Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/22 20:28:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617655.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_SRR8617655 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617655_1.fastq.gz SRR8617655_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 22 20:28:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617655.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,583,290
Mapped reads	37,756,200 / 97.86%
Unmapped reads	827,090 / 2.14%
Mapped paired reads	37,756,200 / 97.86%
Mapped reads, first in pair	19,062,343 / 49.41%
Mapped reads, second in pair	18,693,857 / 48.45%
Mapped reads, both in pair	37,273,744 / 96.61%
Mapped reads, singletons	482,456 / 1.25%
Secondary alignments	0
Supplementary alignments	441,165 / 1.14%
Read min/max/mean length	30 / 150 / 150.54
Duplicated reads (estimated)	10,452,687 / 27.09%
Duplication rate	20.95%
Clipped reads	17,307,880 / 44.86%

2.2. ACGT Content

Number/percentage of A's	1,486,890,418 / 29.09%
Number/percentage of C's	968,952,361 / 18.96%
Number/percentage of T's	1,524,477,243 / 29.82%
Number/percentage of G's	1,131,063,322 / 22.13%
Number/percentage of N's	205,107 / 0%

GC Percentage	41.08%

2.3. Coverage

Mean	1.6522
Standard Deviation	14.6772

2.4. Mapping Quality

Mean Mapping Quality	53.82

2.5. Insert size

Mean	76,923.48
Standard Deviation	2,670,854.1
P25/Median/P75	225 / 279 / 349

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	58,464,547
Insertions	754,587
Mapped reads with at least one insertion	1.91%
Deletions	1,758,435
Mapped reads with at least one deletion	4.5%
Homopolymer indels	47.78%

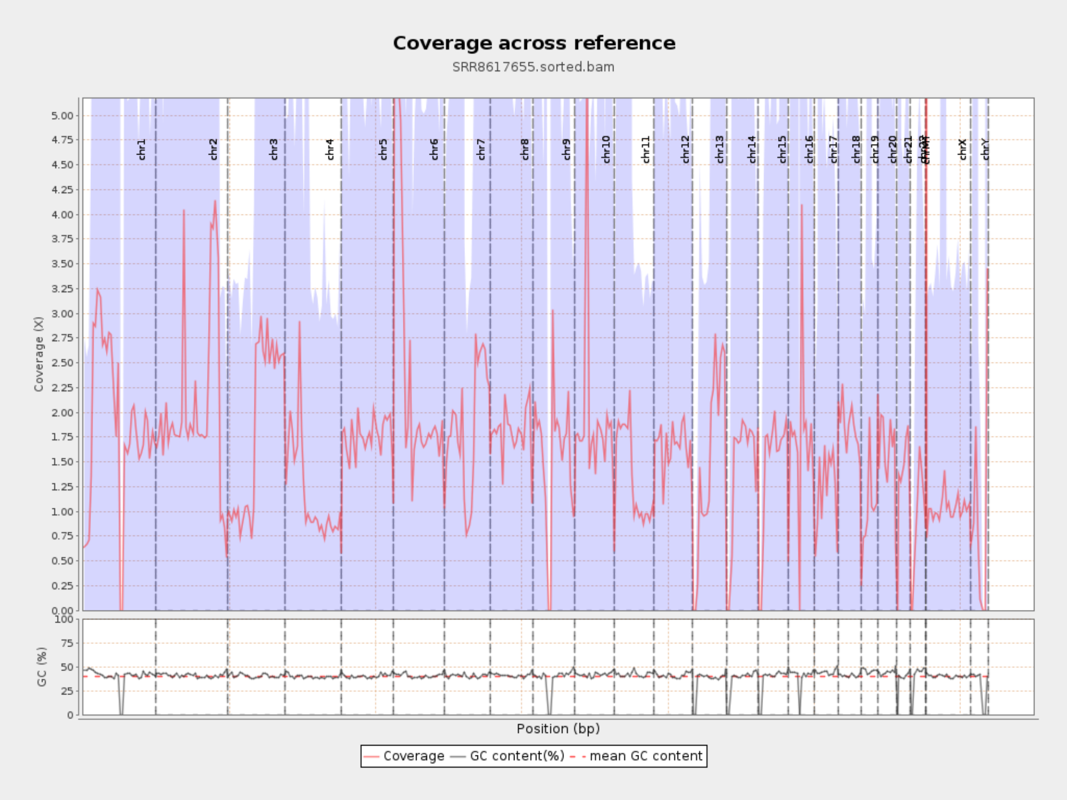
2.7. Chromosome stats

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

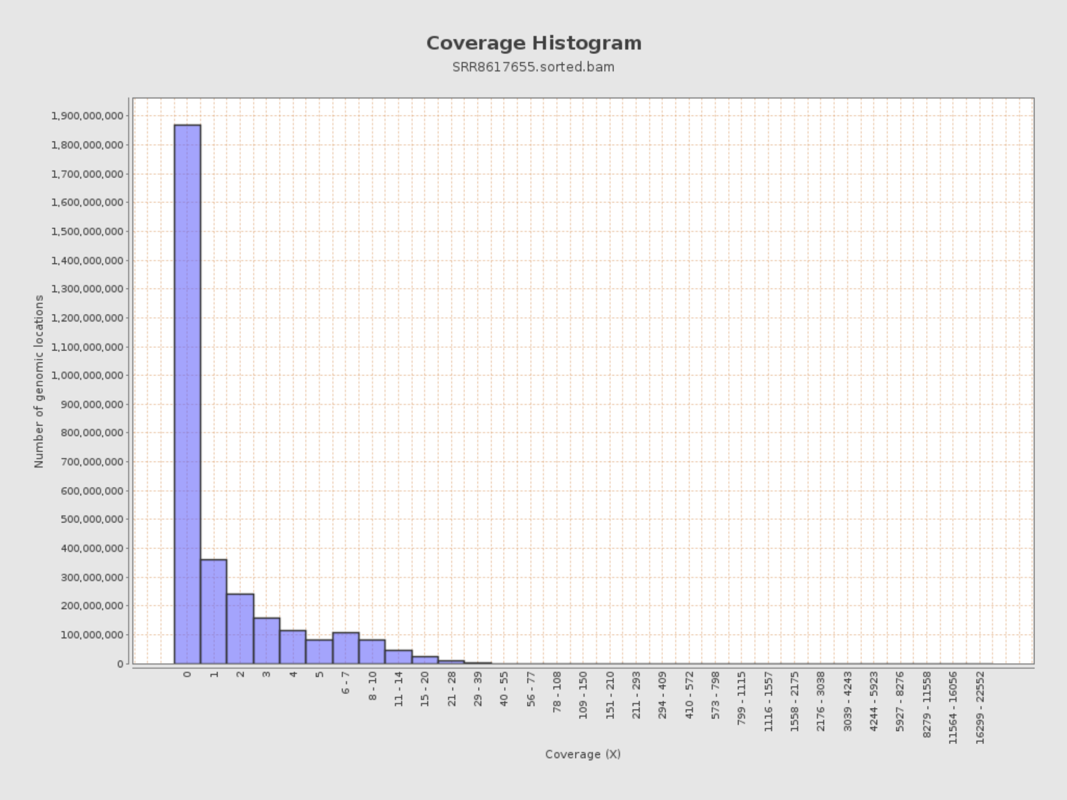
		bases	coverage	deviation
chr1	249250621	468347183	1.879	14.8155
chr2	243199373	503232063	2.0692	15.7368
chr3	198022430	360194660	1.819	3.6247
chr4	191154276	229006407	1.198	9.6215
chr5	180915260	317400159	1.7544	3.3794
chr6	171115067	411845946	2.4068	11.64
chr7	159138663	295465800	1.8567	16.3797
chr8	146364022	263846313	1.8027	5.4583
chr9	141213431	221582983	1.5691	32.0719
chr10	135534747	263649189	1.9453	33.2041
chr11	135006516	183654112	1.3603	15.7195
chr12	133851895	222975583	1.6658	5.9141
chr13	115169878	177430732	1.5406	3.2856
chr14	107349540	152631391	1.4218	3.2663
chr15	102531392	146922658	1.433	3.7879
chr16	90354753	153935533	1.7037	18.282
chr17	81195210	100500899	1.2378	13.1334
chr18	78077248	145045787	1.8577	23.5913
chr19	59128983	63310434	1.0707	9.75
chr20	63025520	103850692	1.6478	4.292
chr21	48129895	64396842	1.338	5.8471
chr22	51304566	47022224	0.9165	2.6479
chrMT	16571	877661	52.9637	34.3245
chrX	155270560	159169776	1.0251	4.4416

chrY	59373566	58496047	0.9852	19.5847

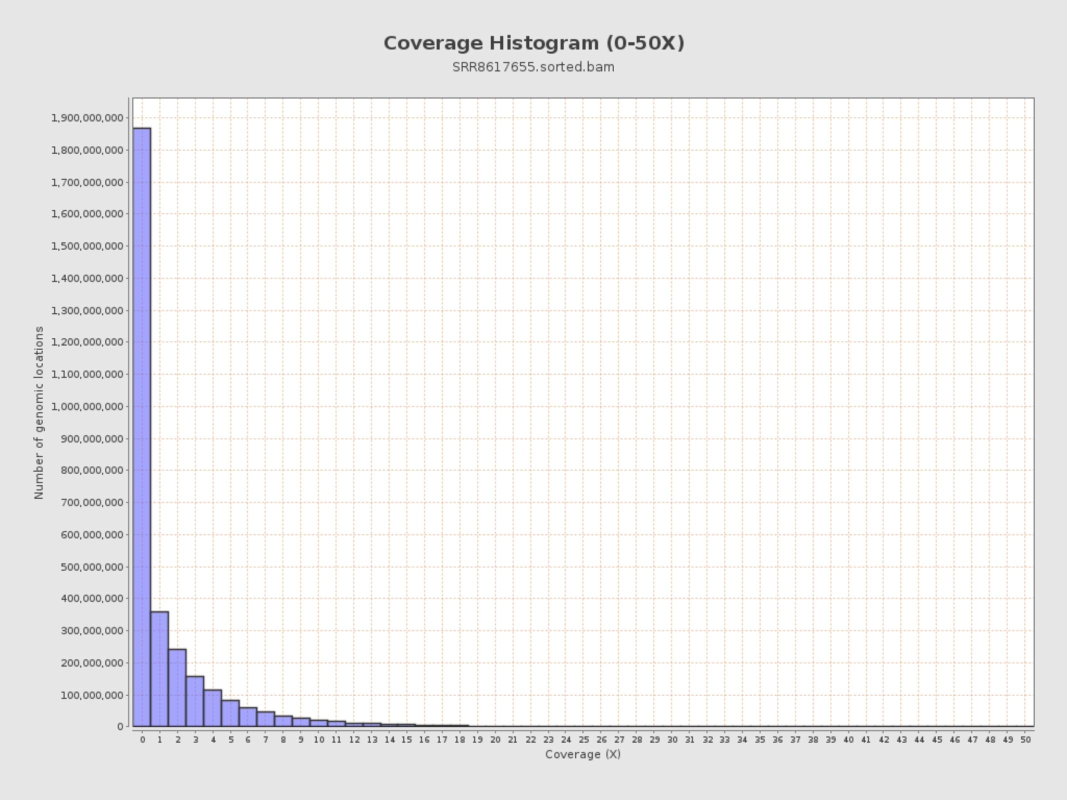
3. Results : Coverage across reference



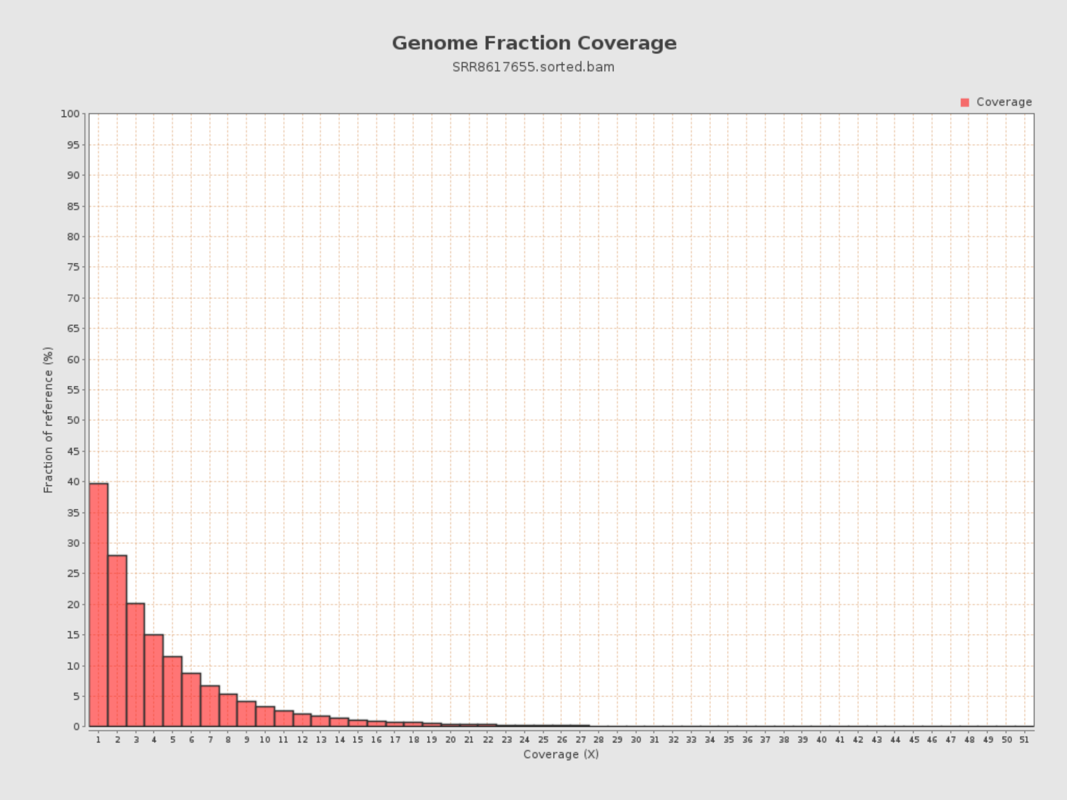
4. Results : Coverage Histogram



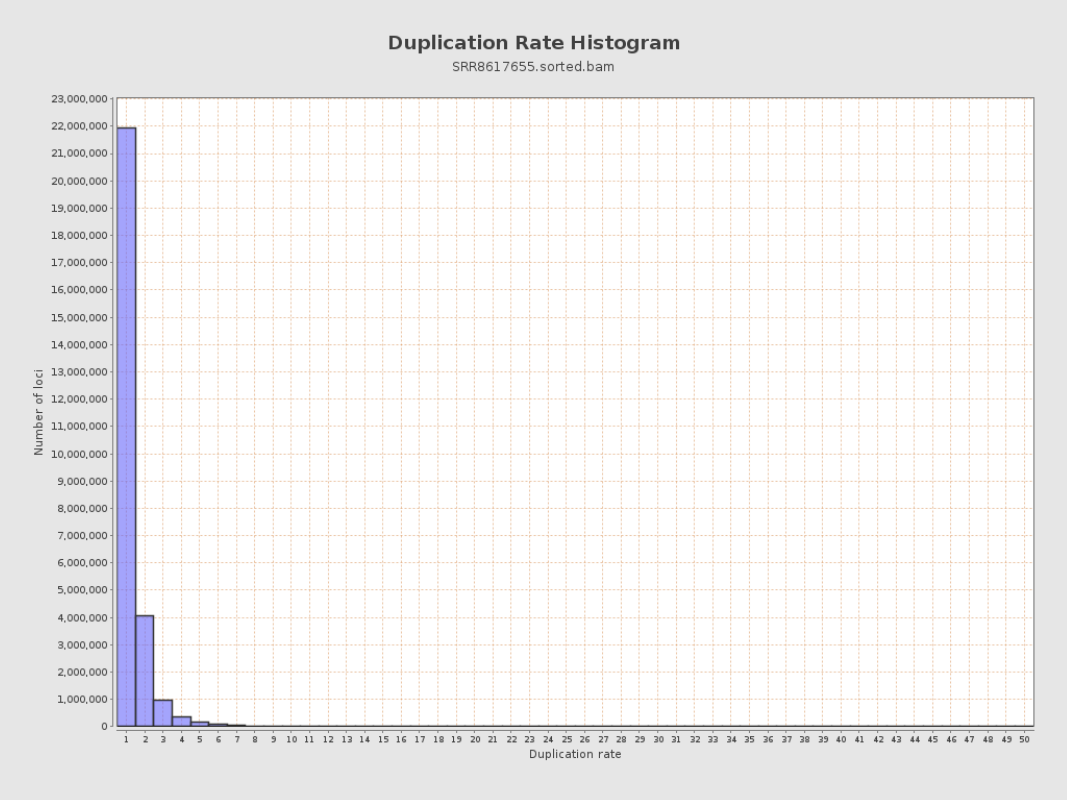
5. Results : Coverage Histogram (0-50X)



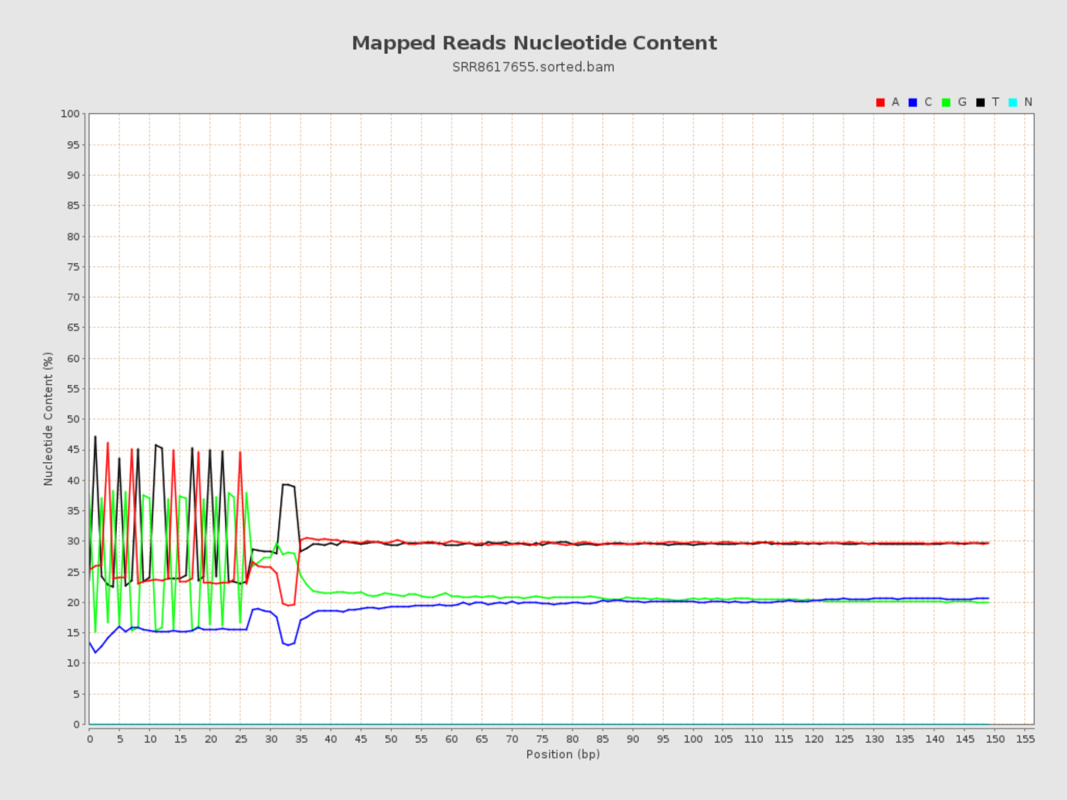
6. Results : Genome Fraction Coverage



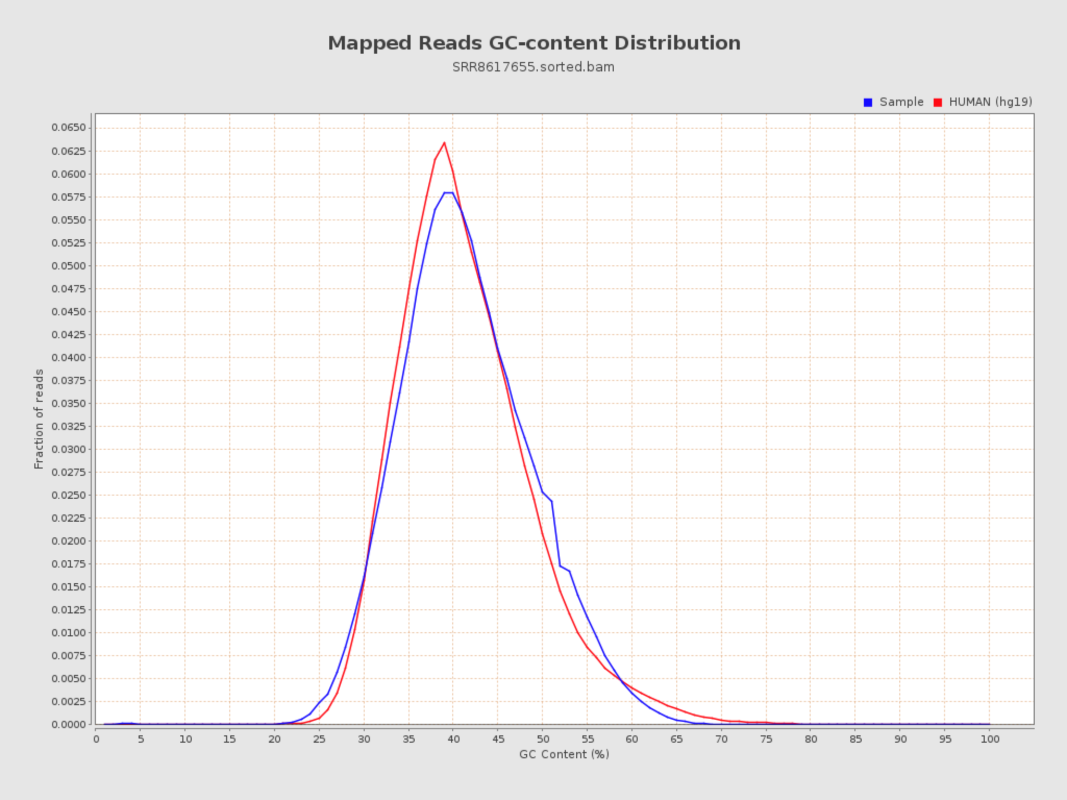
7. Results : Duplication Rate Histogram



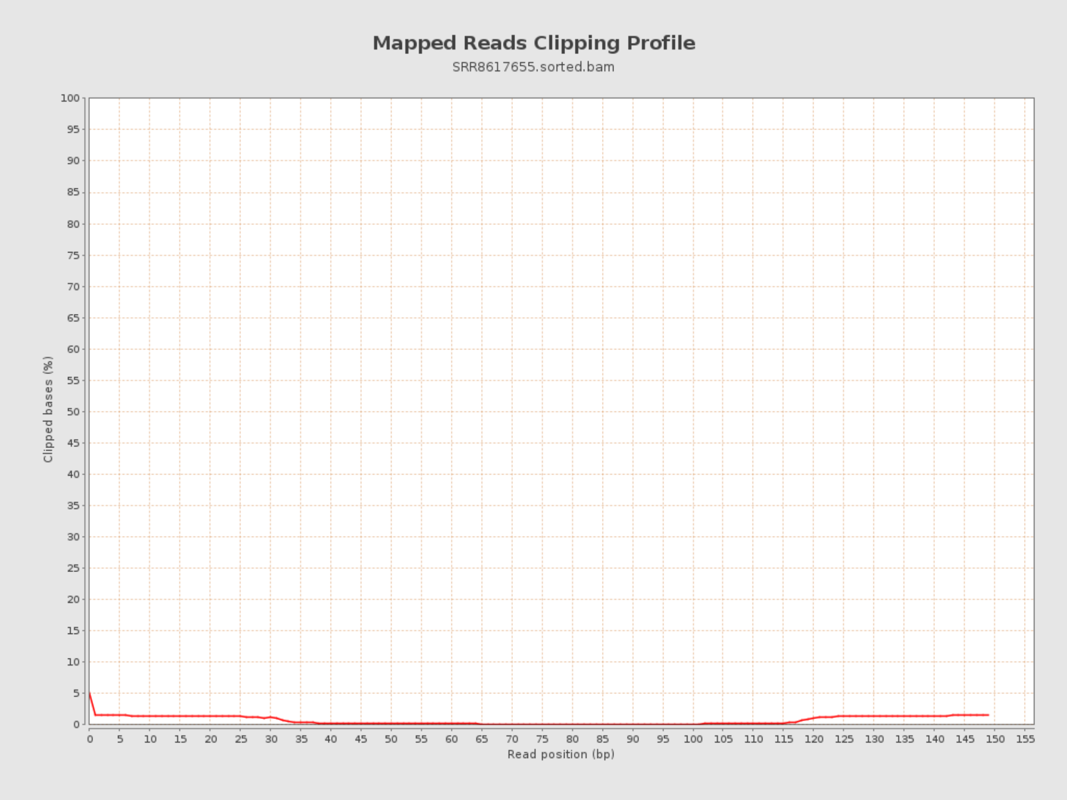
8. Results : Mapped Reads Nucleotide Content



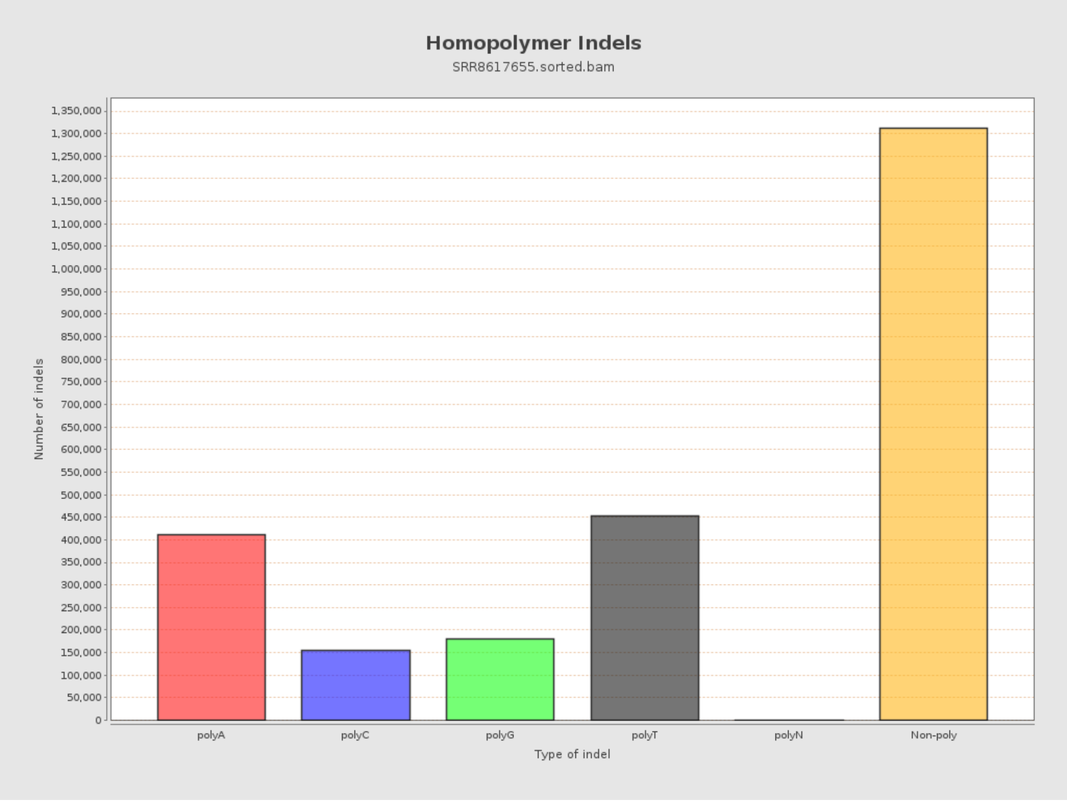
9. Results : Mapped Reads GC-content Distribution



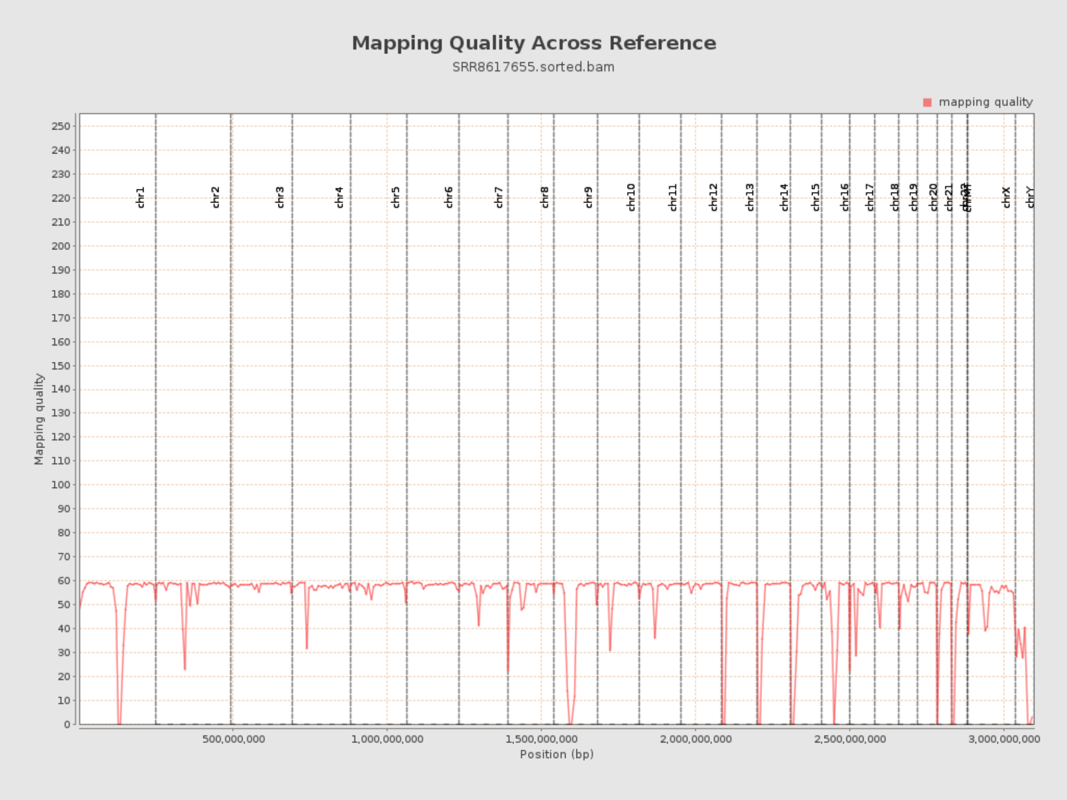
10. Results : Mapped Reads Clipping Profile



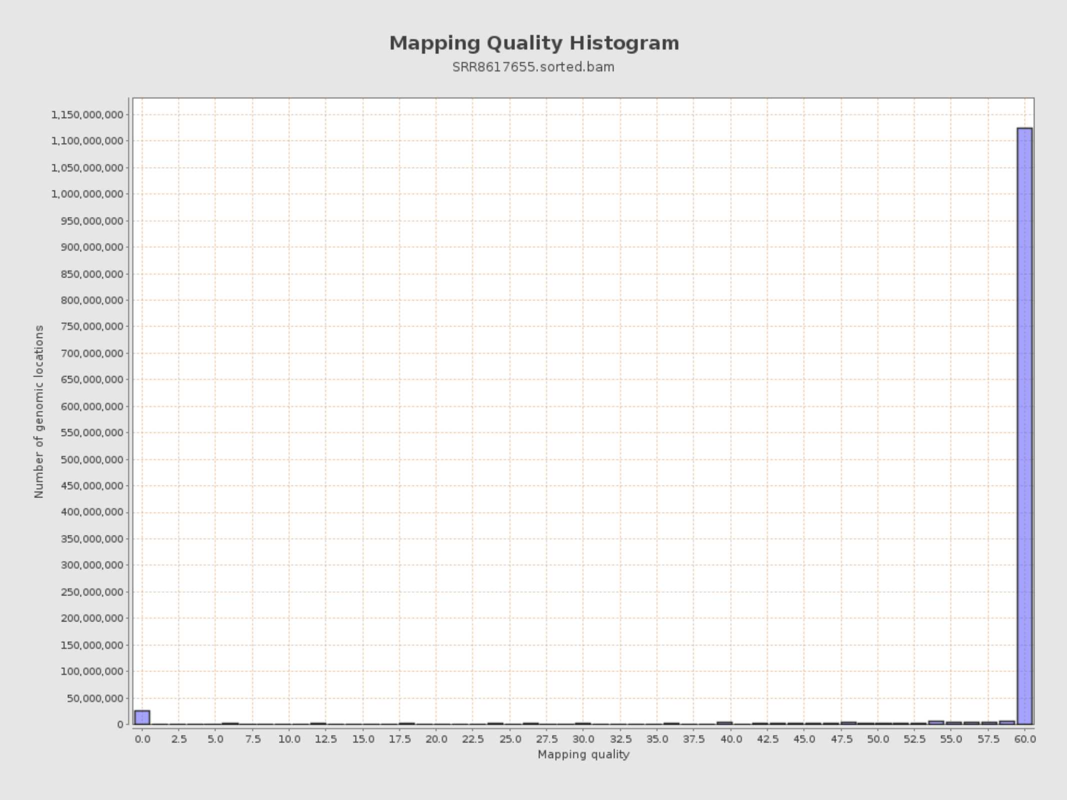
11. Results : Homopolymer Indels



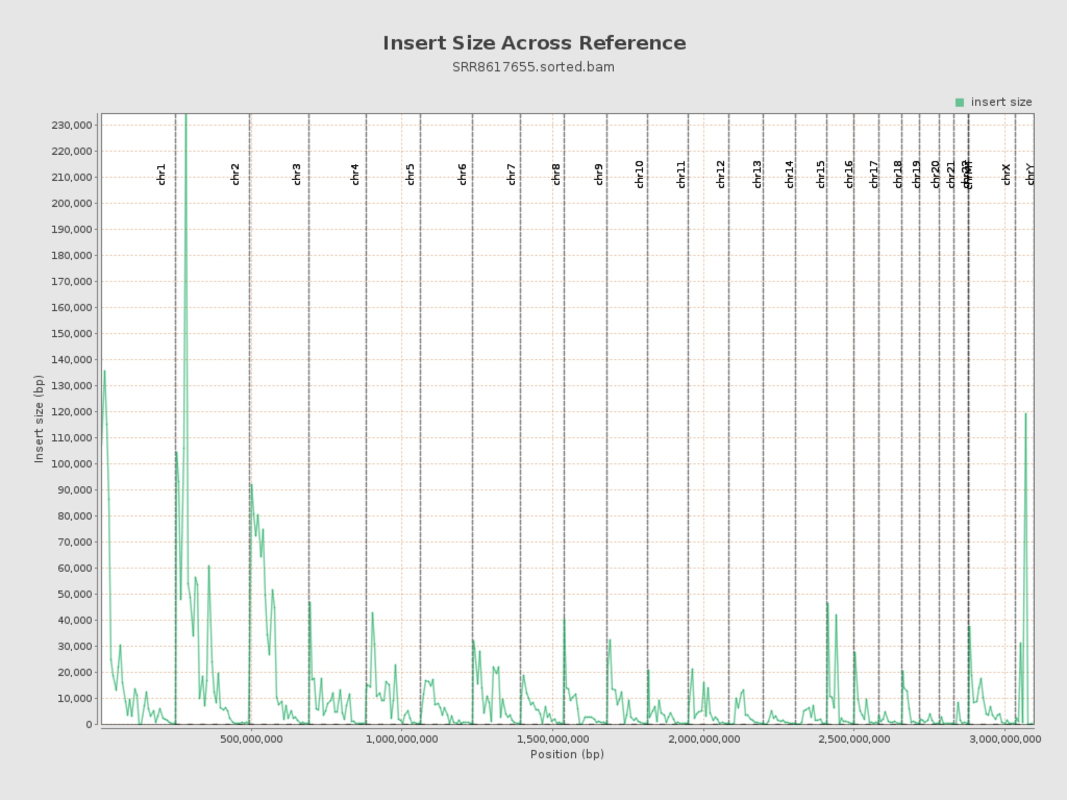
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram