Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 17:25:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617649.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_SRR617649 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617649_1.fastq.gz SRR617649_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 17:25:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617649.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,496,656 / 95.3%
Unmapped reads	1,503,344 / 4.7%
Mapped paired reads	30,496,656 / 95.3%
Mapped reads, first in pair	15,262,514 / 47.7%
Mapped reads, second in pair	15,234,142 / 47.61%
Mapped reads, both in pair	29,917,156 / 93.49%
Mapped reads, singletons	579,500 / 1.81%
Secondary alignments	0
Supplementary alignments	143,449 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	7,055,245 / 22.05%
Duplication rate	10.78%
Clipped reads	6,323,303 / 19.76%

2.2. ACGT Content

Number/percentage of A's	881,526,432 / 29.76%
Number/percentage of C's	590,969,855 / 19.95%
Number/percentage of T's	880,215,675 / 29.72%
Number/percentage of G's	607,412,015 / 20.51%
Number/percentage of N's	1,904,512 / 0.06%

GC Percentage	40.46%

2.3. Coverage

Mean	0.9574
Standard Deviation	10.7836

2.4. Mapping Quality

Mean Mapping Quality	52.69

2.5. Insert size

Mean	32,421.25
Standard Deviation	1,646,001.64
P25/Median/P75	180 / 224 / 291

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	42,233,051
Insertions	462,847
Mapped reads with at least one insertion	1.49%
Deletions	1,090,086
Mapped reads with at least one deletion	3.5%
Homopolymer indels	47.7%

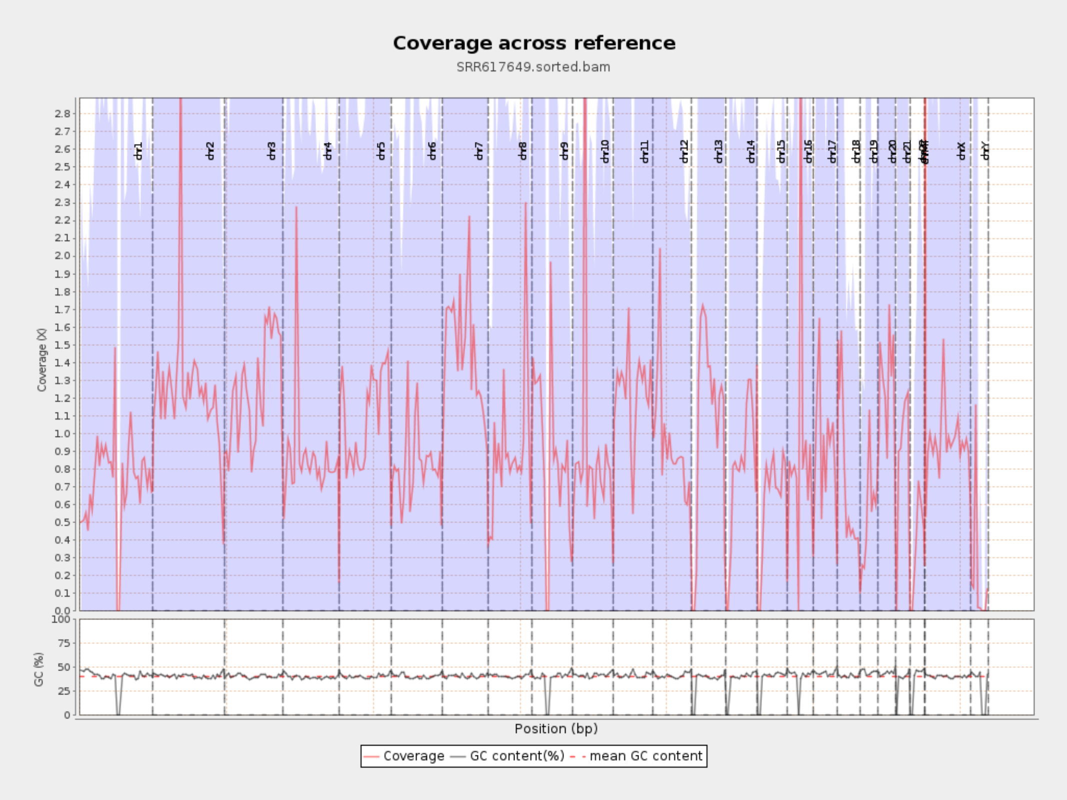
2.7. Chromosome stats

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

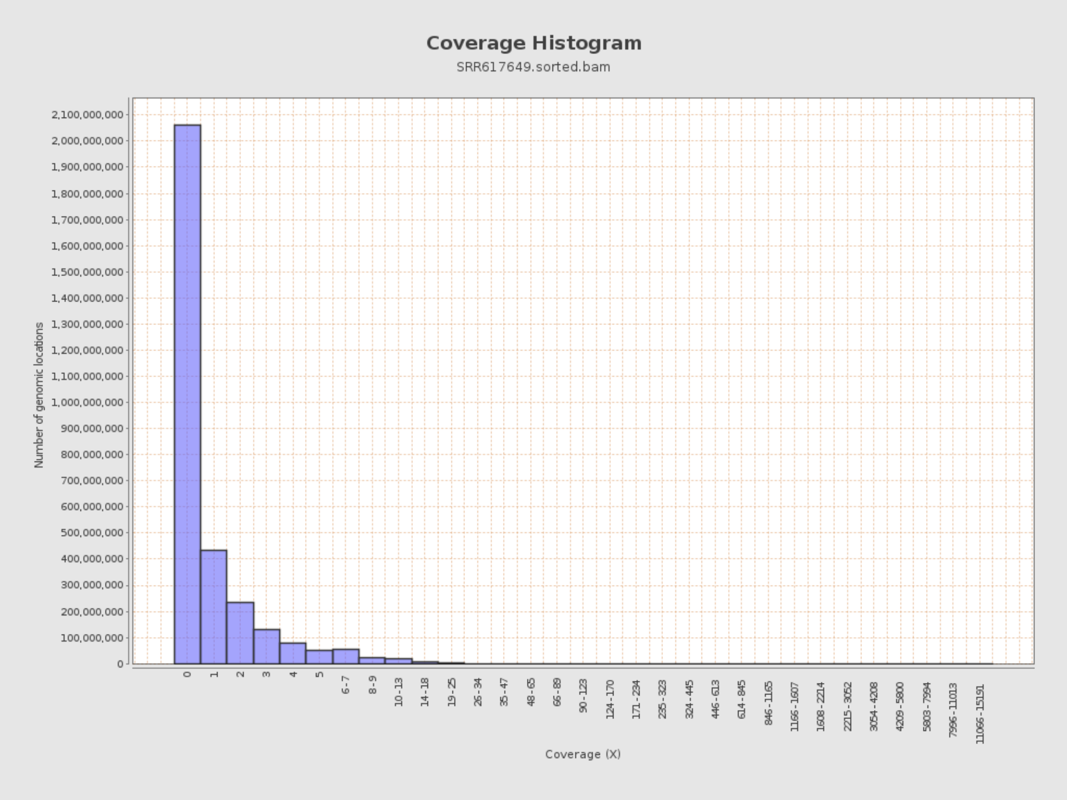
		bases	**coverage**	**deviation**
chr1	249250621	181657728	0.7288	10.4251
chr2	243199373	306089348	1.2586	12.3198
chr3	198022430	248240632	1.2536	2.5001
chr4	191154276	165336677	0.8649	8.5612
chr5	180915260	195822716	1.0824	2.3436
chr6	171115067	143645067	0.8395	5.8903
chr7	159138663	232093138	1.4584	13.5009
chr8	146364022	131650246	0.8995	4.1345
chr9	141213431	121754725	0.8622	21.0367
chr10	135534747	125820729	0.9283	21.8256
chr11	135006516	162899423	1.2066	12.0411
chr12	133851895	126621046	0.946	2.1598
chr13	115169878	127420878	1.1064	2.3112
chr14	107349540	84891240	0.7908	2.4656
chr15	102531392	63327659	0.6176	1.5852
chr16	90354753	82373923	0.9117	17.0353
chr17	81195210	73244146	0.9021	12.9823
chr18	78077248	54731156	0.701	18.6269
chr19	59128983	31486761	0.5325	6.0792
chr20	63025520	80132229	1.2714	3.1149
chr21	48129895	43170930	0.897	4.4277
chr22	51304566	19121796	0.3727	1.2813
chrMT	16571	3192525	192.6574	133.2259
chrX	155270560	147185628	0.9479	4.3804

chrY	59373566	11927168	0.2009	17.7073

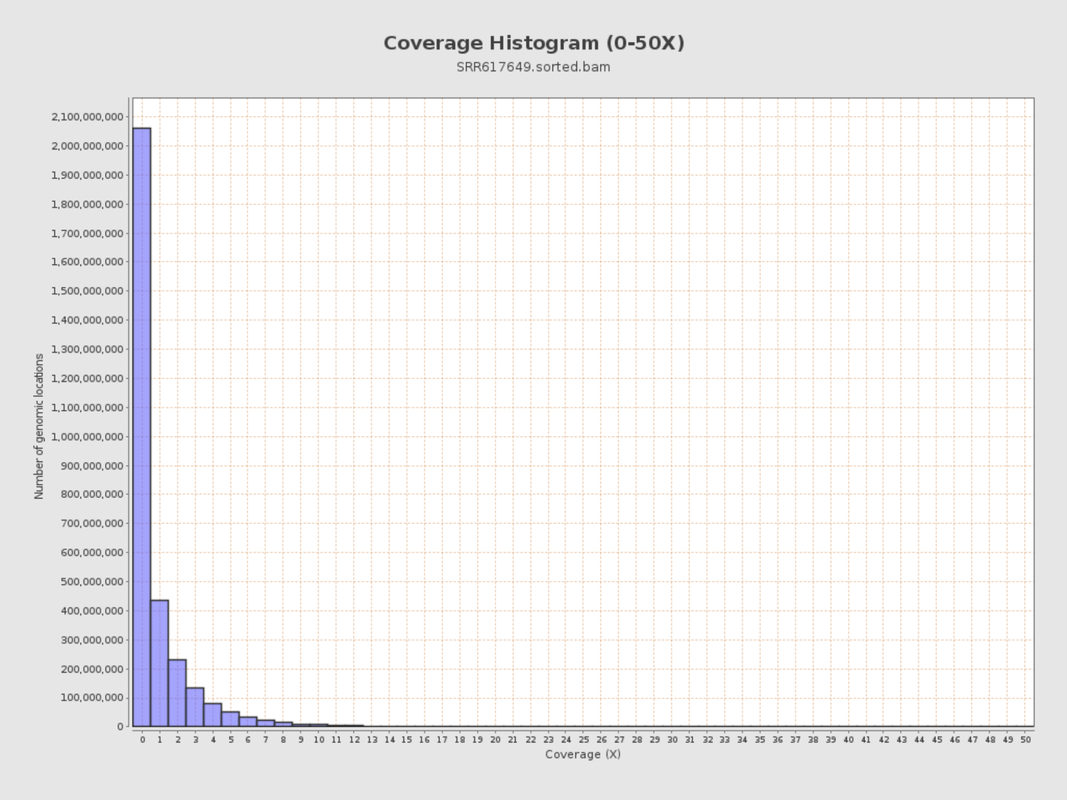
3. Results : Coverage across reference



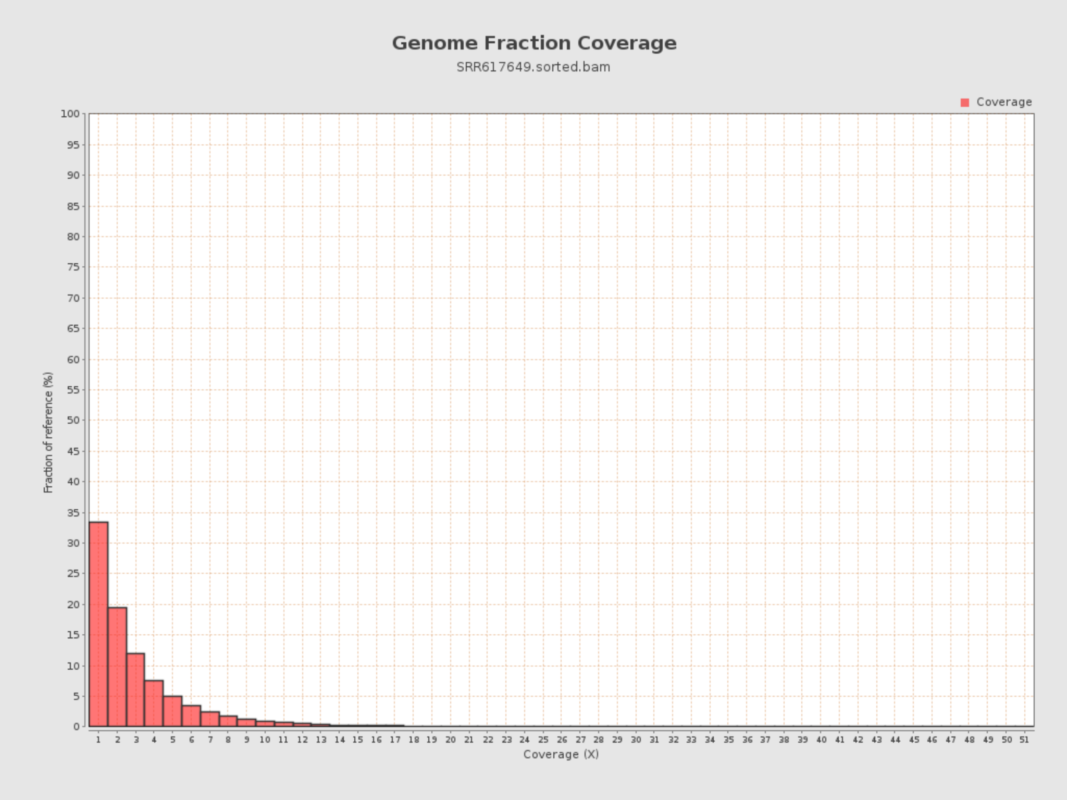
4. Results : Coverage Histogram



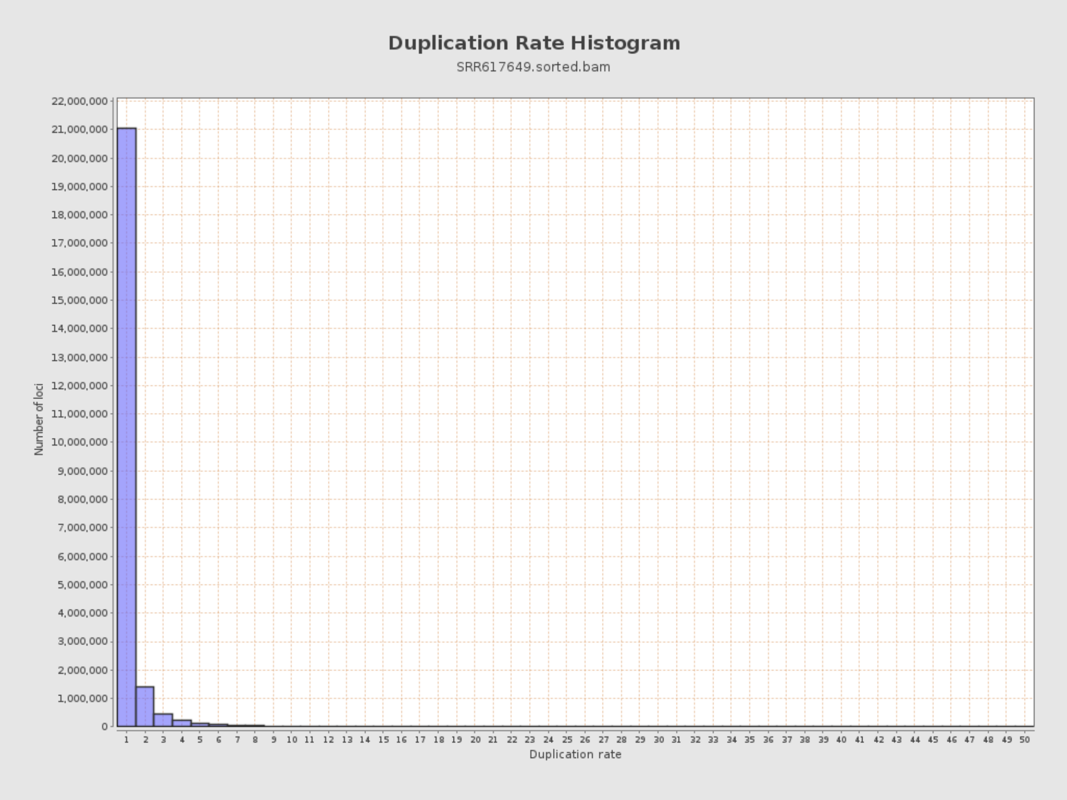
5. Results : Coverage Histogram (0-50X)



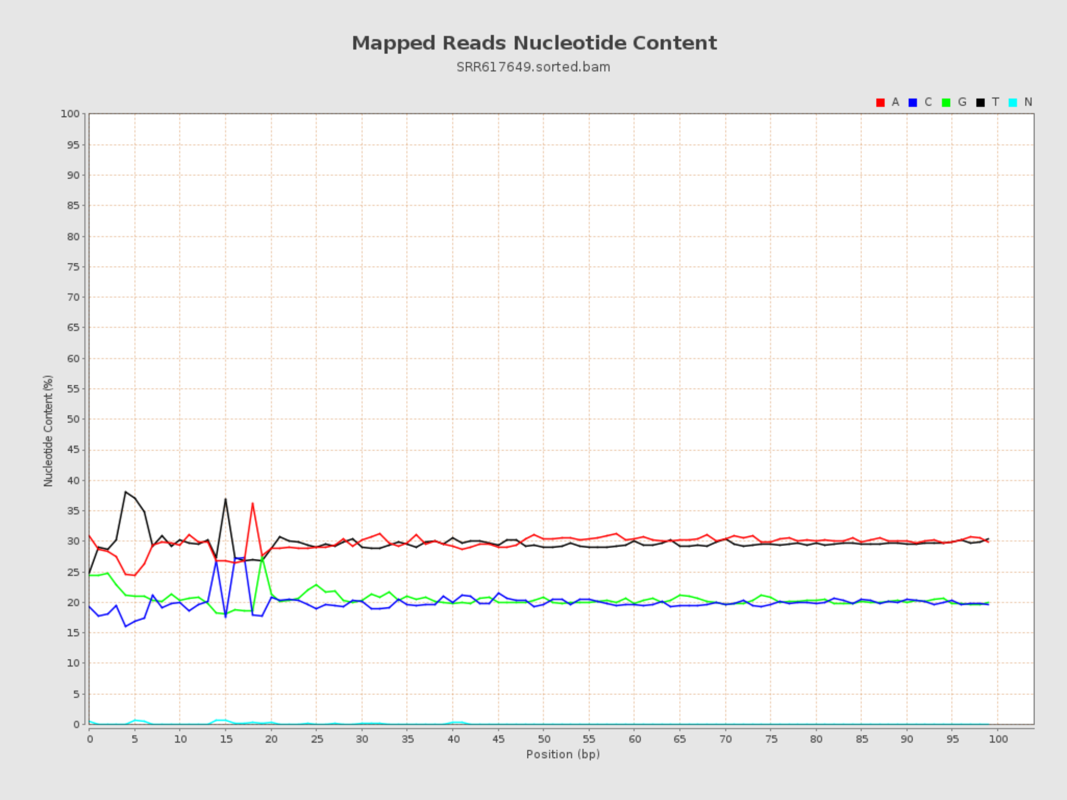
6. Results : Genome Fraction Coverage



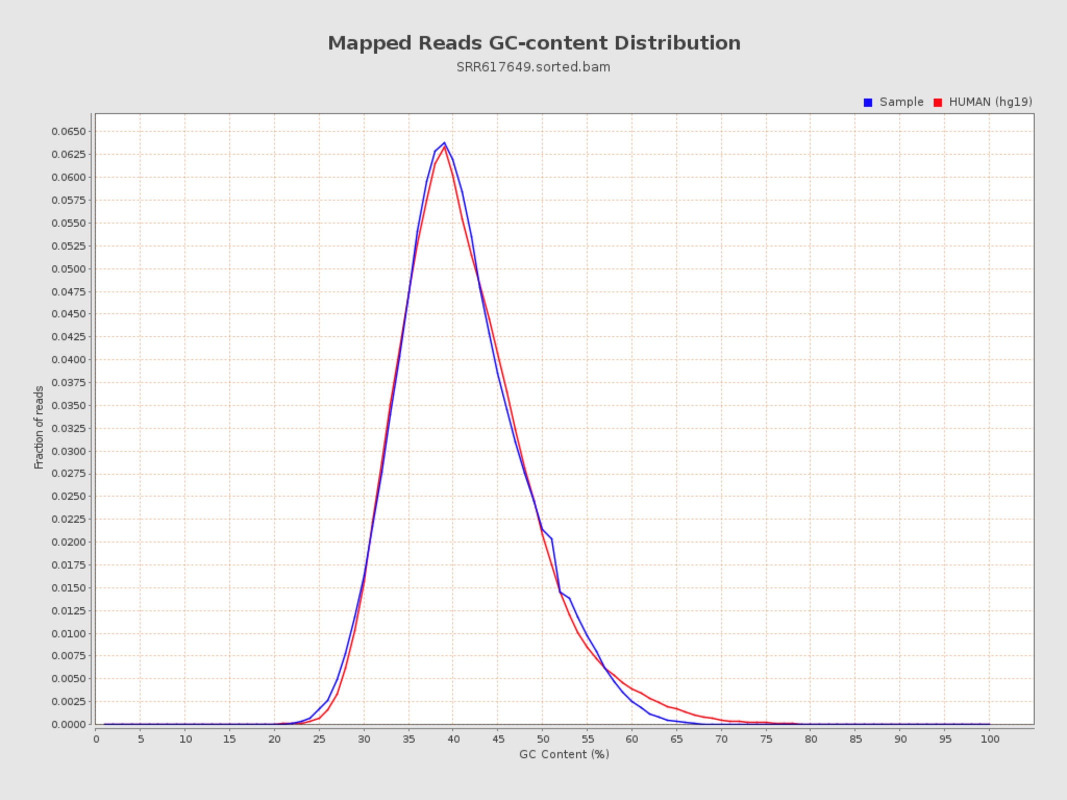
7. Results : Duplication Rate Histogram



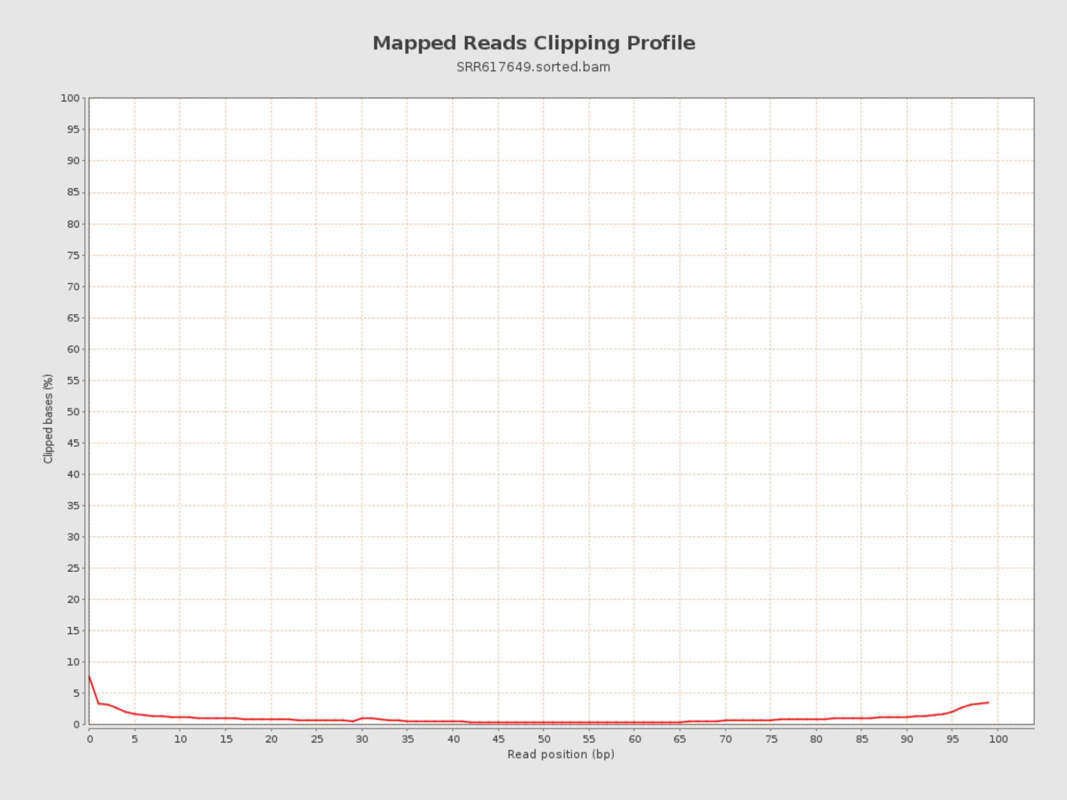
8. Results : Mapped Reads Nucleotide Content



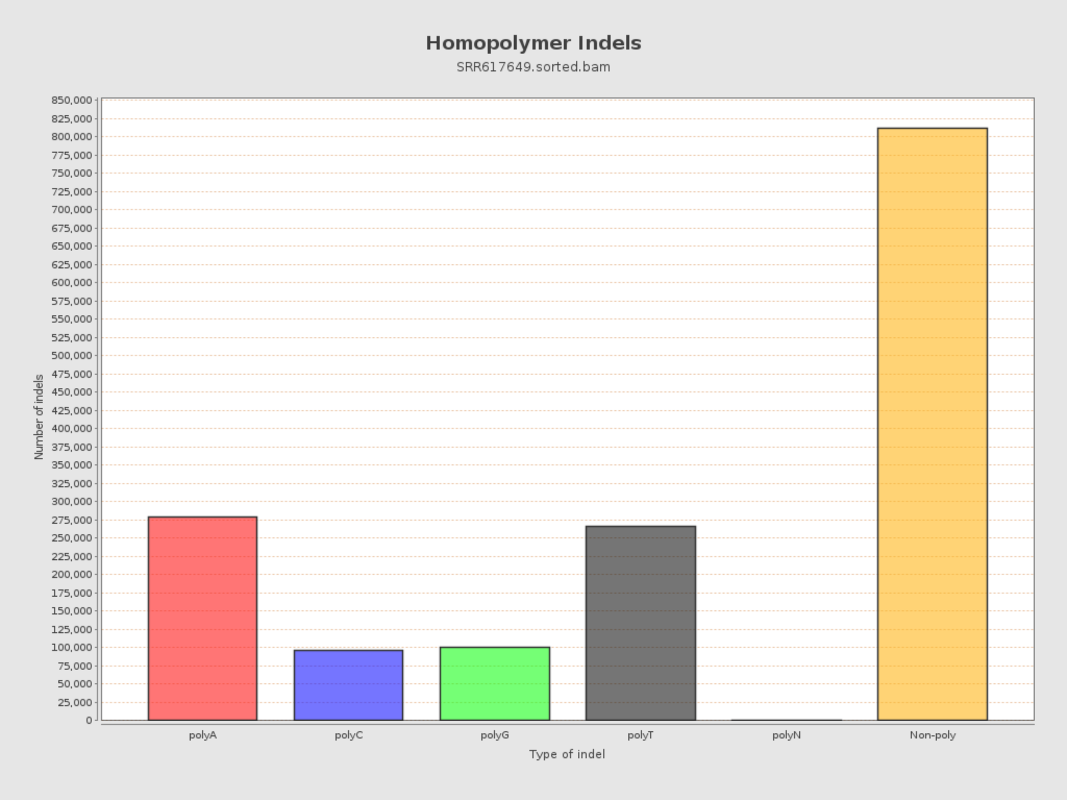
9. Results : Mapped Reads GC-content Distribution



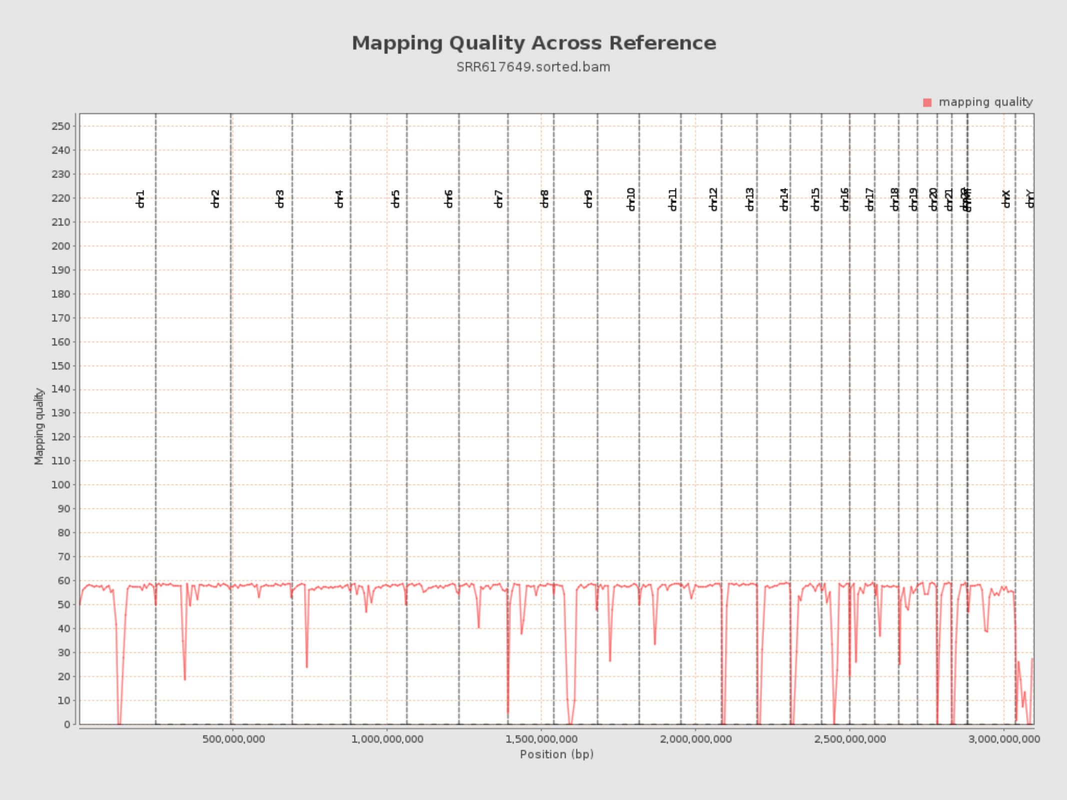
10. Results : Mapped Reads Clipping Profile



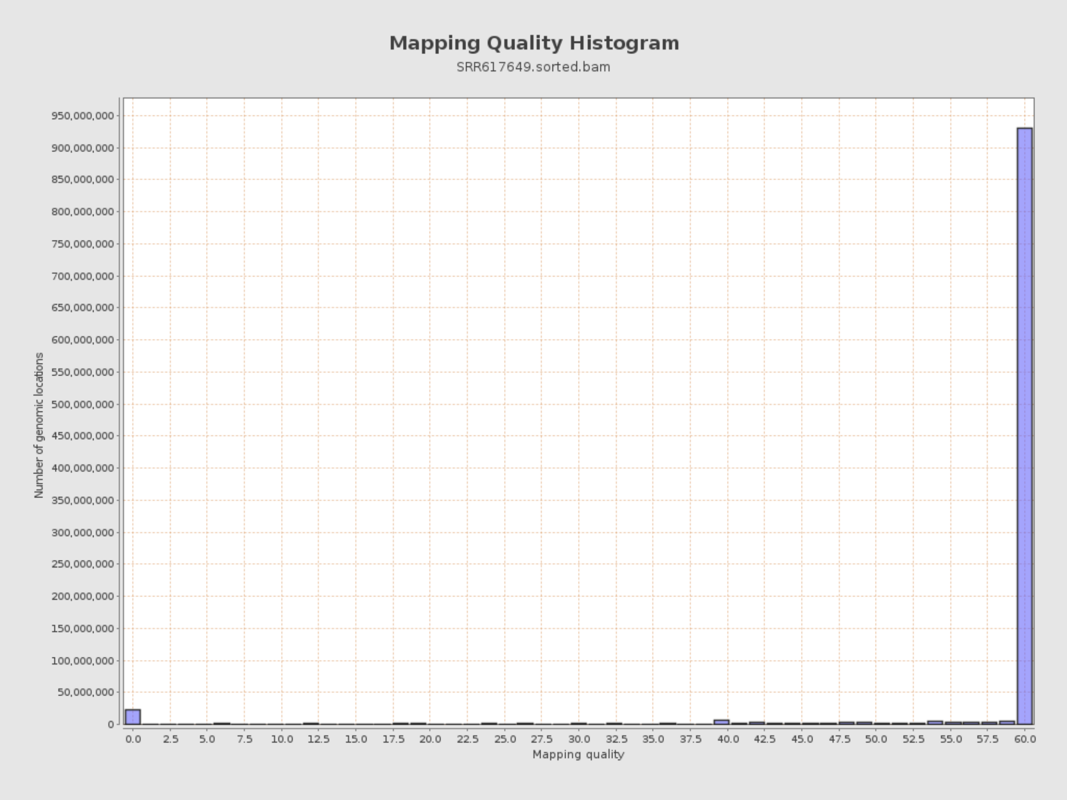
11. Results : Homopolymer Indels



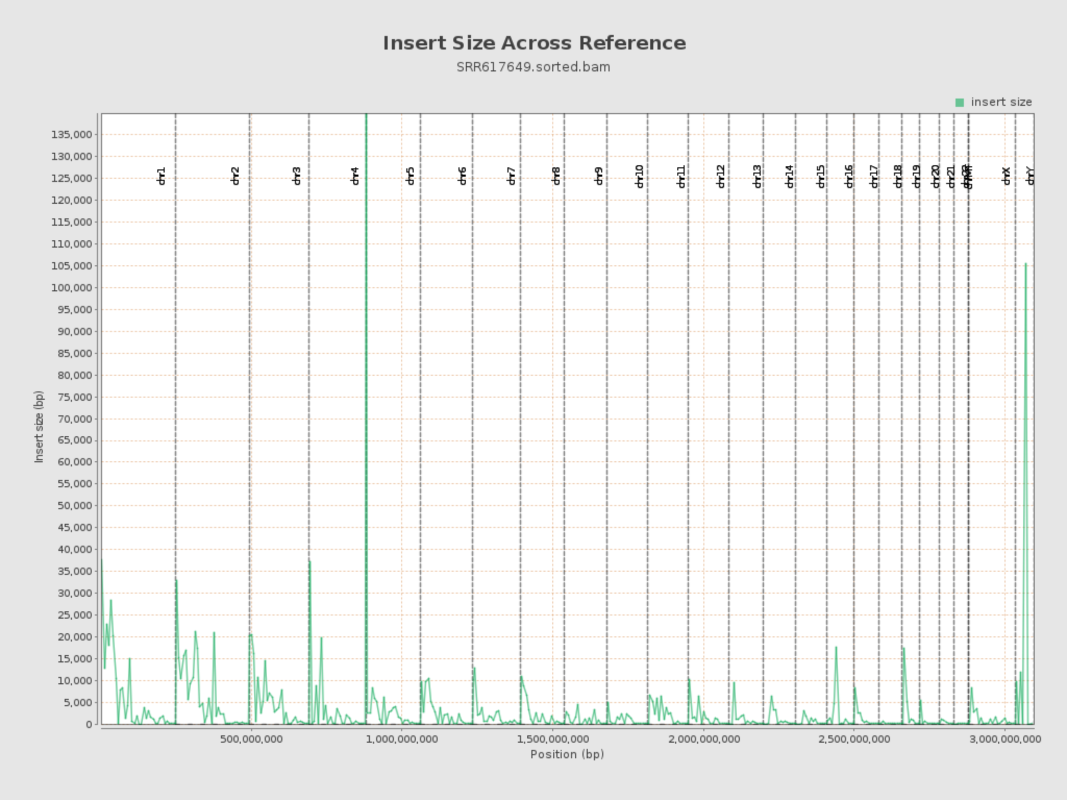
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram