Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 09:19:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617732.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_SRR8617732 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617732_1.fastq.gz SRR8617732_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 09:19:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617732.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,073,224
Mapped reads	34,355,656 / 97.95%
Unmapped reads	717,568 / 2.05%
Mapped paired reads	34,355,656 / 97.95%
Mapped reads, first in pair	17,327,113 / 49.4%
Mapped reads, second in pair	17,028,543 / 48.55%
Mapped reads, both in pair	33,928,632 / 96.74%
Mapped reads, singletons	427,024 / 1.22%
Secondary alignments	0
Supplementary alignments	1,351,817 / 3.85%
Read min/max/mean length	30 / 150 / 151.87
Duplicated reads (estimated)	11,633,522 / 33.17%
Duplication rate	22.94%
Clipped reads	20,981,839 / 59.82%

2.2. ACGT Content

Number/percentage of A's	1,324,422,456 / 29.38%
Number/percentage of C's	840,338,134 / 18.64%
Number/percentage of T's	1,358,884,287 / 30.14%
Number/percentage of G's	984,376,646 / 21.84%
Number/percentage of N's	166,559 / 0%

GC Percentage	40.48%

2.3. Coverage

Mean	1.4574
Standard Deviation	15.339

2.4. Mapping Quality

Mean Mapping Quality	52.87

2.5. Insert size

Mean	296,742.61
Standard Deviation	5,278,936.17
P25/Median/P75	209 / 278 / 354

2.6. Mismatches and indels

General error rate	1.28%
Mismatches	55,328,004
Insertions	866,908
Mapped reads with at least one insertion	2.37%
Deletions	1,861,018
Mapped reads with at least one deletion	5.19%
Homopolymer indels	45.89%

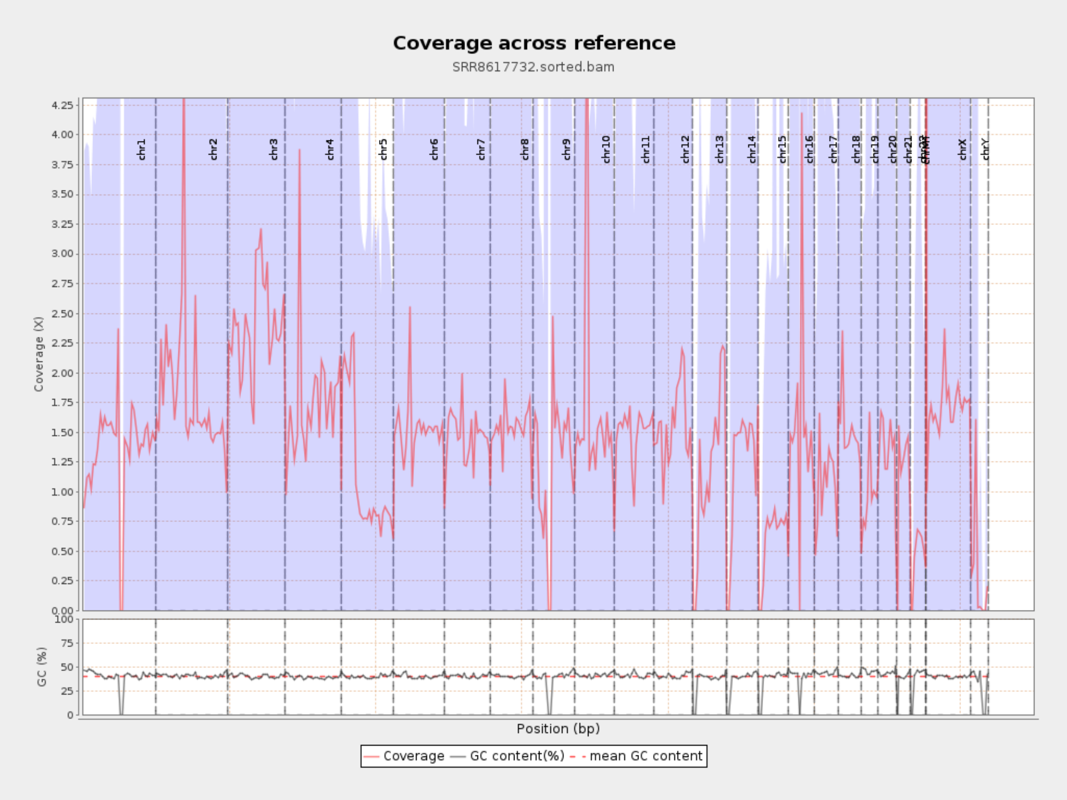
2.7. Chromosome stats

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

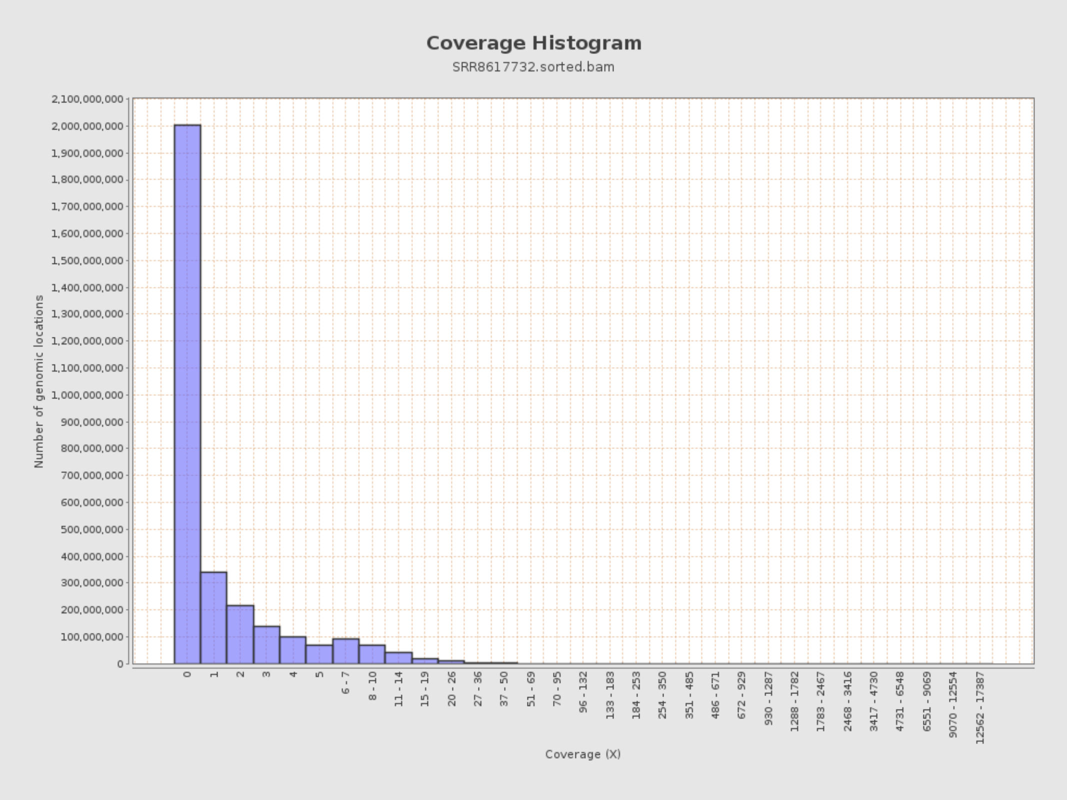
		bases	coverage	deviation
chr1	249250621	337563207	1.3543	15.9729
chr2	243199373	447091255	1.8384	21.1806
chr3	198022430	472980754	2.3885	4.4143
chr4	191154276	334110429	1.7479	16.9284
chr5	180915260	207405495	1.1464	3.3728
chr6	171115067	263219282	1.5383	11.9033
chr7	159138663	233449677	1.467	14.4965
chr8	146364022	223824509	1.5292	5.4123
chr9	141213431	174372654	1.2348	28.0553
chr10	135534747	224048786	1.6531	32.0273
chr11	135006516	200963611	1.4885	10.3404
chr12	133851895	208010352	1.554	8.2153
chr13	115169878	139329980	1.2098	2.9478
chr14	107349540	129982610	1.2108	3.3726
chr15	102531392	61373848	0.5986	3.9758
chr16	90354753	135994416	1.5051	21.5836
chr17	81195210	86389699	1.064	14.7519
chr18	78077248	120067192	1.5378	23.6589
chr19	59128983	57361339	0.9701	9.2134
chr20	63025520	87496858	1.3883	5.798
chr21	48129895	57415378	1.1929	8.5215
chr22	51304566	23419772	0.4565	2.5964
chrMT	16571	1770639	106.8517	58.629
chrX	155270560	265049453	1.707	6.3179

chrY	59373566	19104585	0.3218	23.9726

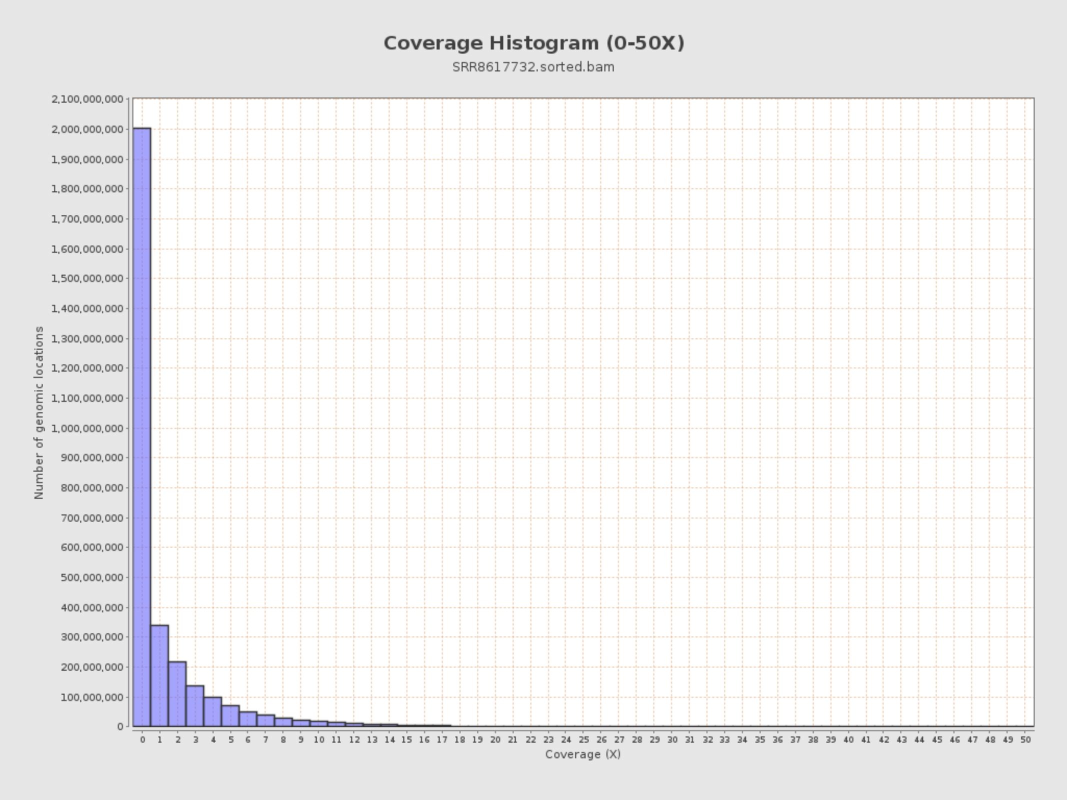
3. Results : Coverage across reference



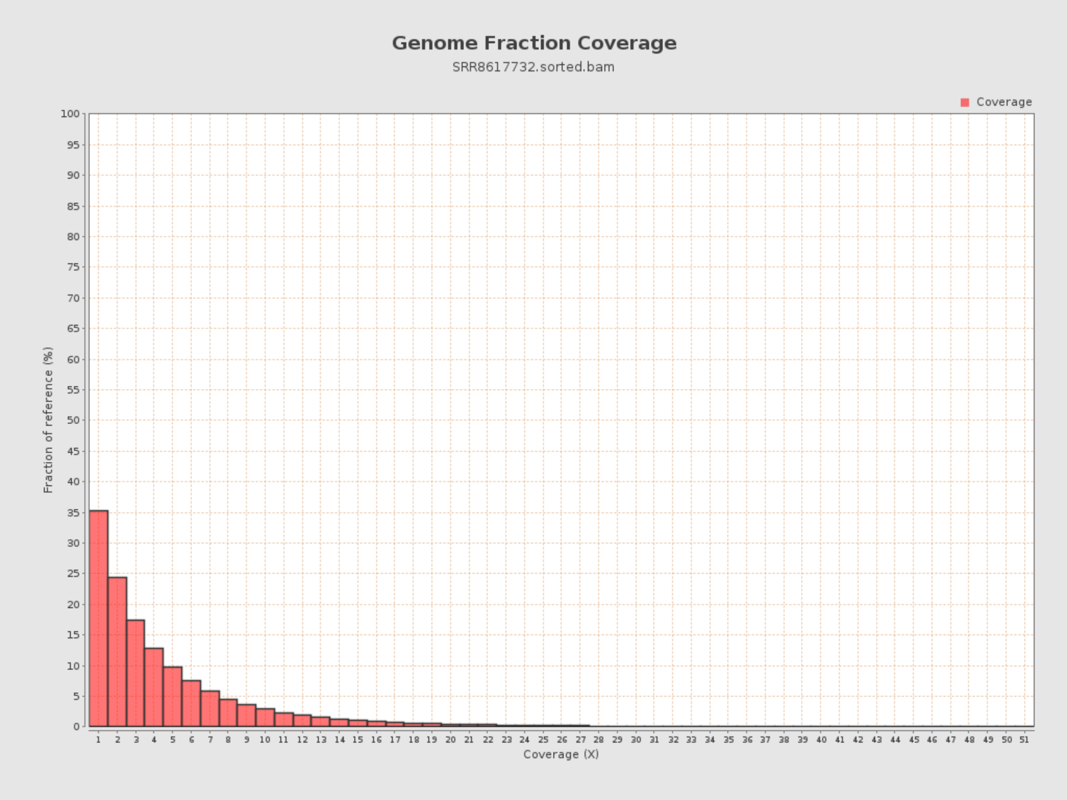
4. Results : Coverage Histogram



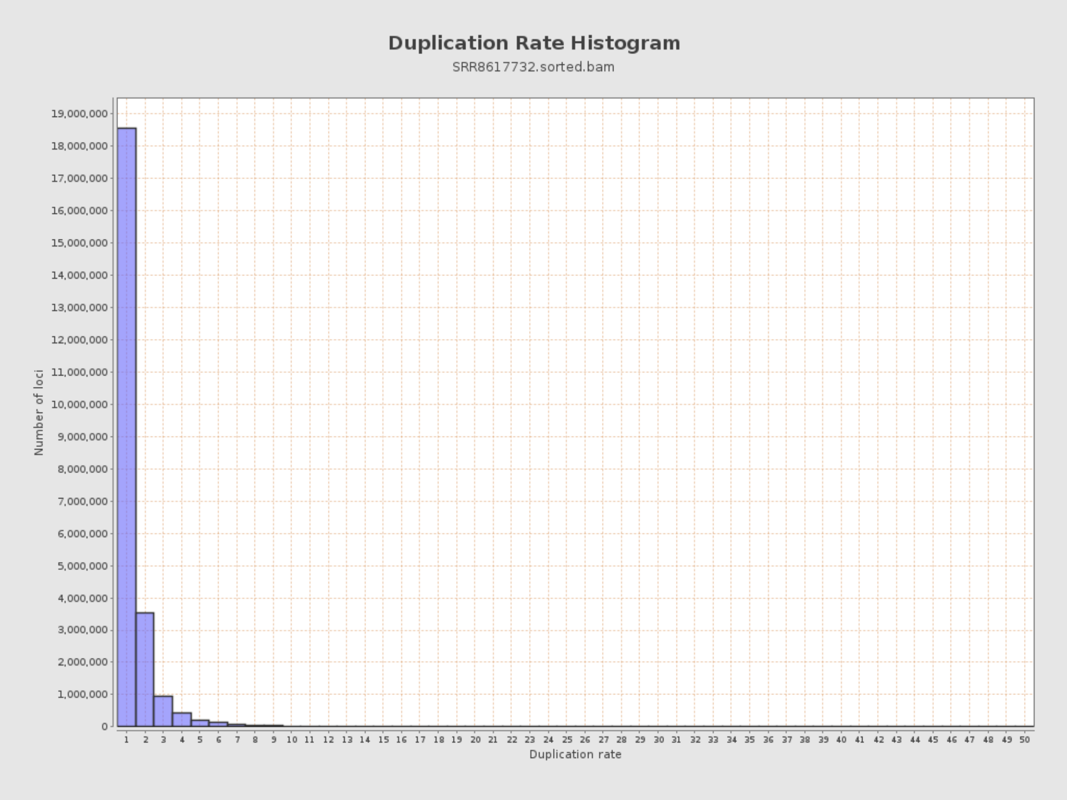
5. Results : Coverage Histogram (0-50X)



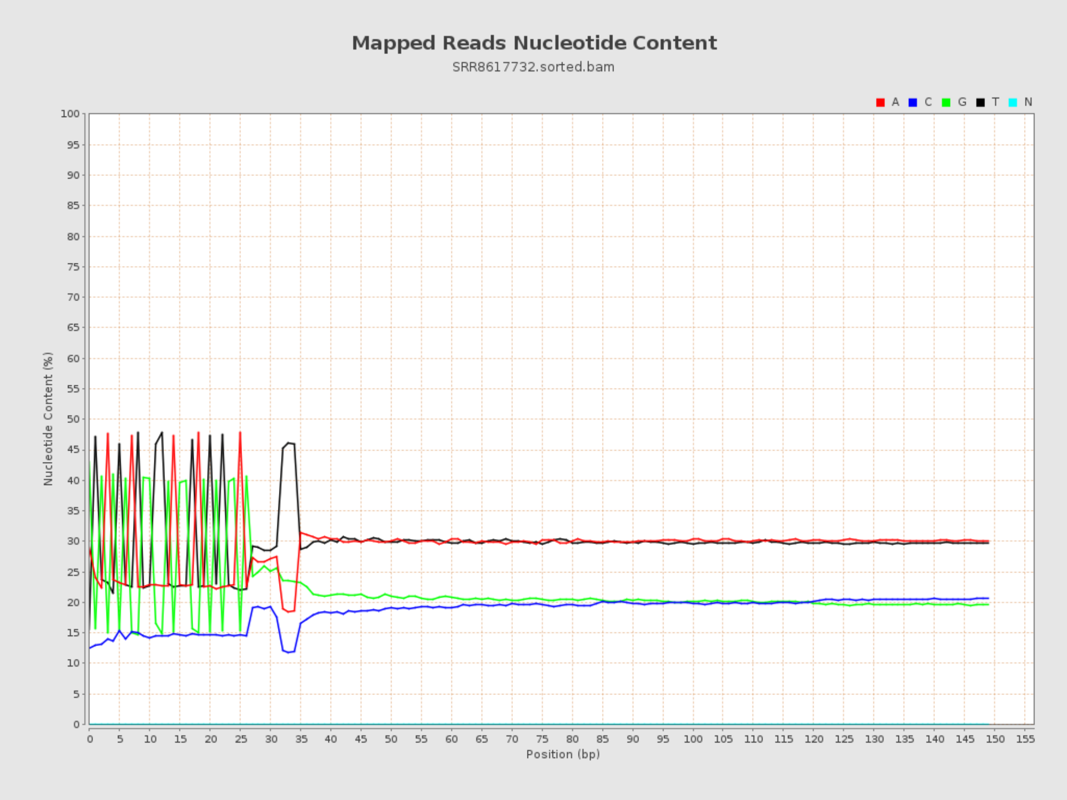
6. Results : Genome Fraction Coverage



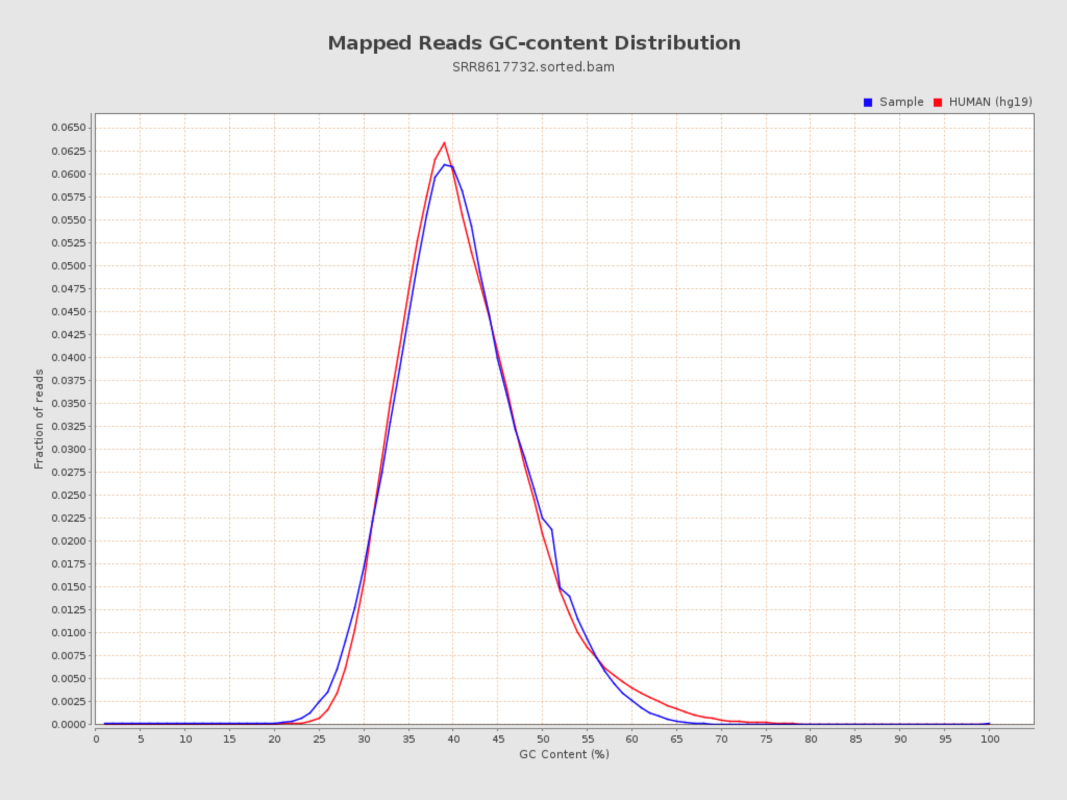
7. Results : Duplication Rate Histogram



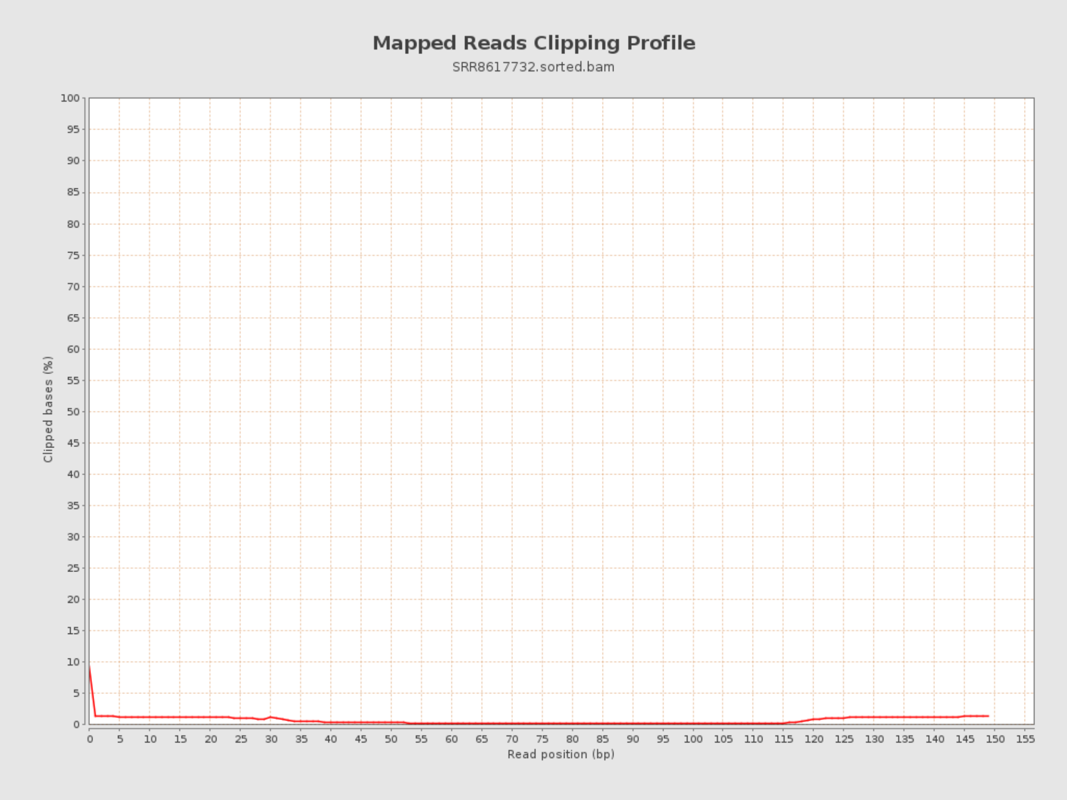
8. Results : Mapped Reads Nucleotide Content



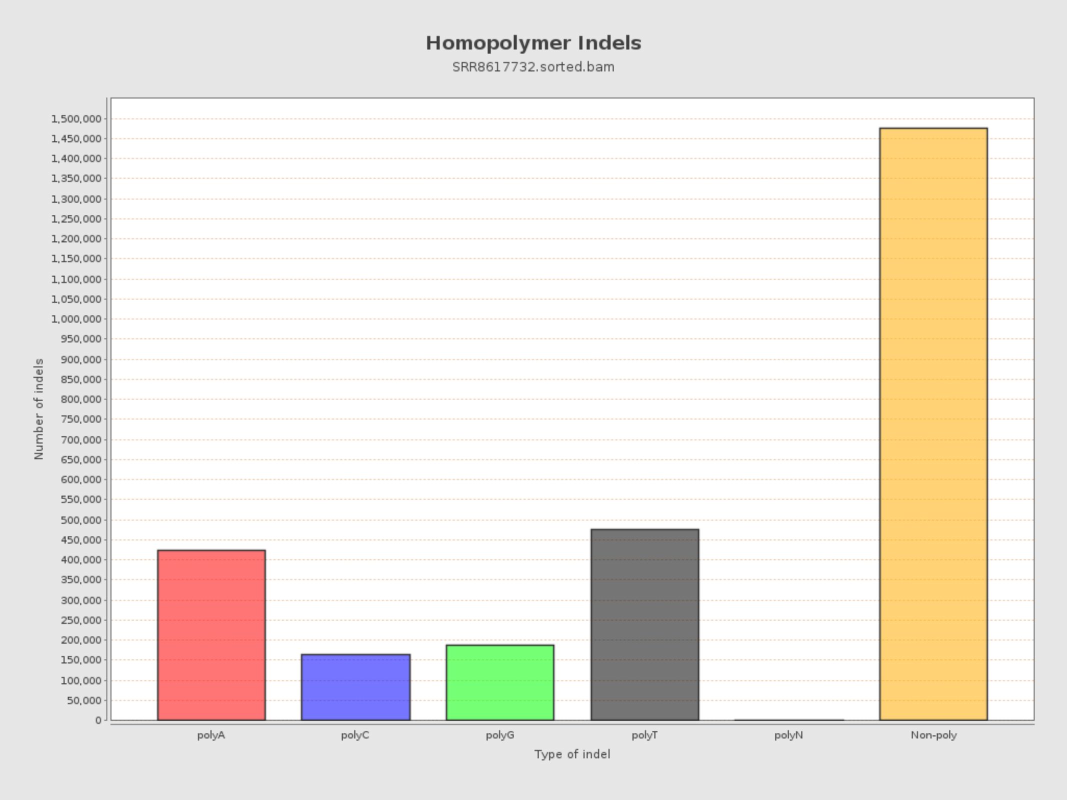
9. Results : Mapped Reads GC-content Distribution



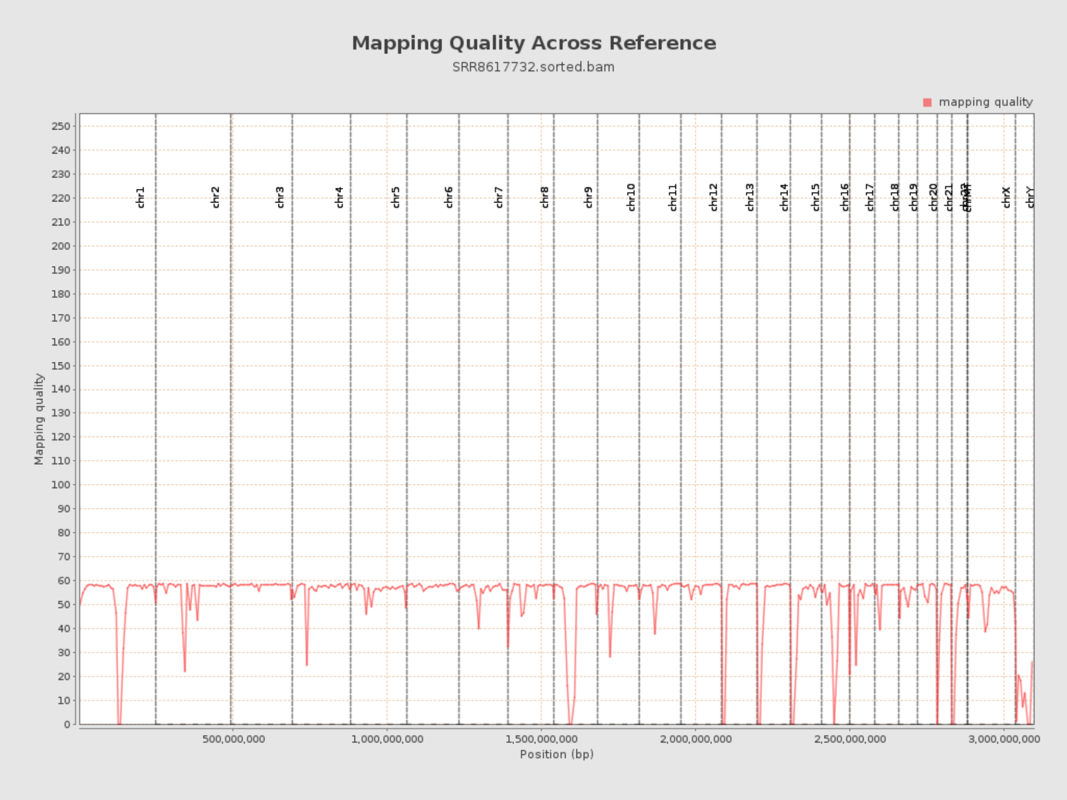
10. Results : Mapped Reads Clipping Profile



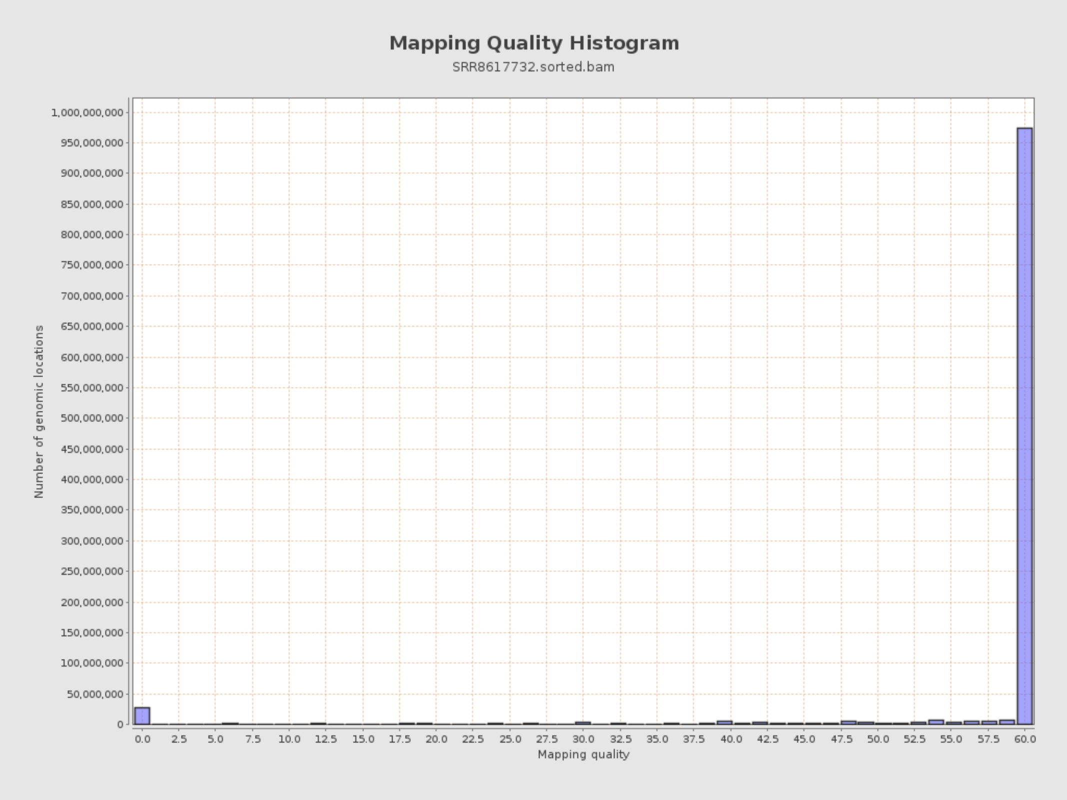
11. Results : Homopolymer Indels



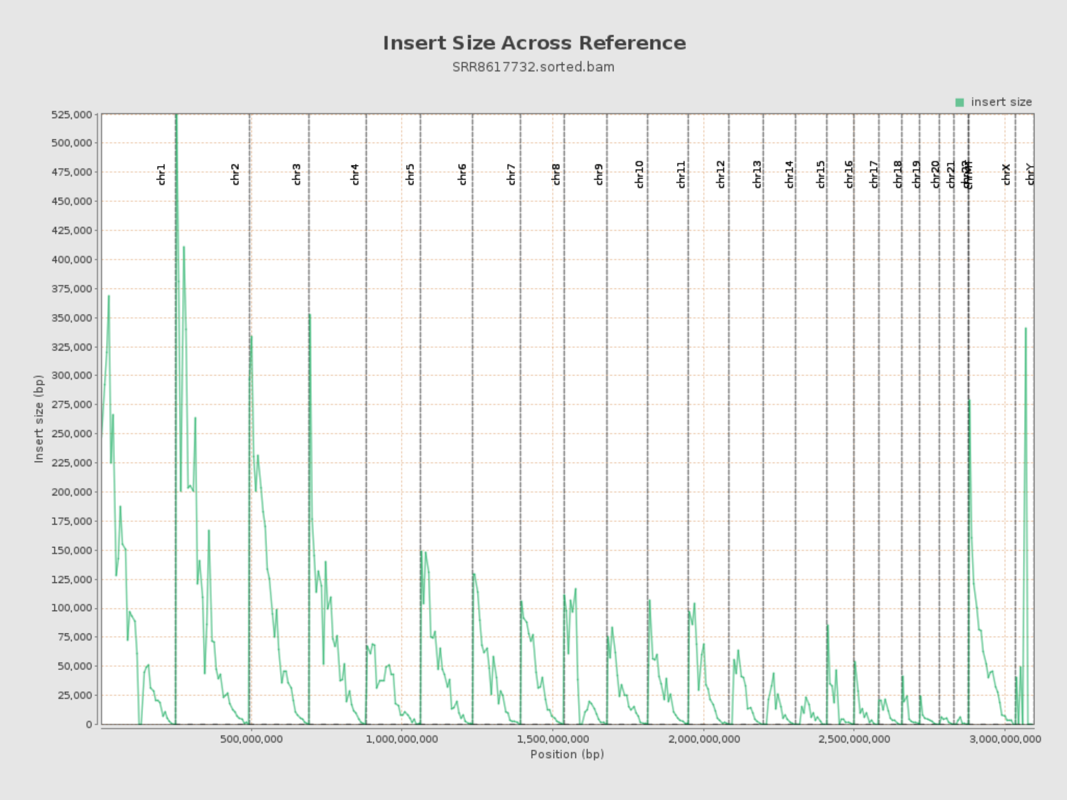
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram