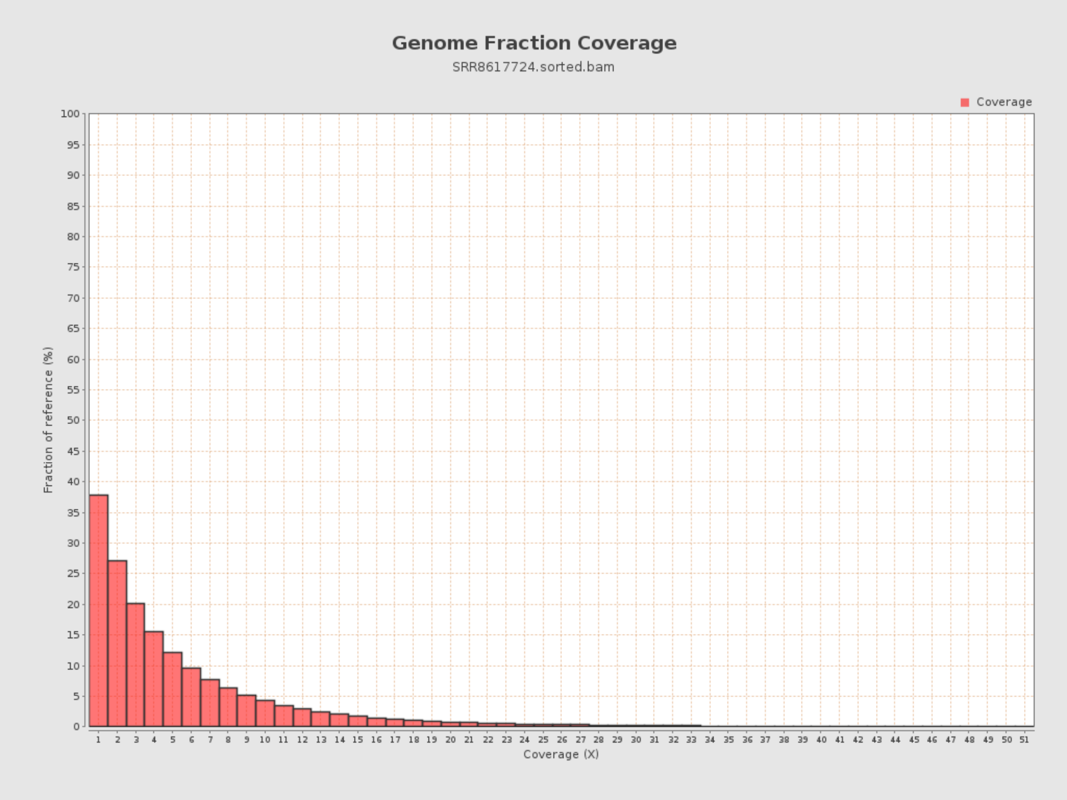
4. Results : Coverage Histogram



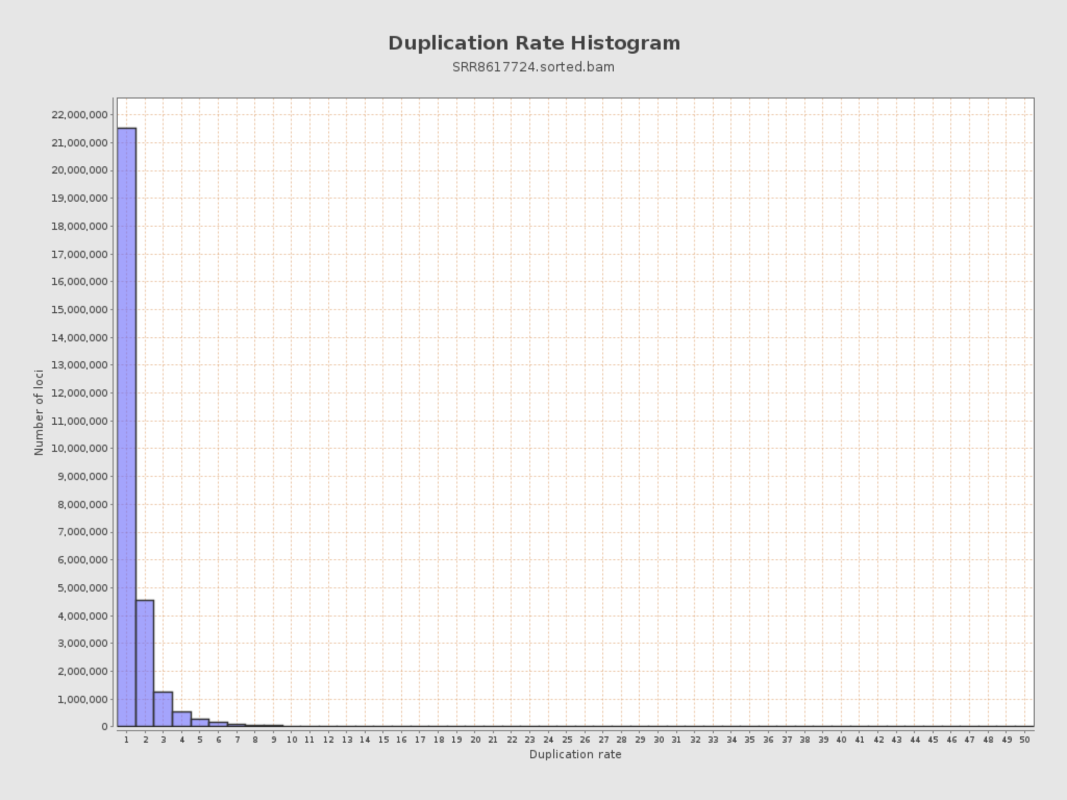
5. Results : Coverage Histogram (0-50X)



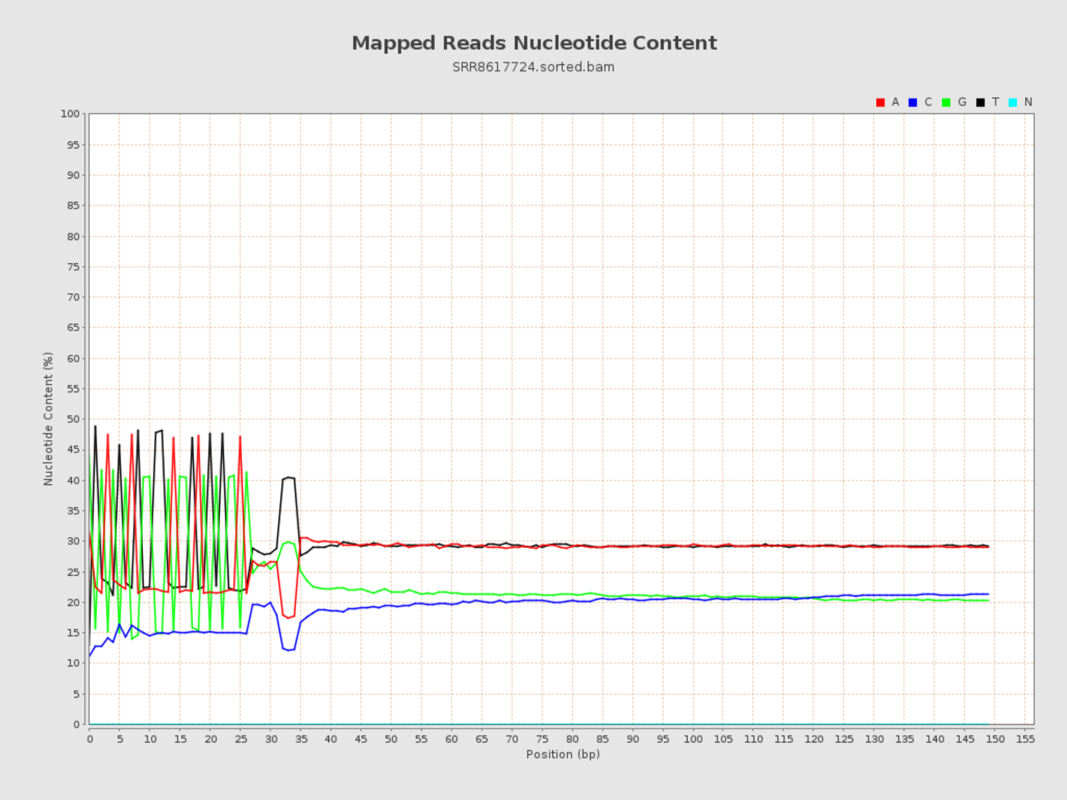
6. Results : Genome Fraction Coverage



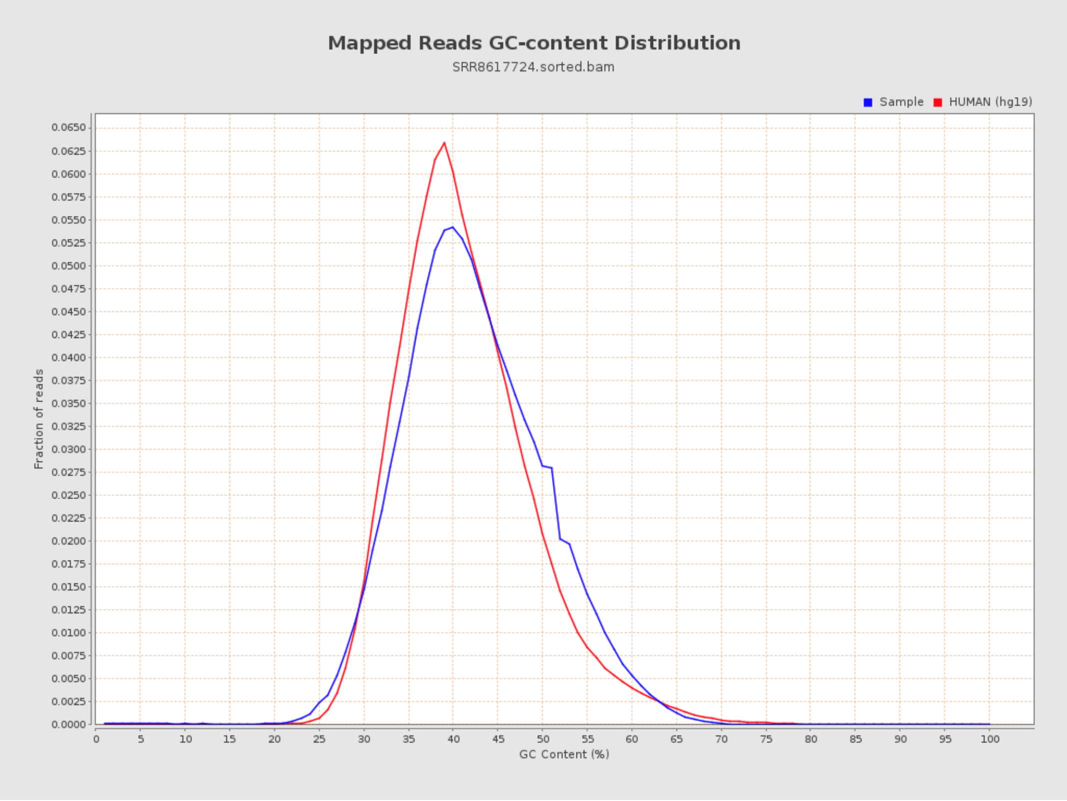
7. Results : Duplication Rate Histogram



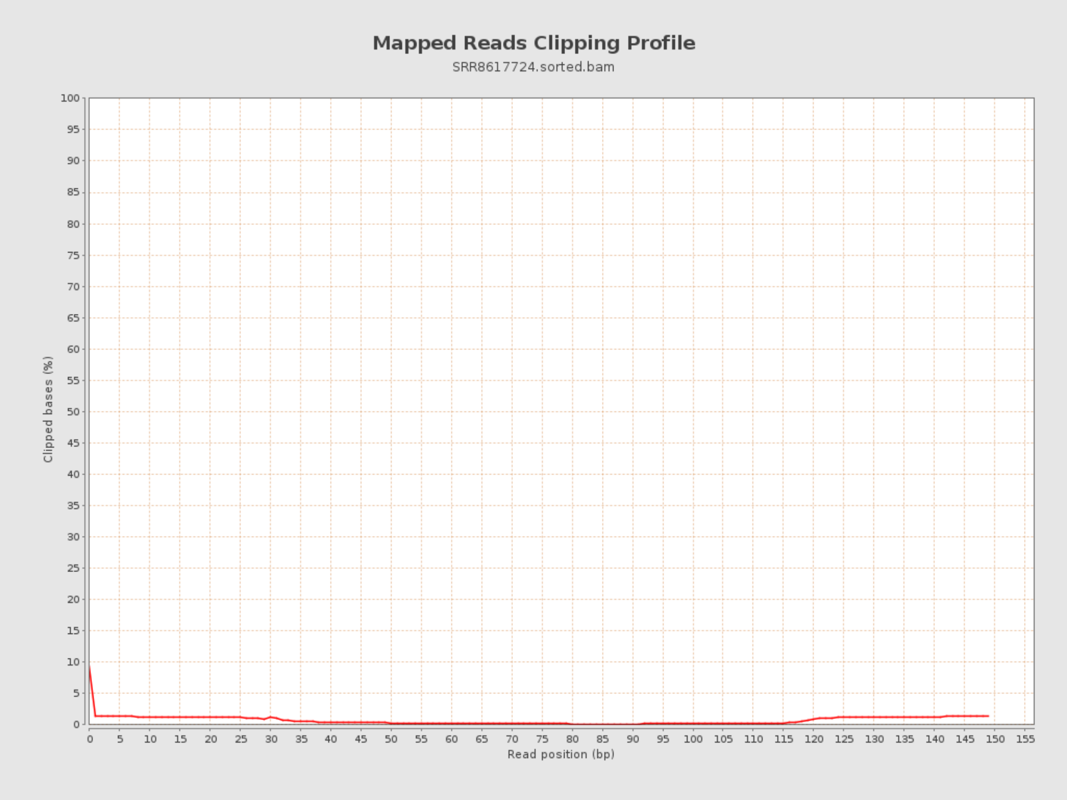
8. Results : Mapped Reads Nucleotide Content



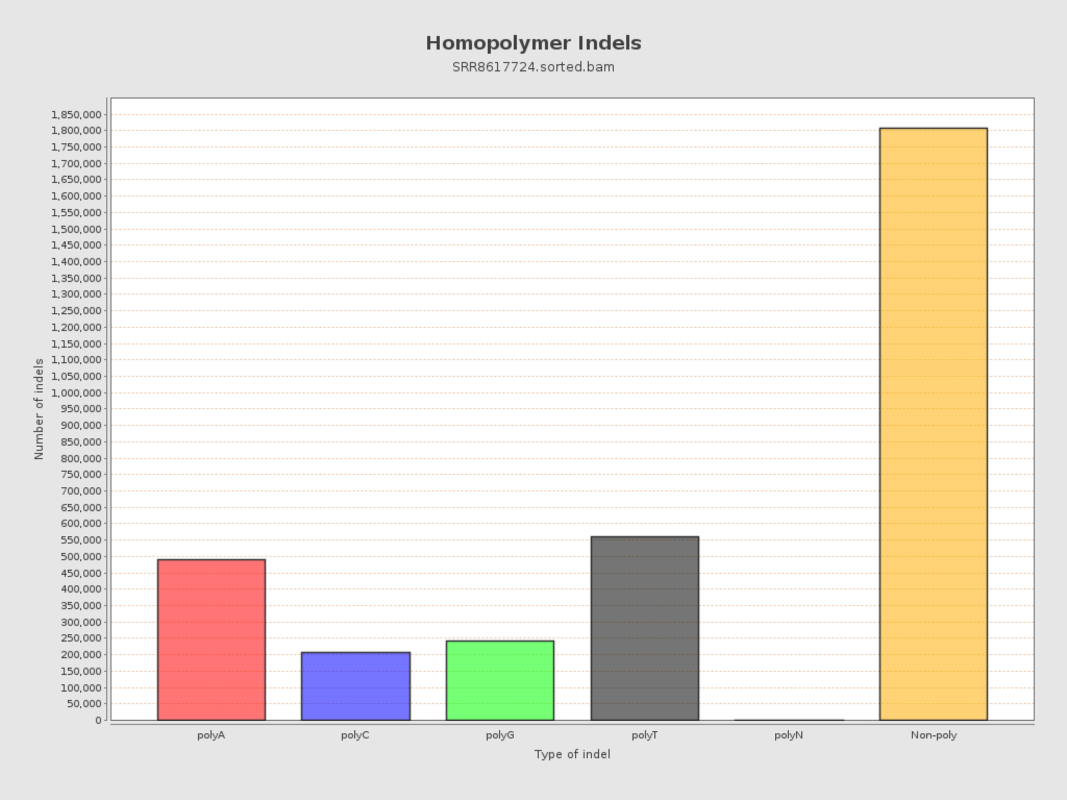
9. Results : Mapped Reads GC-content Distribution



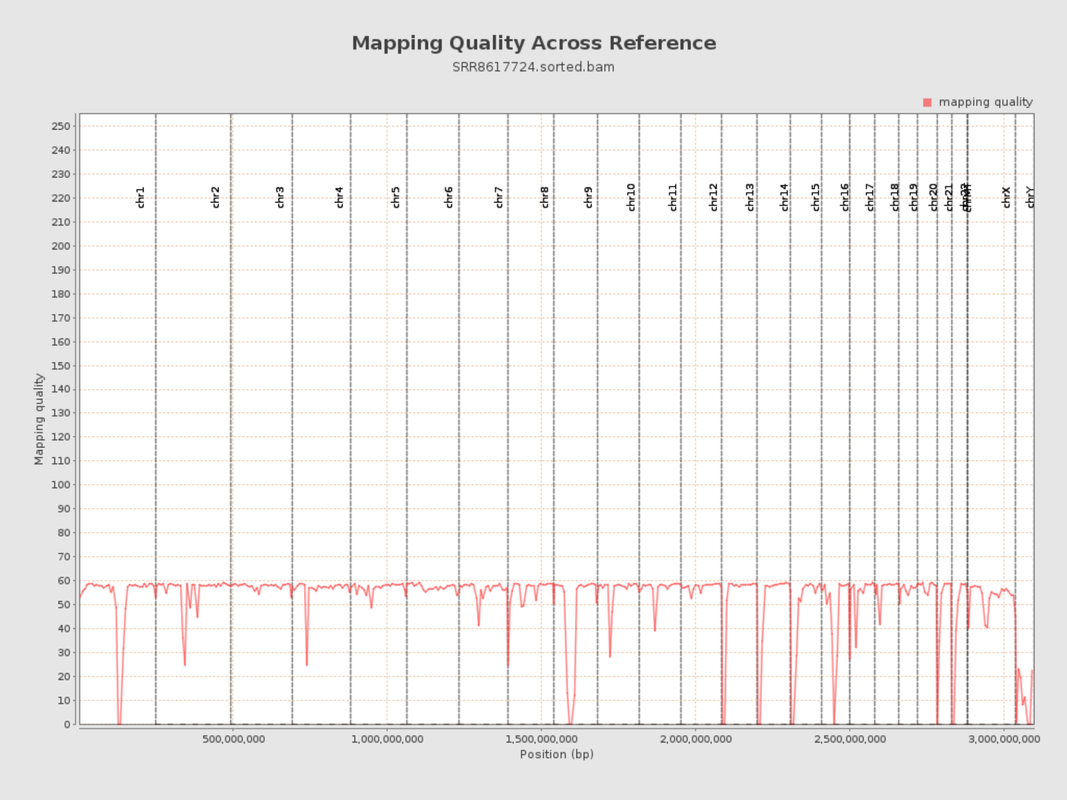
10. Results : Mapped Reads Clipping Profile



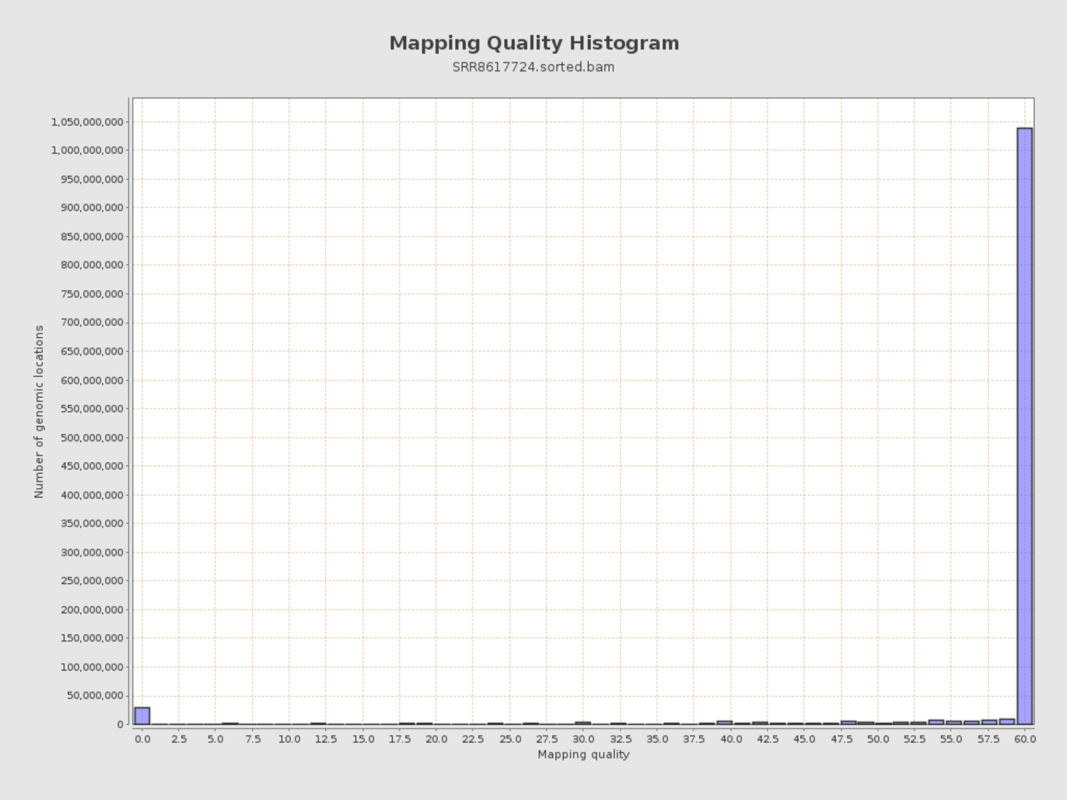
11. Results : Homopolymer Indels



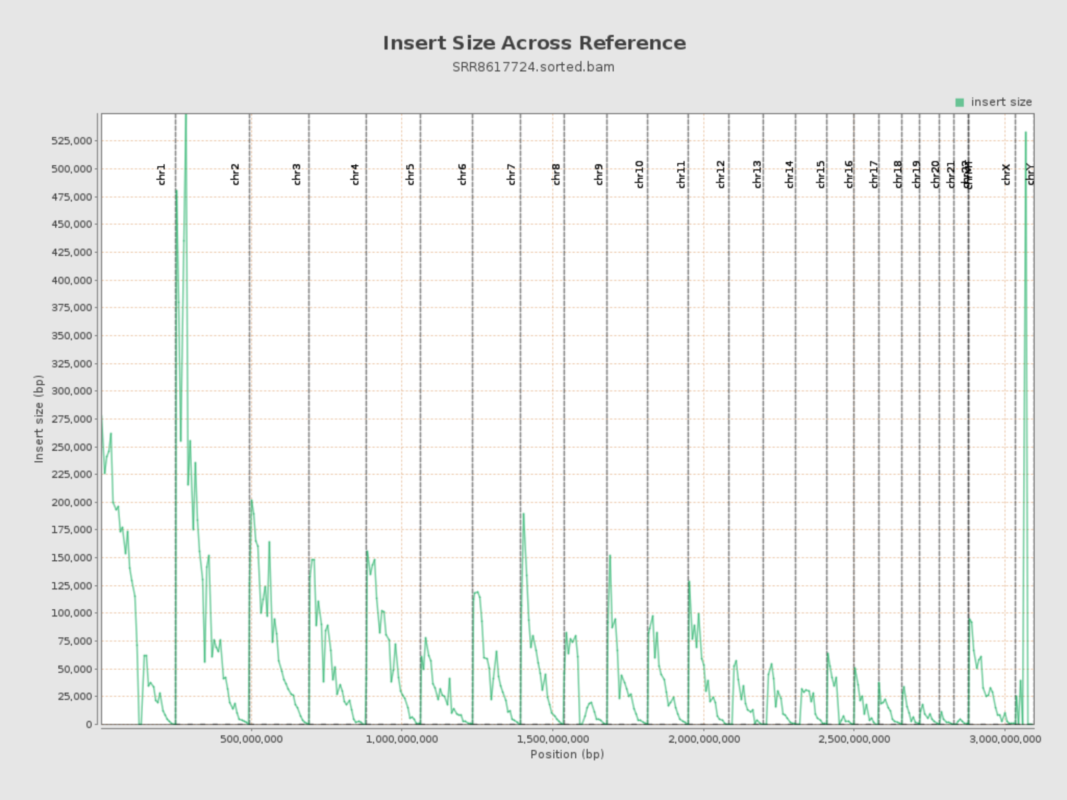
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram