Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 05:32:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617702.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_SRR8617702 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617702_1.fastq.gz SRR8617702_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 05:32:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617702.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	39,409,852
Mapped reads	38,006,063 / 96.44%
Unmapped reads	1,403,789 / 3.56%
Mapped paired reads	38,006,063 / 96.44%
Mapped reads, first in pair	19,334,190 / 49.06%
Mapped reads, second in pair	18,671,873 / 47.38%
Mapped reads, both in pair	37,121,564 / 94.19%
Mapped reads, singletons	884,499 / 2.24%
Secondary alignments	0
Supplementary alignments	1,366,318 / 3.47%
Read min/max/mean length	30 / 150 / 151.74
Duplicated reads (estimated)	10,765,816 / 27.32%
Duplication rate	16.63%
Clipped reads	18,642,659 / 47.3%

2.2. ACGT Content

Number/percentage of A's	1,489,926,801 / 29.02%
Number/percentage of C's	1,002,799,657 / 19.53%
Number/percentage of T's	1,518,207,703 / 29.57%
Number/percentage of G's	1,122,965,741 / 21.87%
Number/percentage of N's	20,685 / 0%

GC Percentage	41.41%

2.3. Coverage

Mean	1.6597
Standard Deviation	26.2251

2.4. Mapping Quality

Mean Mapping Quality	52.75

2.5. Insert size

Mean	257,528.92
Standard Deviation	4,703,382.04
P25/Median/P75	215 / 277 / 353

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	71,799,209
Insertions	974,380
Mapped reads with at least one insertion	2.39%
Deletions	1,960,375
Mapped reads with at least one deletion	4.94%
Homopolymer indels	45.07%

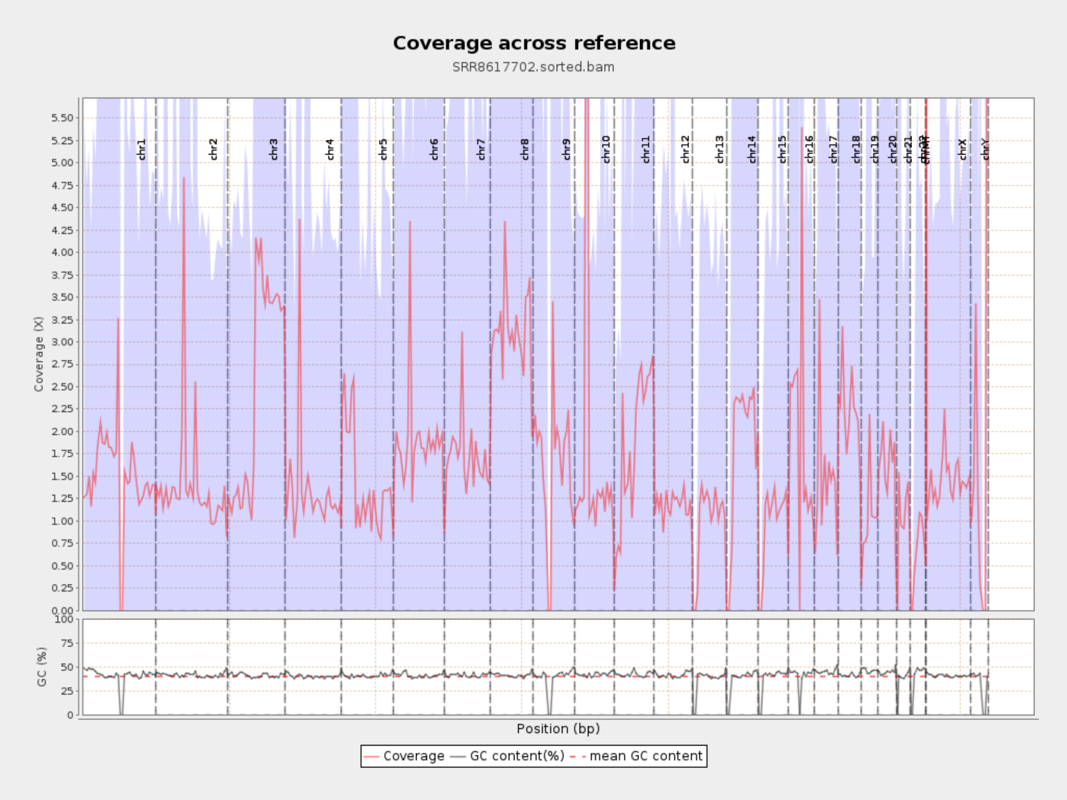
2.7. Chromosome stats

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

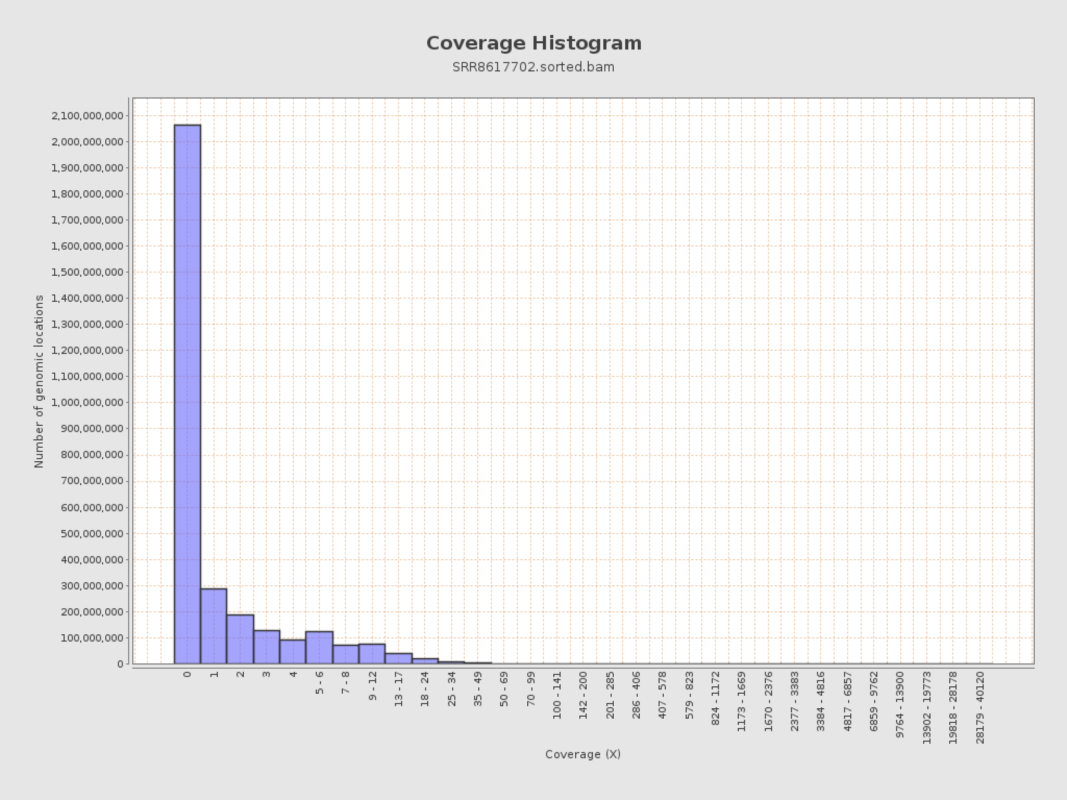
		bases	coverage	deviation
chr1	249250621	376002180	1.5085	27.5063
chr2	243199373	342248329	1.4073	24.1559
chr3	198022430	491408092	2.4816	5.8038
chr4	191154276	258409353	1.3518	20.2908
chr5	180915260	258642132	1.4296	3.9364
chr6	171115067	325449475	1.9019	26.4009
chr7	159138663	273221369	1.7169	21.9993
chr8	146364022	457221213	3.1239	13.2173
chr9	141213431	231471887	1.6392	36.9911
chr10	135534747	240457457	1.7741	83.3114
chr11	135006516	250047071	1.8521	11.0899
chr12	133851895	157756584	1.1786	6.9252
chr13	115169878	113314719	0.9839	2.7289
chr14	107349540	201027228	1.8726	4.7001
chr15	102531392	99102942	0.9666	4.5049
chr16	90354753	170712629	1.8894	27.6276
chr17	81195210	121030512	1.4906	24.0888
chr18	78077248	176167674	2.2563	30.4875
chr19	59128983	63010977	1.0657	15.0238
chr20	63025520	105053700	1.6668	7.2483
chr21	48129895	50435859	1.0479	10.0858
chr22	51304566	33549147	0.6539	3.2049
chrMT	16571	783997	47.3114	29.0465
chrX	155270560	224058013	1.443	6.1506

chrY	59373566	117337404	1.9763	42.8156

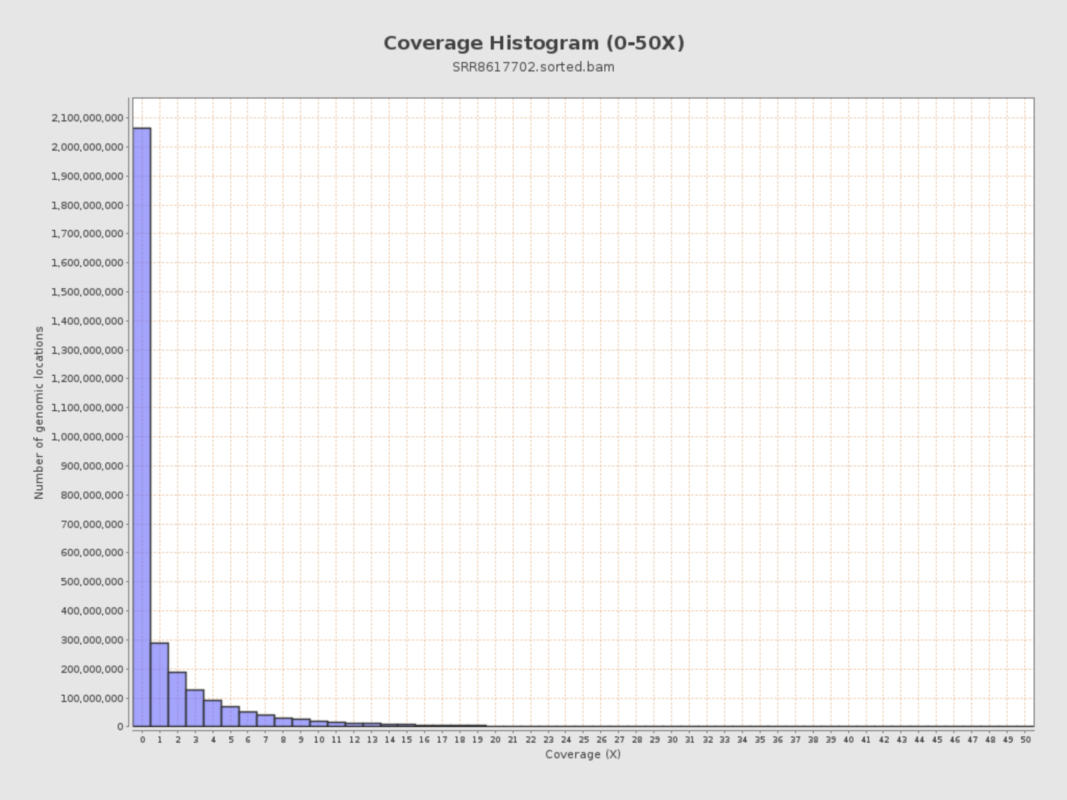
3. Results : Coverage across reference



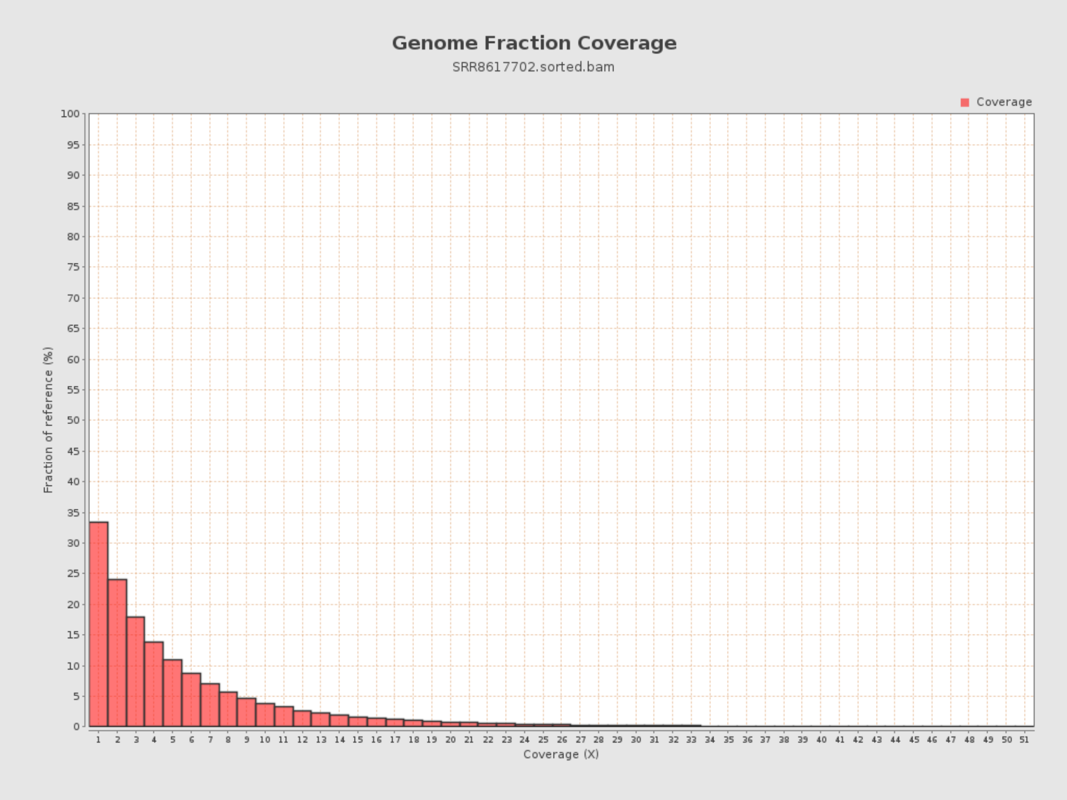
4. Results : Coverage Histogram



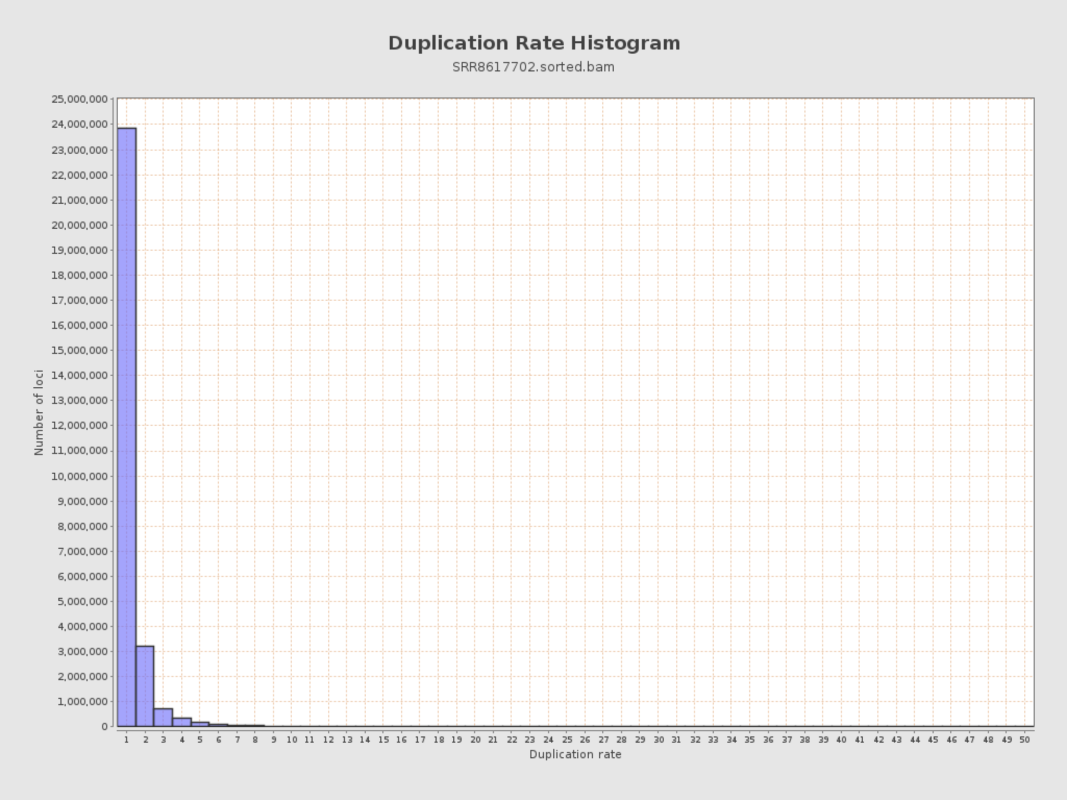
5. Results : Coverage Histogram (0-50X)



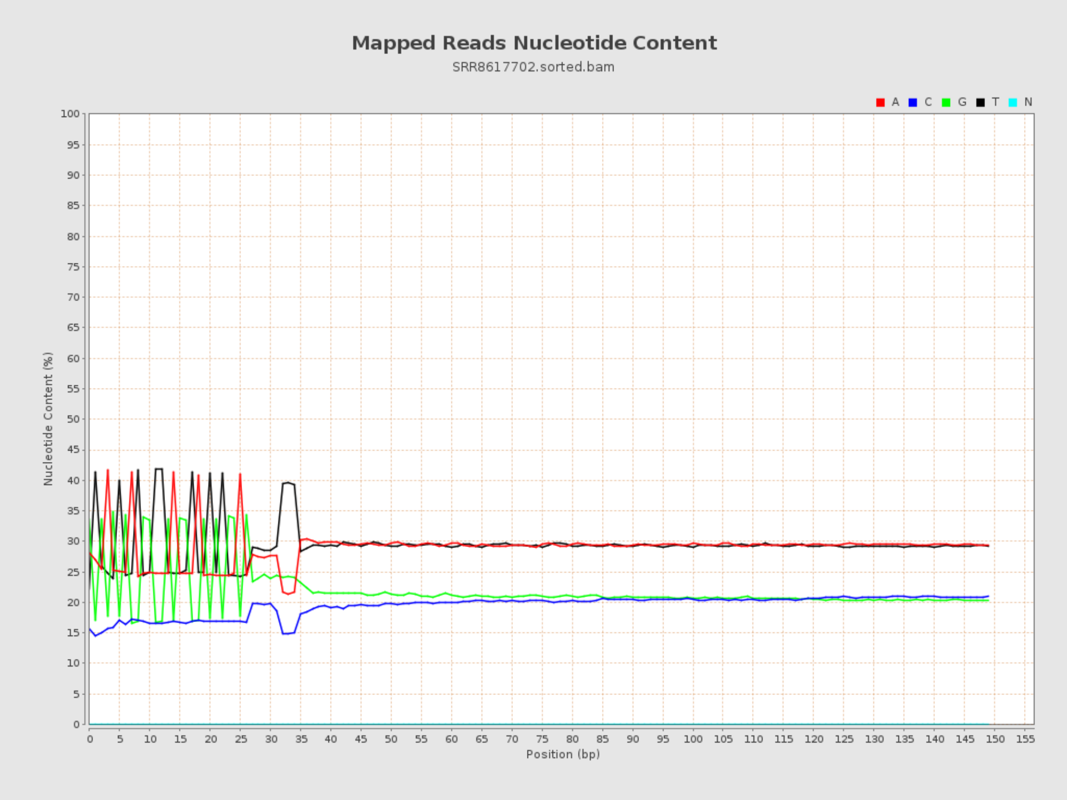
6. Results : Genome Fraction Coverage



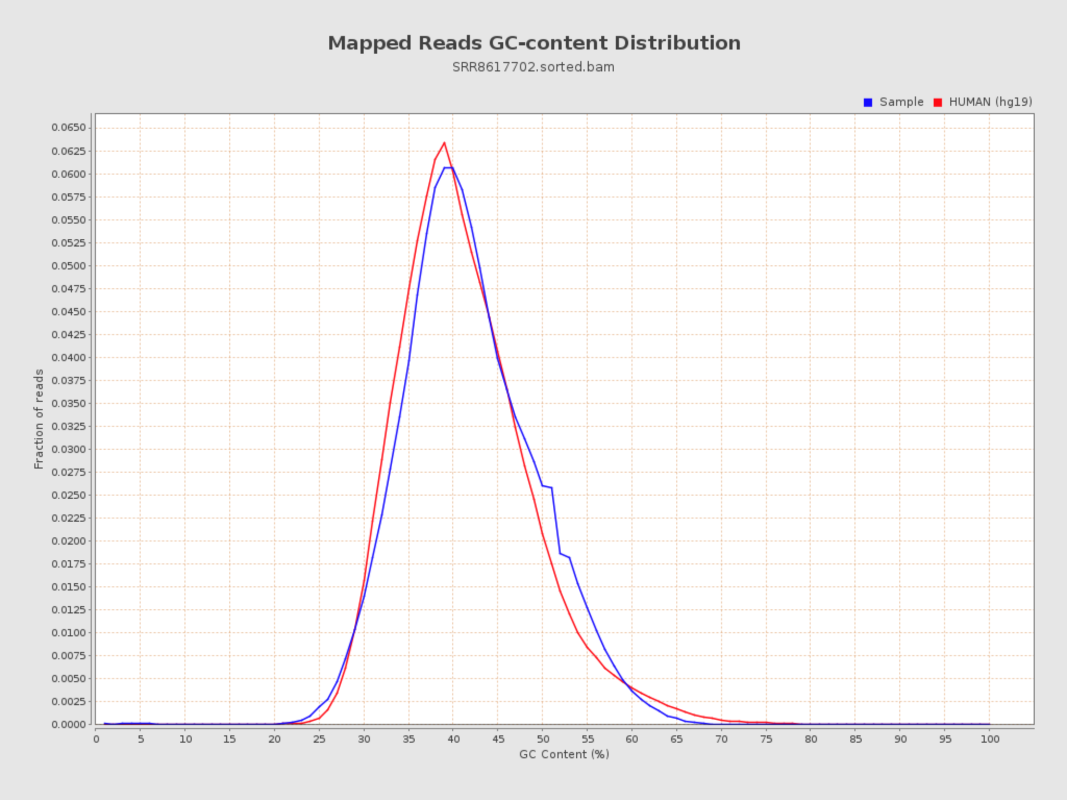
7. Results : Duplication Rate Histogram



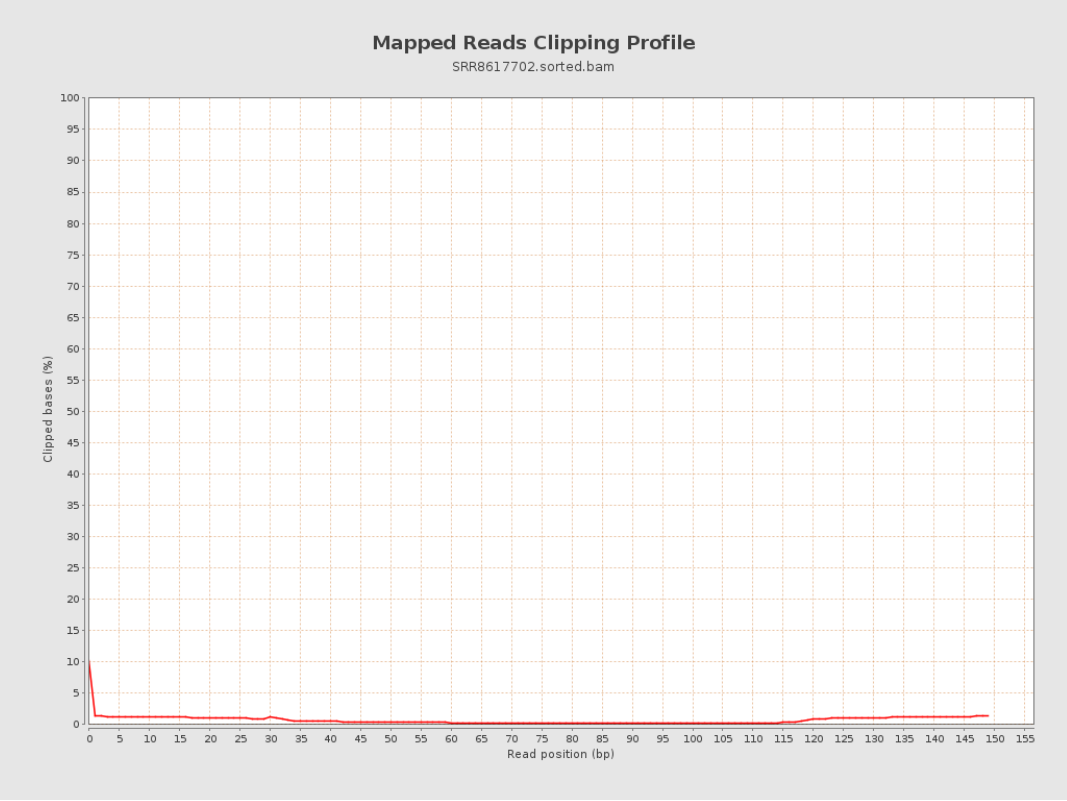
8. Results : Mapped Reads Nucleotide Content



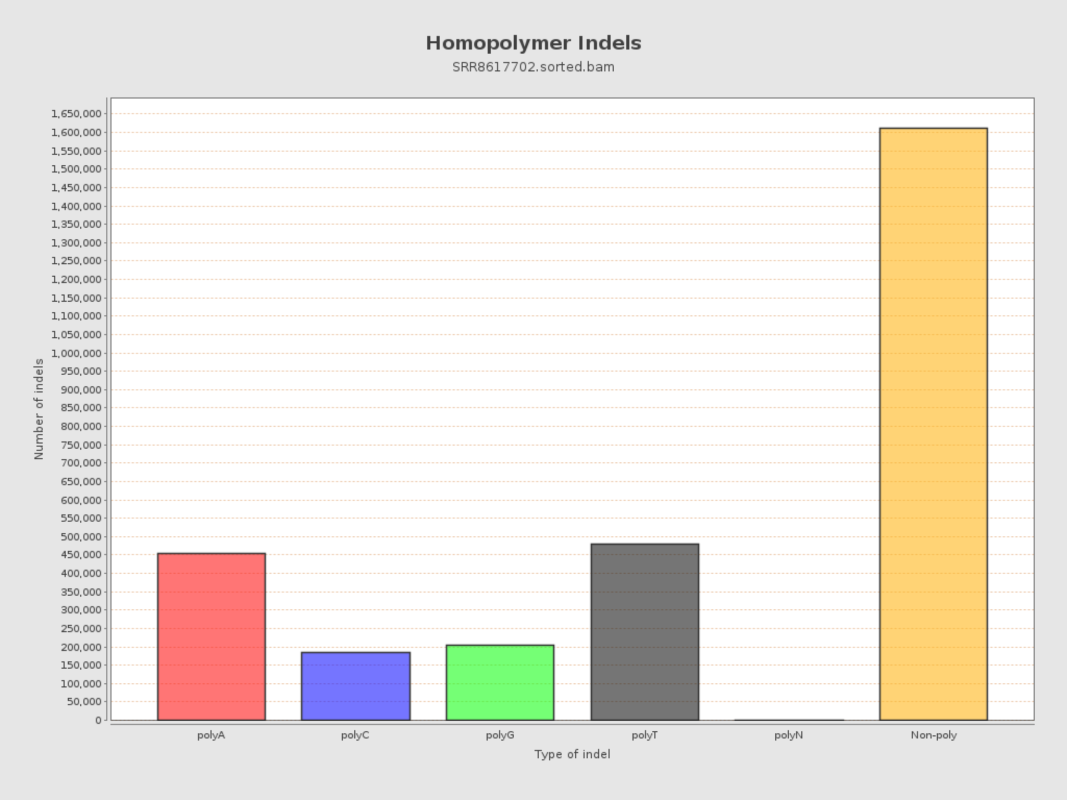
9. Results : Mapped Reads GC-content Distribution



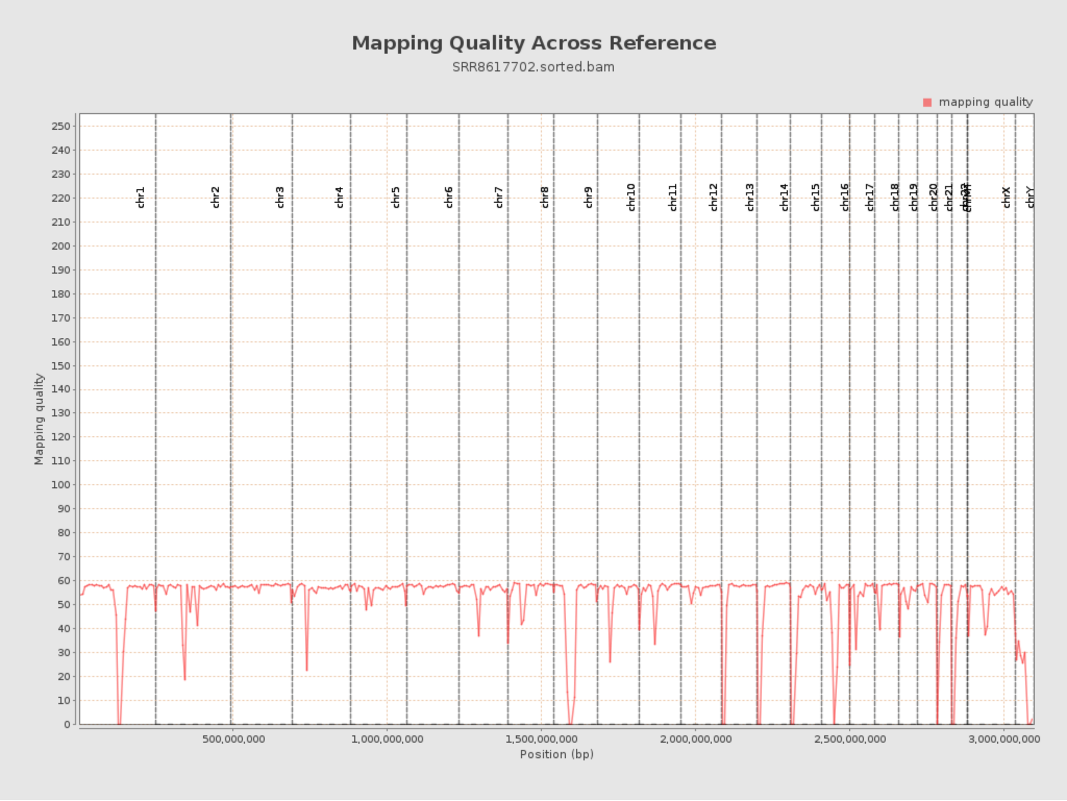
10. Results : Mapped Reads Clipping Profile



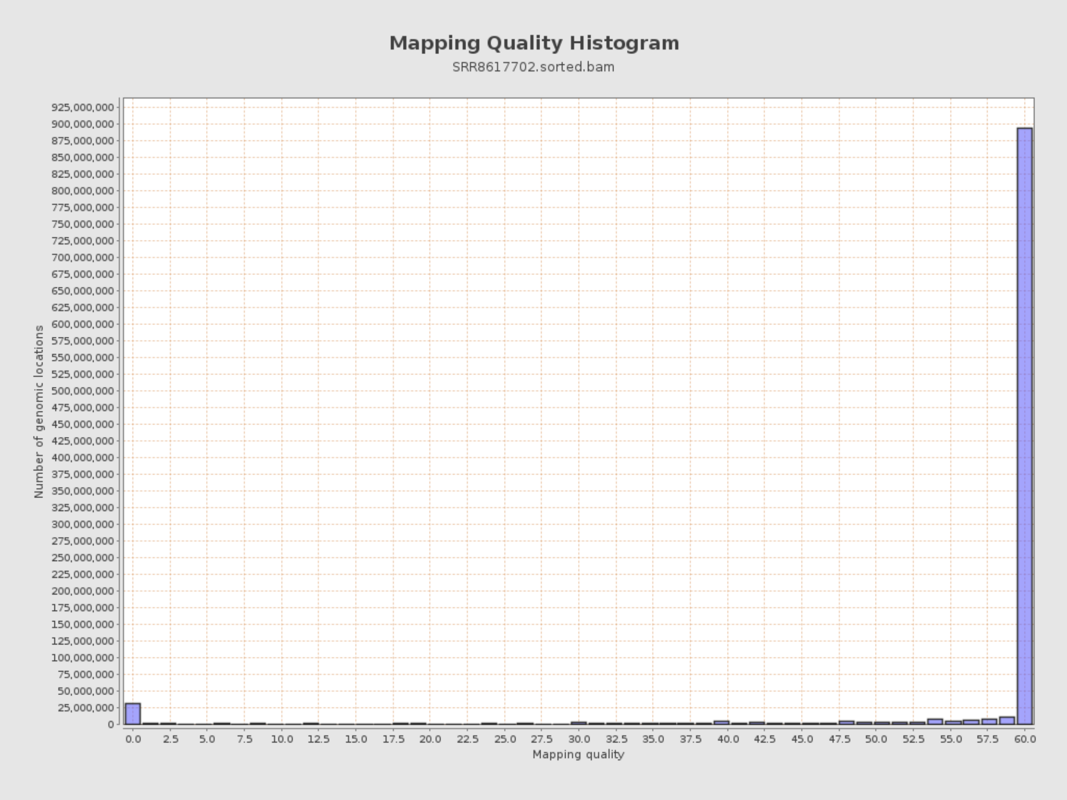
11. Results : Homopolymer Indels



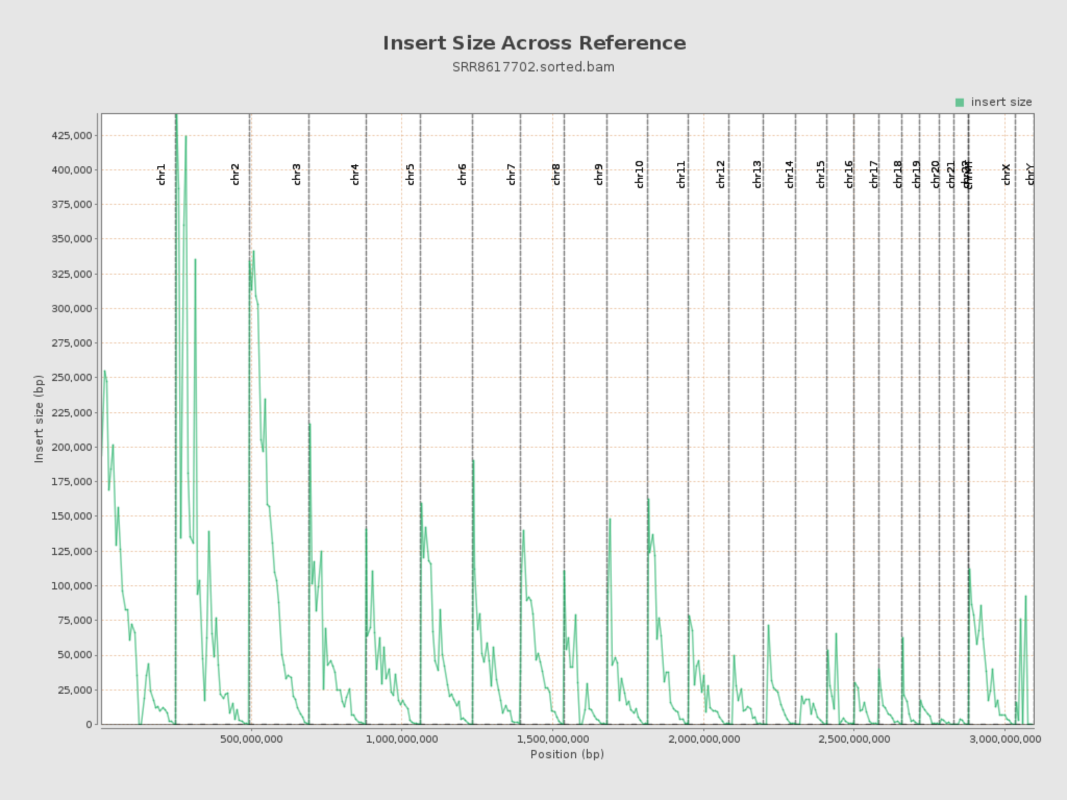
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram