Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 09:18:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617669.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_SRR617669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617669_1.fastq.gz SRR617669_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 09:18:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,312,896 / 94.73%
Unmapped reads	1,687,104 / 5.27%
Mapped paired reads	30,312,896 / 94.73%
Mapped reads, first in pair	15,342,070 / 47.94%
Mapped reads, second in pair	14,970,826 / 46.78%
Mapped reads, both in pair	29,570,212 / 92.41%
Mapped reads, singletons	742,684 / 2.32%
Secondary alignments	0
Supplementary alignments	181,677 / 0.57%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	7,020,641 / 21.94%
Duplication rate	10.81%
Clipped reads	6,601,630 / 20.63%

2.2. ACGT Content

Number/percentage of A's	871,978,870 / 29.77%
Number/percentage of C's	582,972,043 / 19.9%
Number/percentage of T's	871,421,866 / 29.75%
Number/percentage of G's	598,945,656 / 20.45%
Number/percentage of N's	3,857,146 / 0.13%

GC Percentage	40.35%

2.3. Coverage

Mean	0.9468
Standard Deviation	10.6172

2.4. Mapping Quality

Mean Mapping Quality	52.56

2.5. Insert size

Mean	47,776.65
Standard Deviation	2,038,582.93
P25/Median/P75	180 / 224 / 292

2.6. Mismatches and indels

General error rate	1.41%
Mismatches	40,249,537
Insertions	462,861
Mapped reads with at least one insertion	1.5%
Deletions	1,080,032
Mapped reads with at least one deletion	3.49%
Homopolymer indels	47.66%

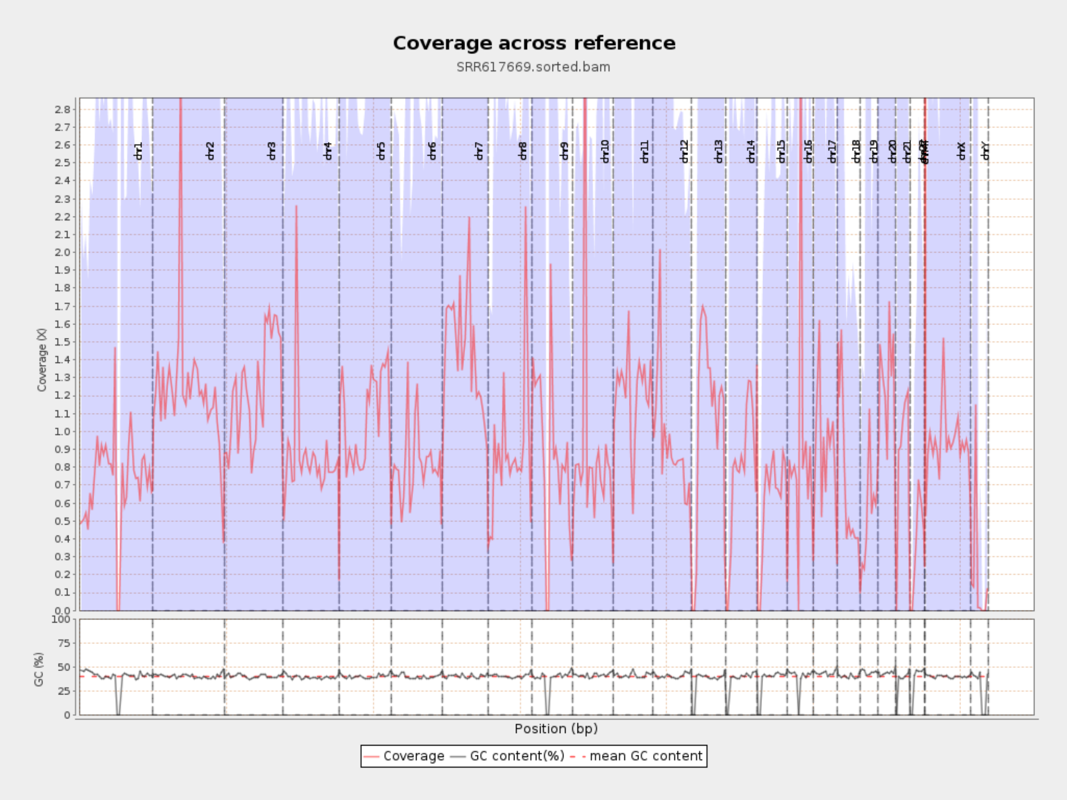
2.7. Chromosome stats

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

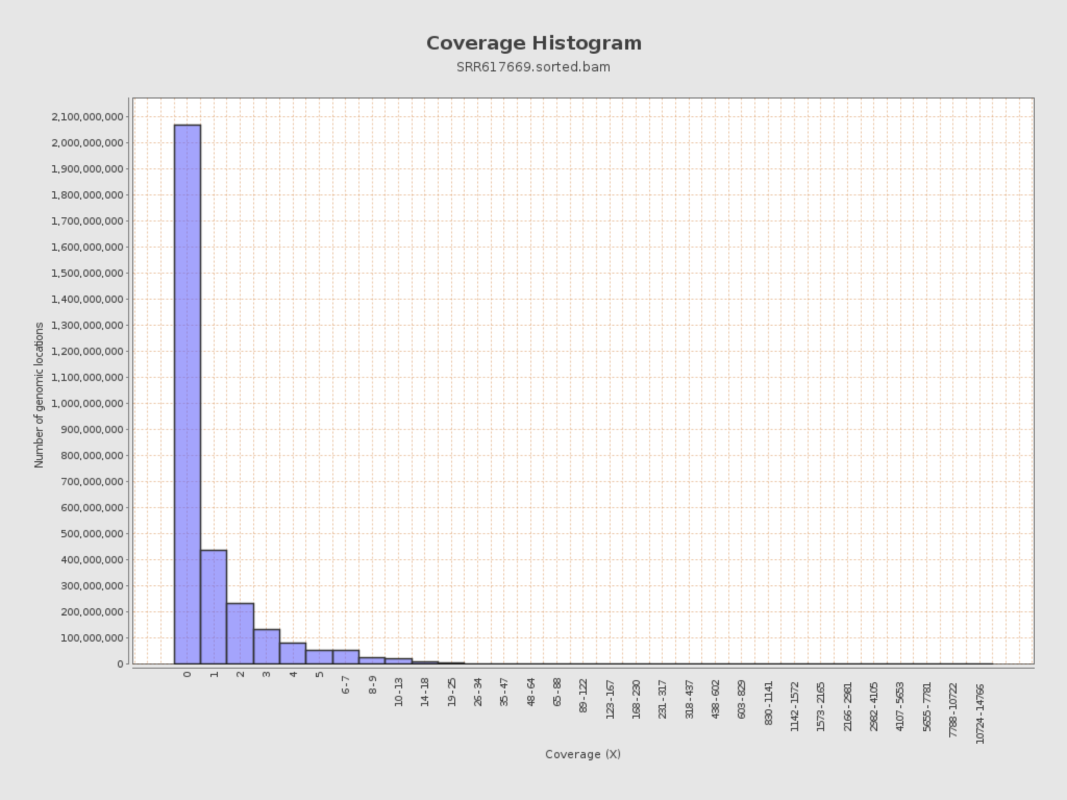
		bases	coverage	deviation
chr1	249250621	179851809	0.7216	10.2025
chr2	243199373	303185145	1.2467	12.1856
chr3	198022430	245349930	1.239	2.4876
chr4	191154276	163903628	0.8574	8.4989
chr5	180915260	193550229	1.0698	2.3346
chr6	171115067	142232595	0.8312	5.7358
chr7	159138663	229373769	1.4413	13.4608
chr8	146364022	129801524	0.8868	4.0864
chr9	141213431	120387141	0.8525	20.6086
chr10	135534747	124413177	0.9179	21.4146
chr11	135006516	161056379	1.193	11.9372
chr12	133851895	125114571	0.9347	2.3744
chr13	115169878	125638096	1.0909	2.3323
chr14	107349540	83812204	0.7807	2.4778
chr15	102531392	62708028	0.6116	1.7861
chr16	90354753	81113429	0.8977	16.6309
chr17	81195210	72429544	0.892	12.7997
chr18	78077248	54246197	0.6948	18.3044
chr19	59128983	31086392	0.5257	6.1022
chr20	63025520	79419245	1.2601	3.0677
chr21	48129895	42862319	0.8906	4.4391
chr22	51304566	18939504	0.3692	1.2976
chrMT	16571	3065139	184.9701	130.4702
chrX	155270560	145565844	0.9375	4.3677

chrY	59373566	11870863	0.1999	17.393

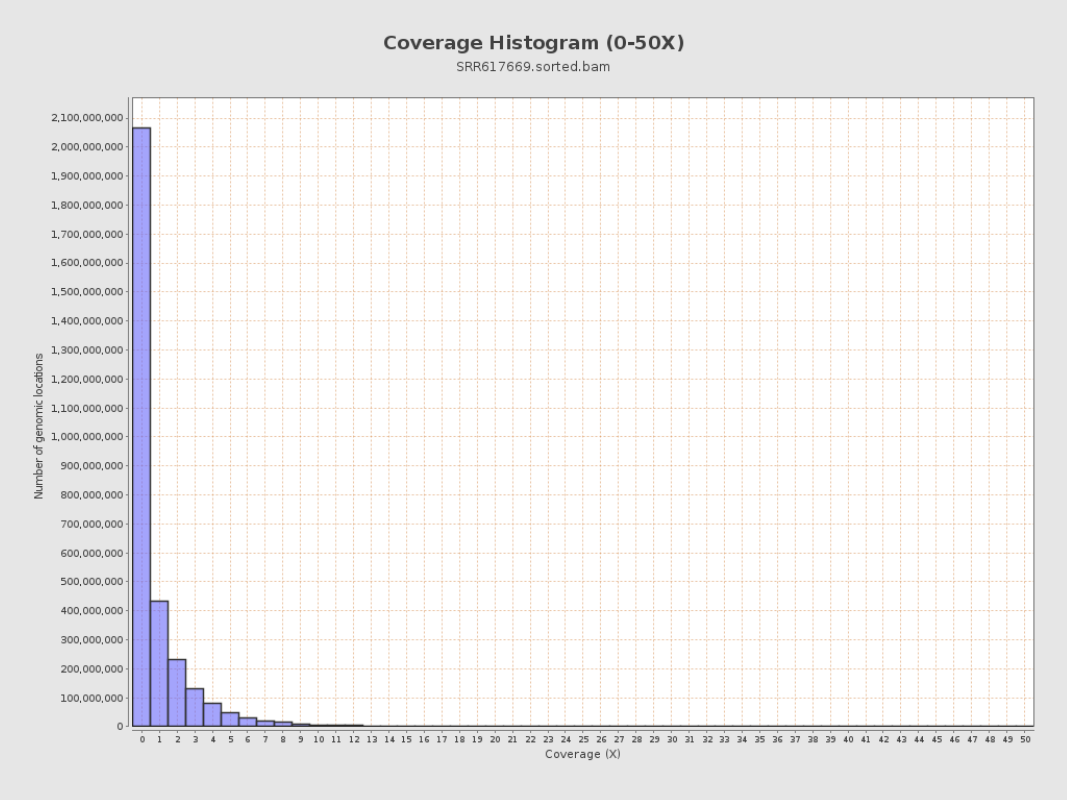
3. Results : Coverage across reference



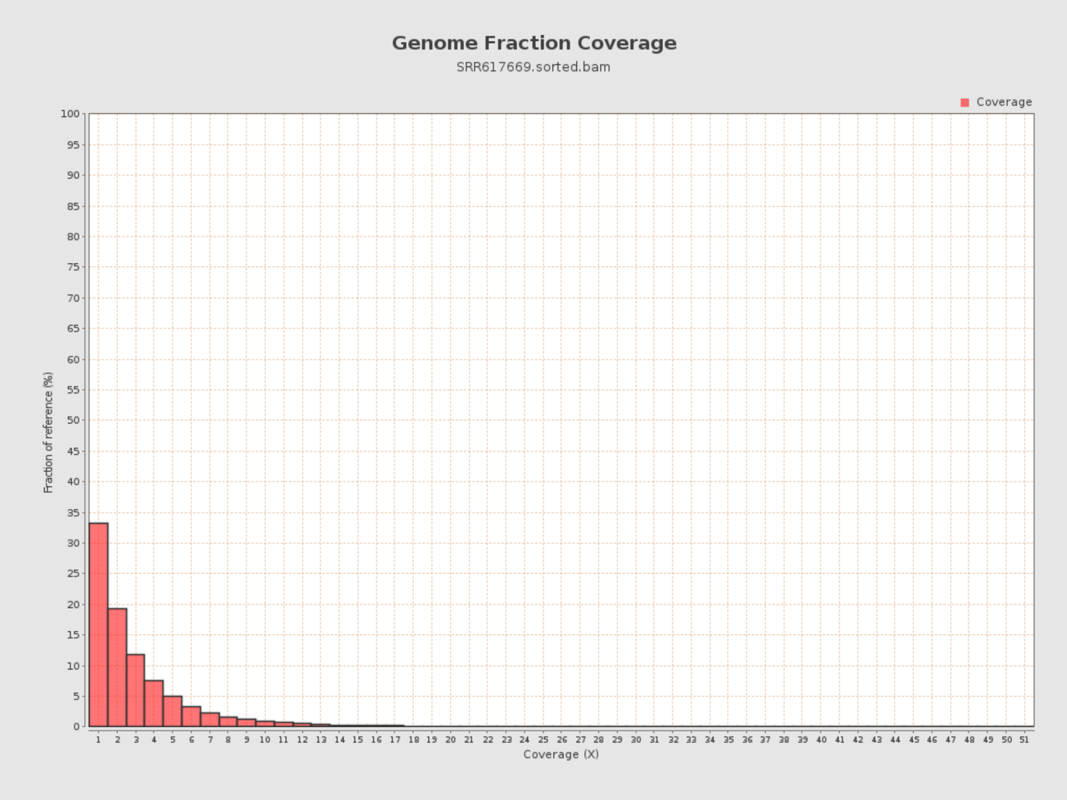
4. Results : Coverage Histogram



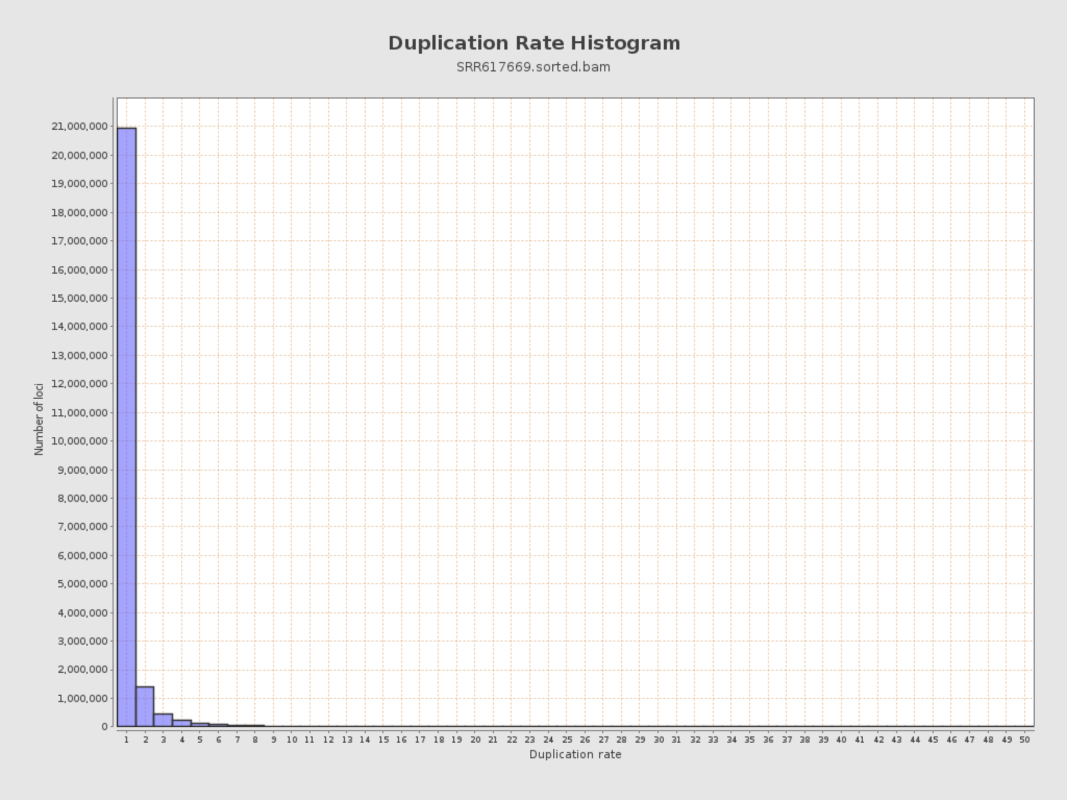
5. Results : Coverage Histogram (0-50X)



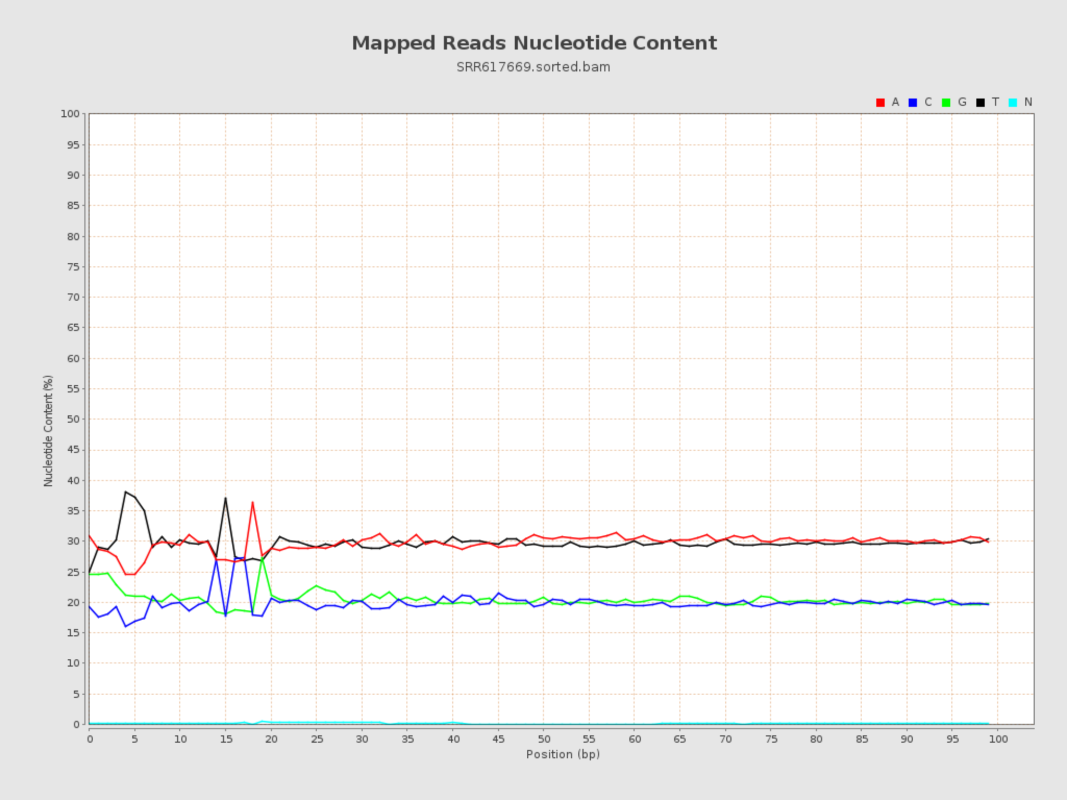
6. Results : Genome Fraction Coverage



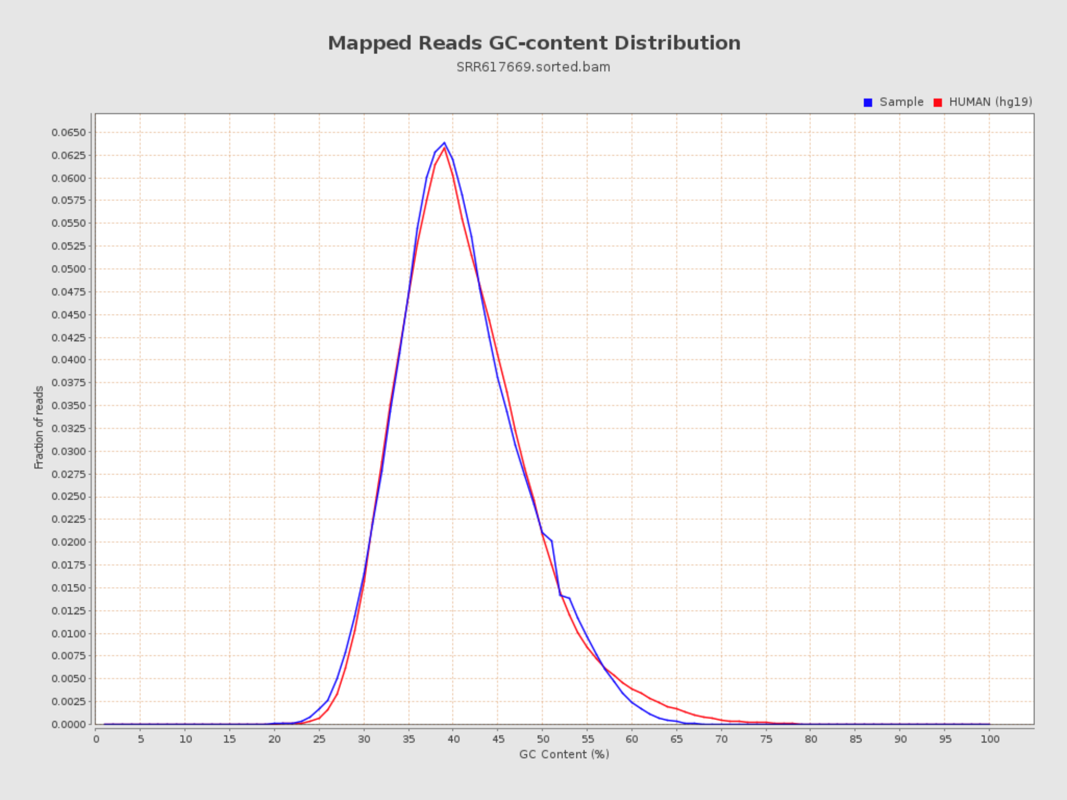
7. Results : Duplication Rate Histogram



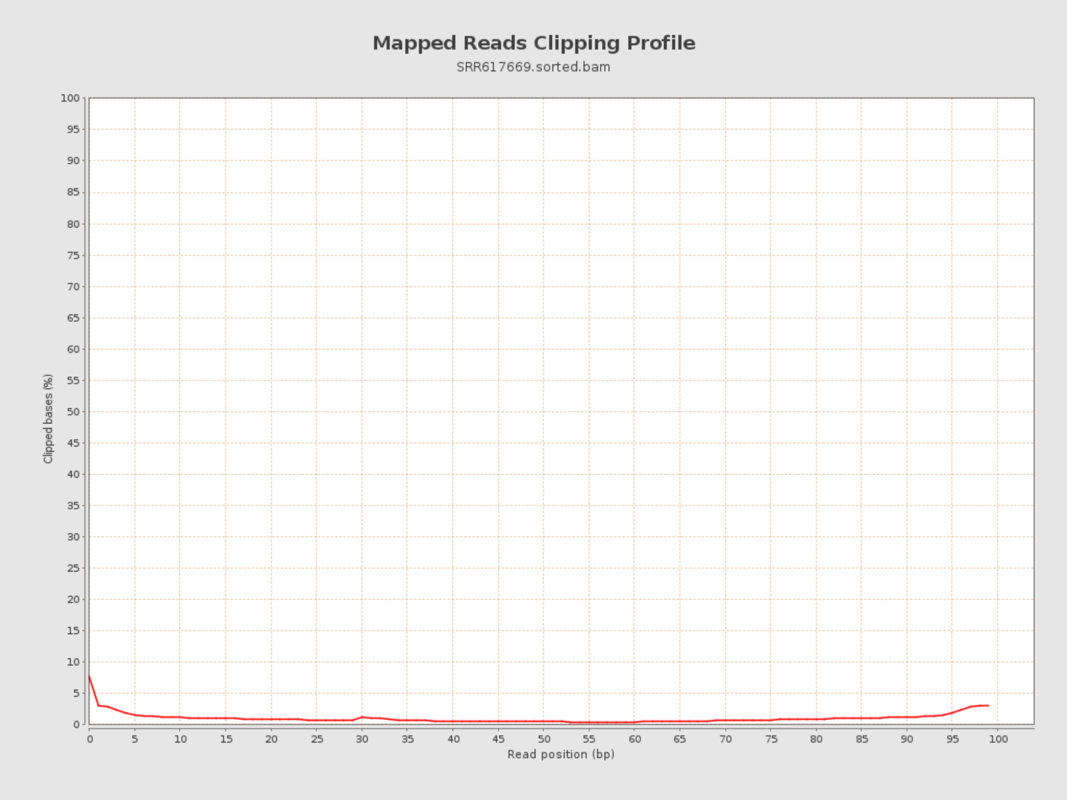
8. Results : Mapped Reads Nucleotide Content



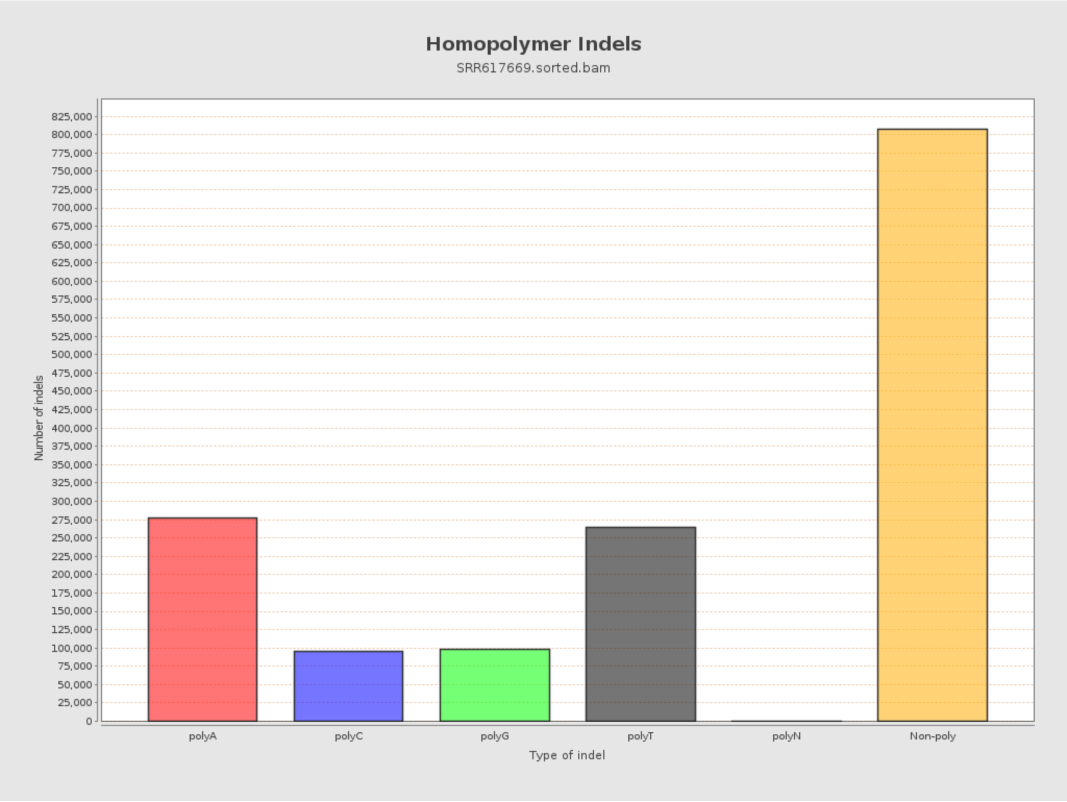
9. Results : Mapped Reads GC-content Distribution



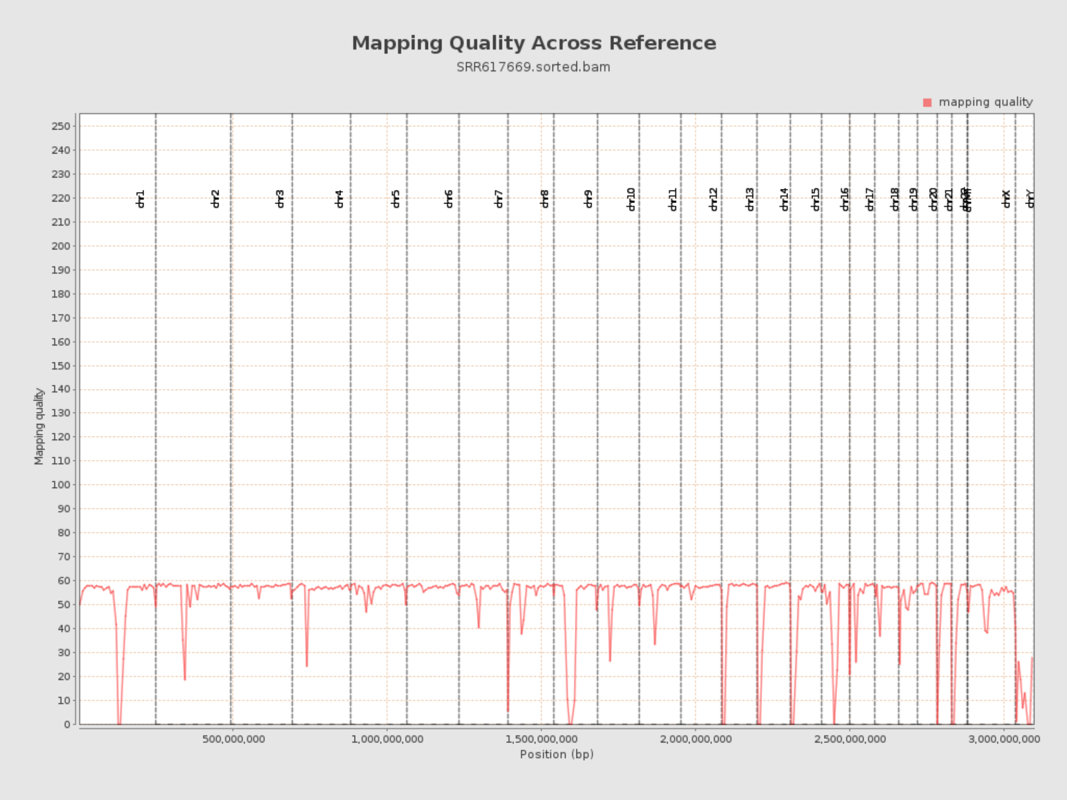
10. Results : Mapped Reads Clipping Profile



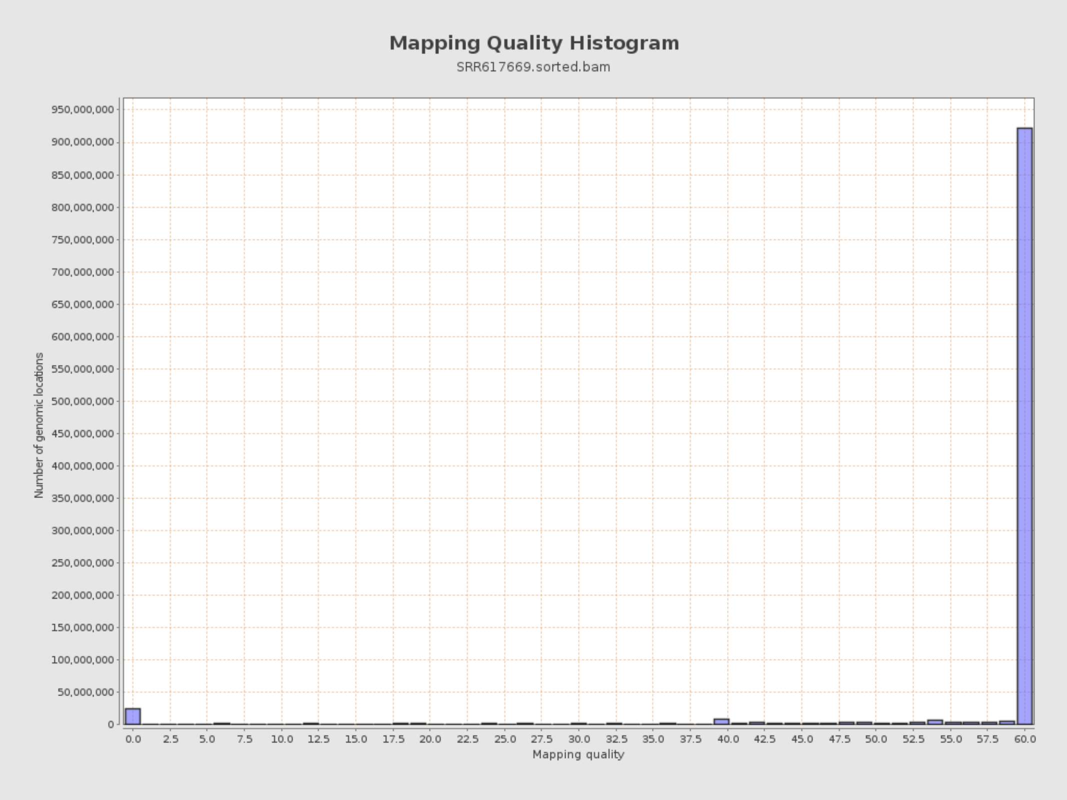
11. Results : Homopolymer Indels



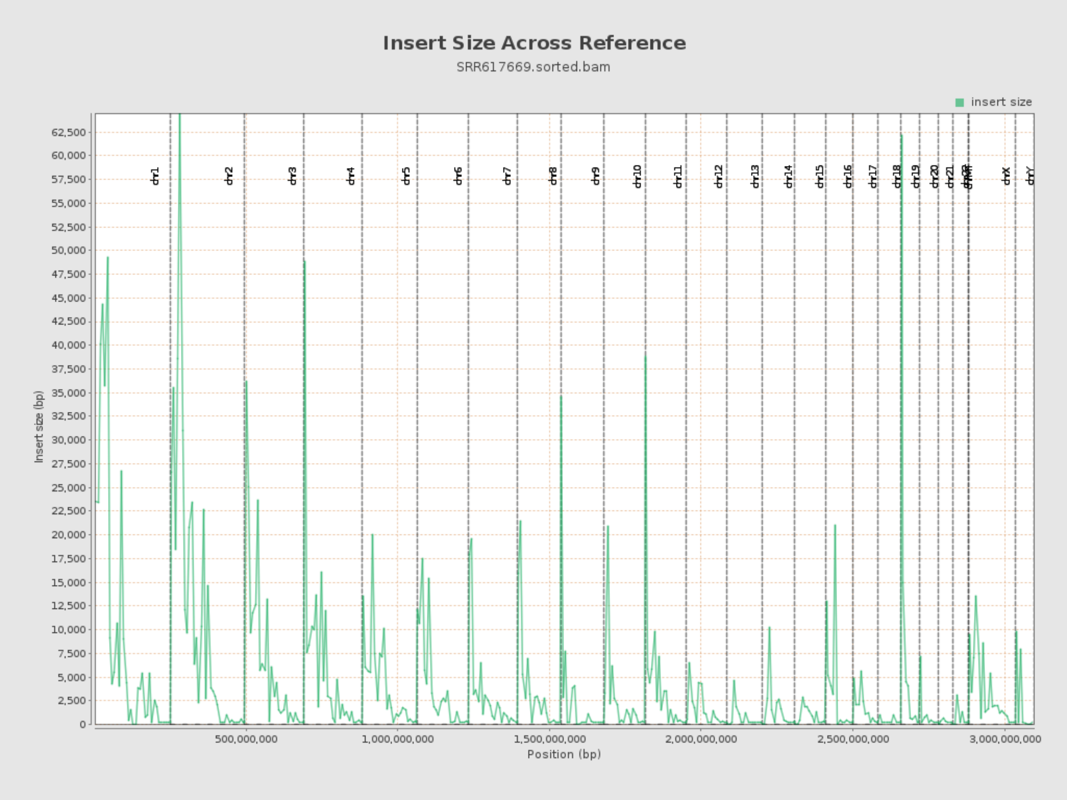
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram