Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 22:50:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617380.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_SRR617380 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617380_1.fastq.gz SRR617380_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 22:50:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617380.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,455,807 / 95.17%
Unmapped reads	1,544,193 / 4.83%
Mapped paired reads	30,455,807 / 95.17%
Mapped reads, first in pair	15,292,153 / 47.79%
Mapped reads, second in pair	15,163,654 / 47.39%
Mapped reads, both in pair	30,021,544 / 93.82%
Mapped reads, singletons	434,263 / 1.36%
Secondary alignments	0
Supplementary alignments	66,615 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,579,286 / 4.94%
Duplication rate	1.48%
Clipped reads	2,358,459 / 7.37%

2.2. ACGT Content

Number/percentage of A's	906,020,859 / 30.28%
Number/percentage of C's	593,839,181 / 19.85%
Number/percentage of T's	893,882,523 / 29.88%
Number/percentage of G's	596,583,014 / 19.94%
Number/percentage of N's	1,454,908 / 0.05%

GC Percentage	39.79%

2.3. Coverage

Mean	0.9667
Standard Deviation	9.8838

2.4. Mapping Quality

Mean Mapping Quality	53.49

2.5. Insert size

Mean	52,498.94
Standard Deviation	2,200,635.7
P25/Median/P75	172 / 213 / 276

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	31,688,813
Insertions	299,511
Mapped reads with at least one insertion	0.95%
Deletions	363,489
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.22%

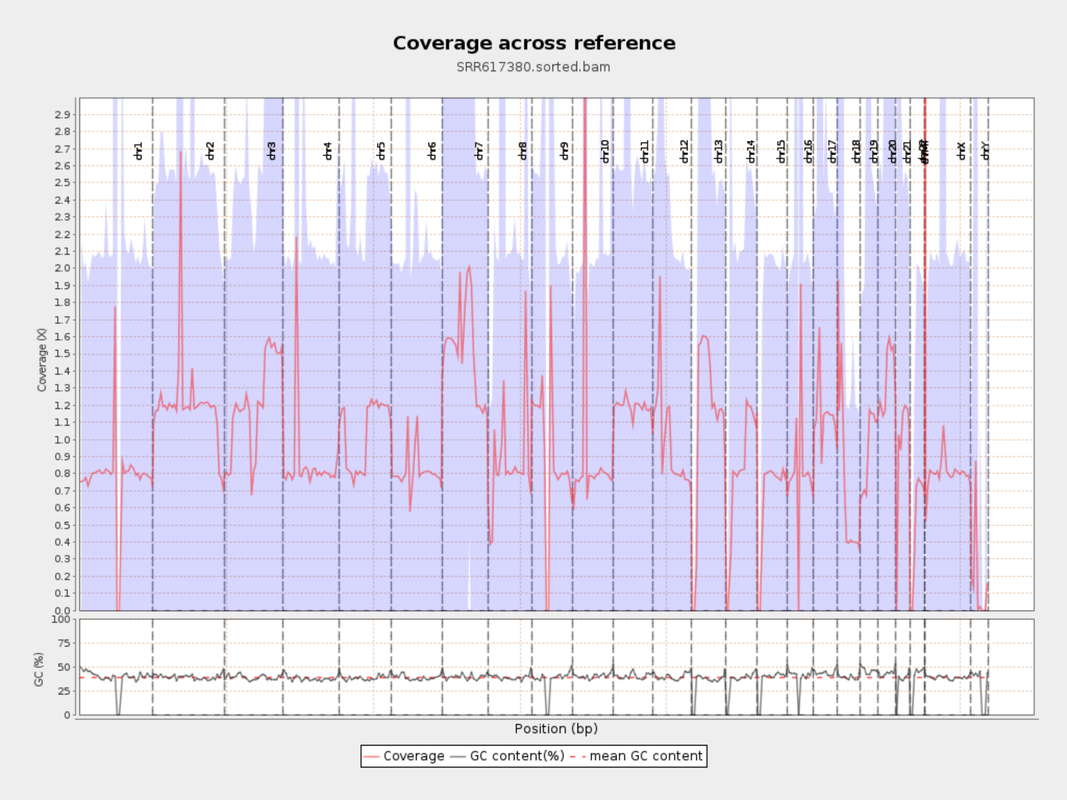
2.7. Chromosome stats

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

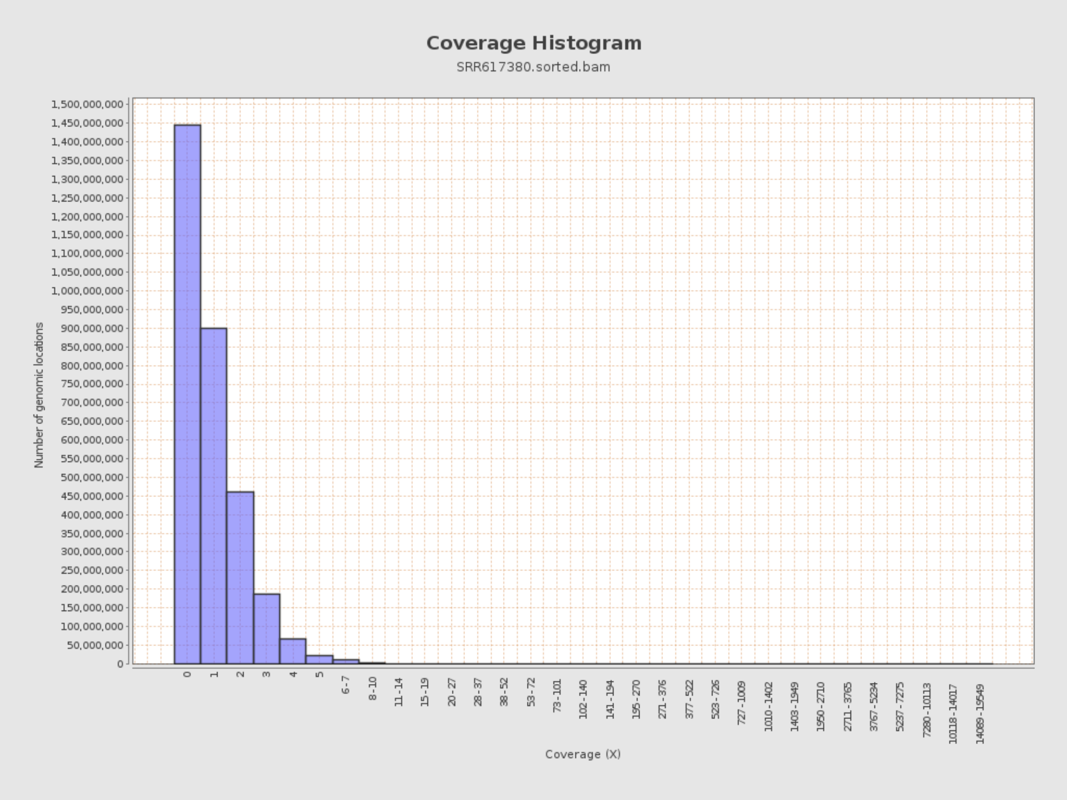
		bases	**coverage**	**deviation**
chr1	249250621	194046060	0.7785	20.0094
chr2	243199373	295720598	1.216	8.9708
chr3	198022430	238166645	1.2027	1.4942
chr4	191154276	164140736	0.8587	9.5622
chr5	180915260	187788329	1.038	1.4755
chr6	171115067	140435371	0.8207	3.6735
chr7	159138663	242965300	1.5268	10.9442
chr8	146364022	126105559	0.8616	7.7155
chr9	141213431	126031747	0.8925	14.9825
chr10	135534747	126022682	0.9298	20.4691
chr11	135006516	160600326	1.1896	5.5964
chr12	133851895	131926661	0.9856	1.3396
chr13	115169878	130452229	1.1327	1.2993
chr14	107349540	86741974	0.808	1.3673
chr15	102531392	67153361	0.655	0.9792
chr16	90354753	75006934	0.8301	7.9428
chr17	81195210	92740533	1.1422	7.2199
chr18	78077248	54122438	0.6932	15.367
chr19	59128983	55462871	0.938	9.8484
chr20	63025520	85867924	1.3624	2.5139
chr21	48129895	47748054	0.9921	3.2563
chr22	51304566	26437503	0.5153	0.9173
chrMT	16571	2060862	124.3656	22.8704
chrX	155270560	124725904	0.8033	3.0689

chrY	59373566	10185336	0.1715	8.4465

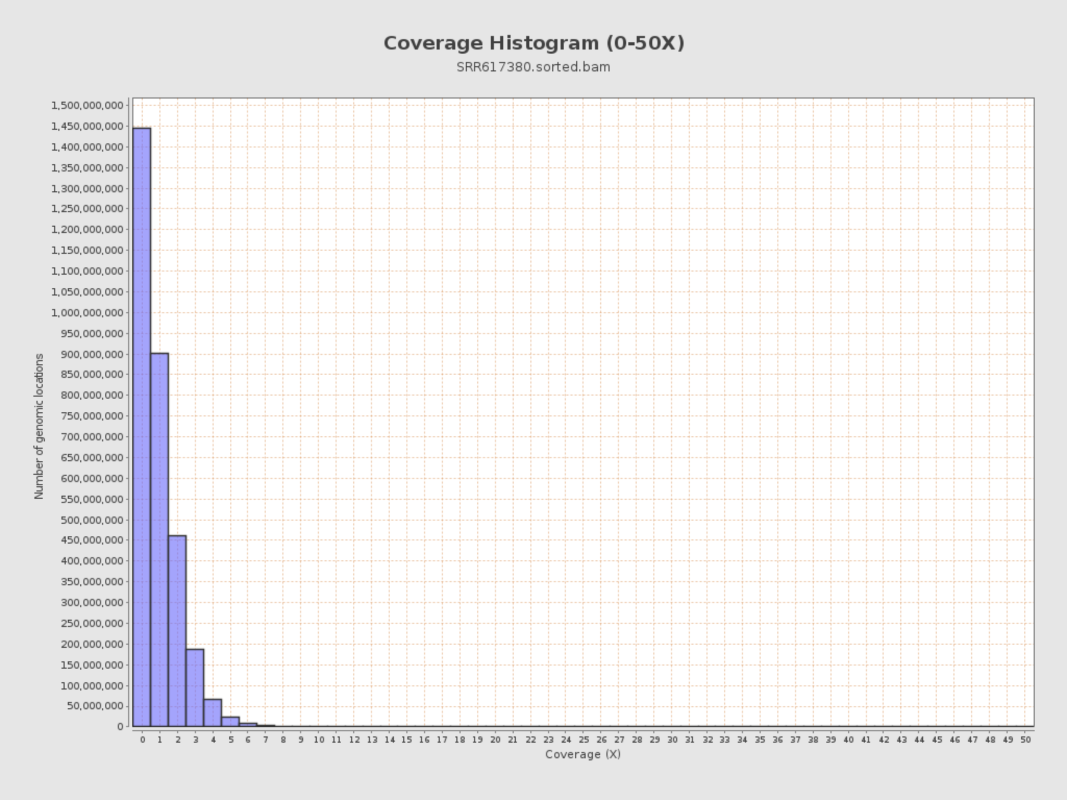
3. Results : Coverage across reference



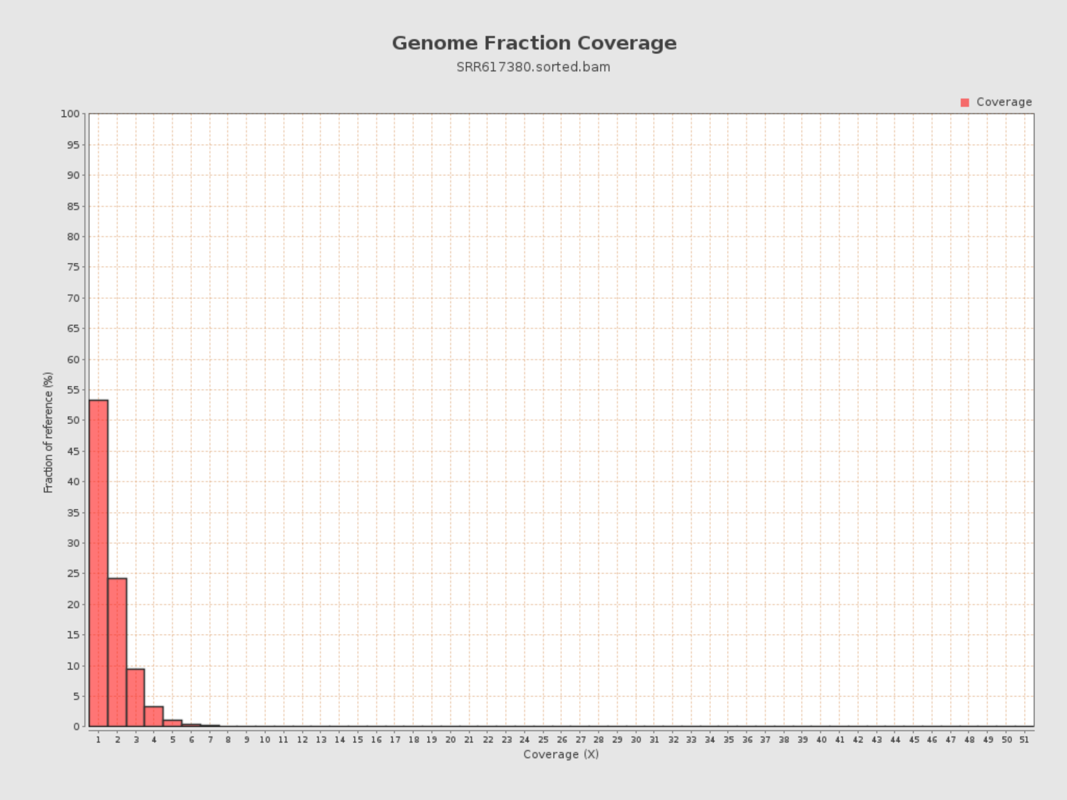
4. Results : Coverage Histogram



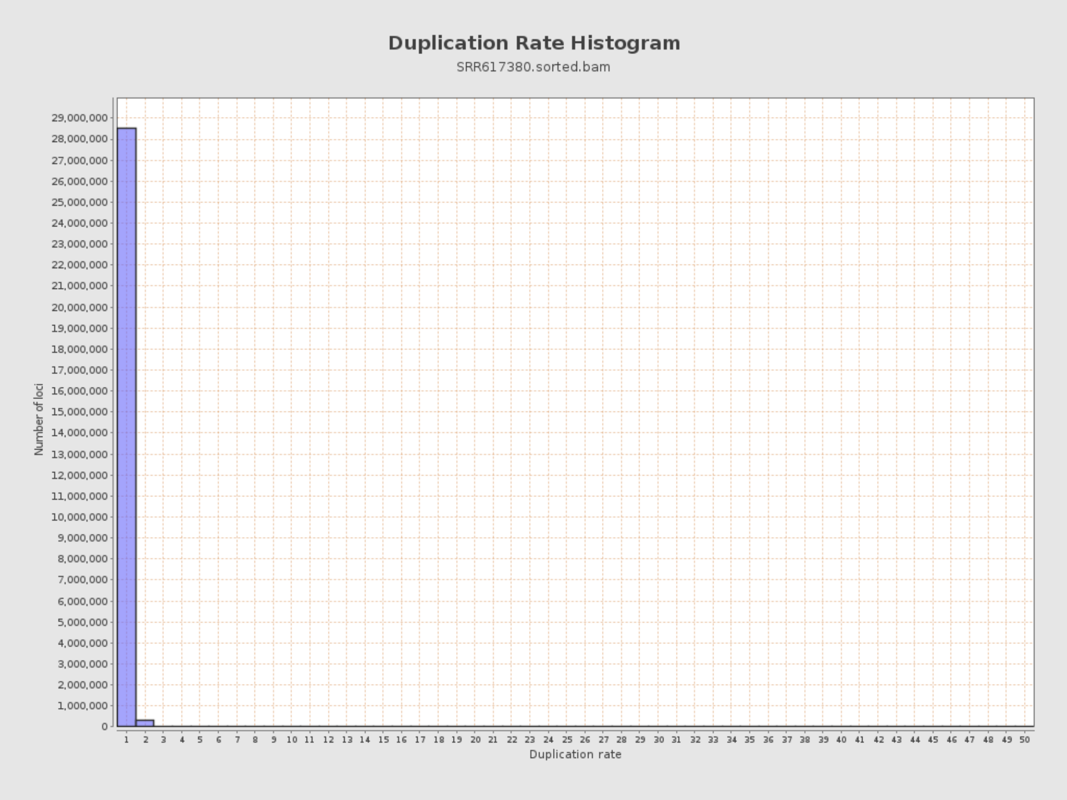
5. Results : Coverage Histogram (0-50X)



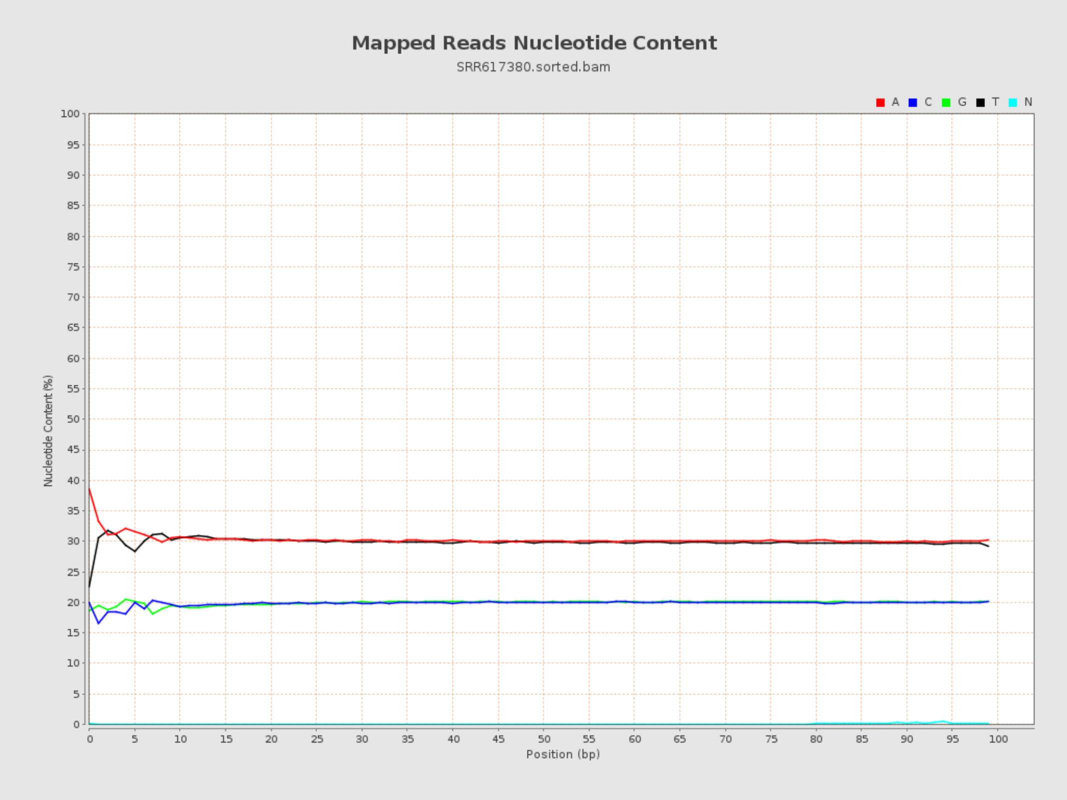
6. Results : Genome Fraction Coverage



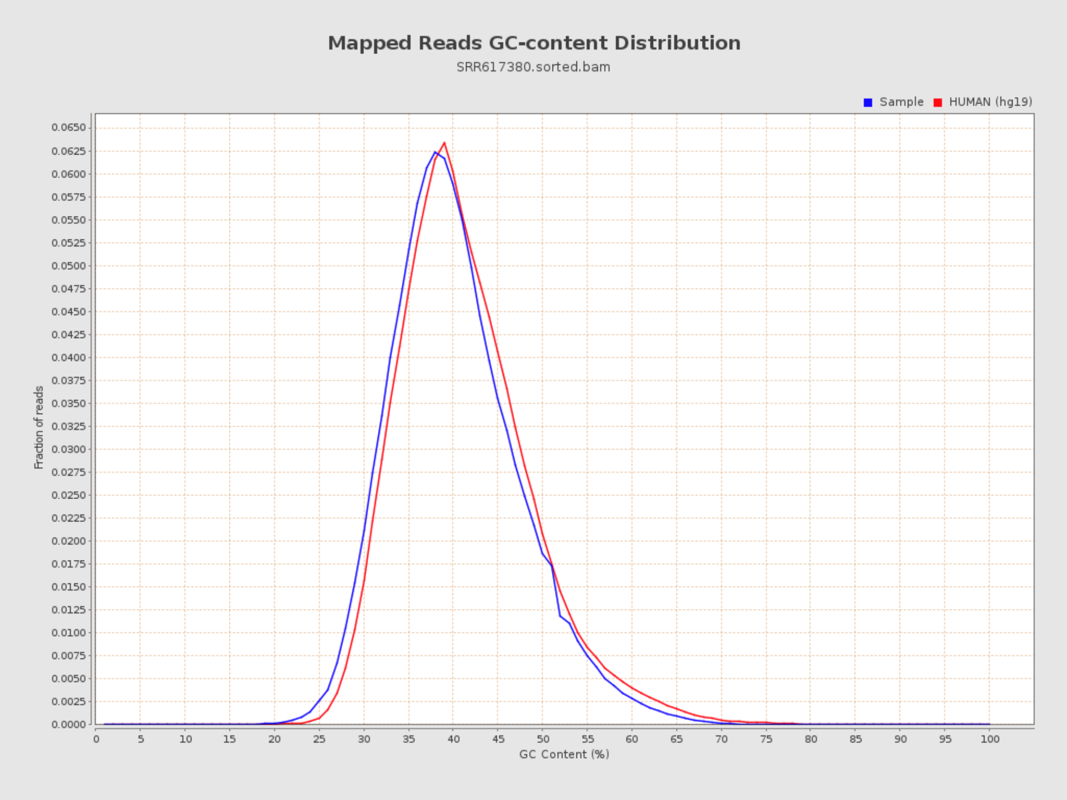
7. Results : Duplication Rate Histogram



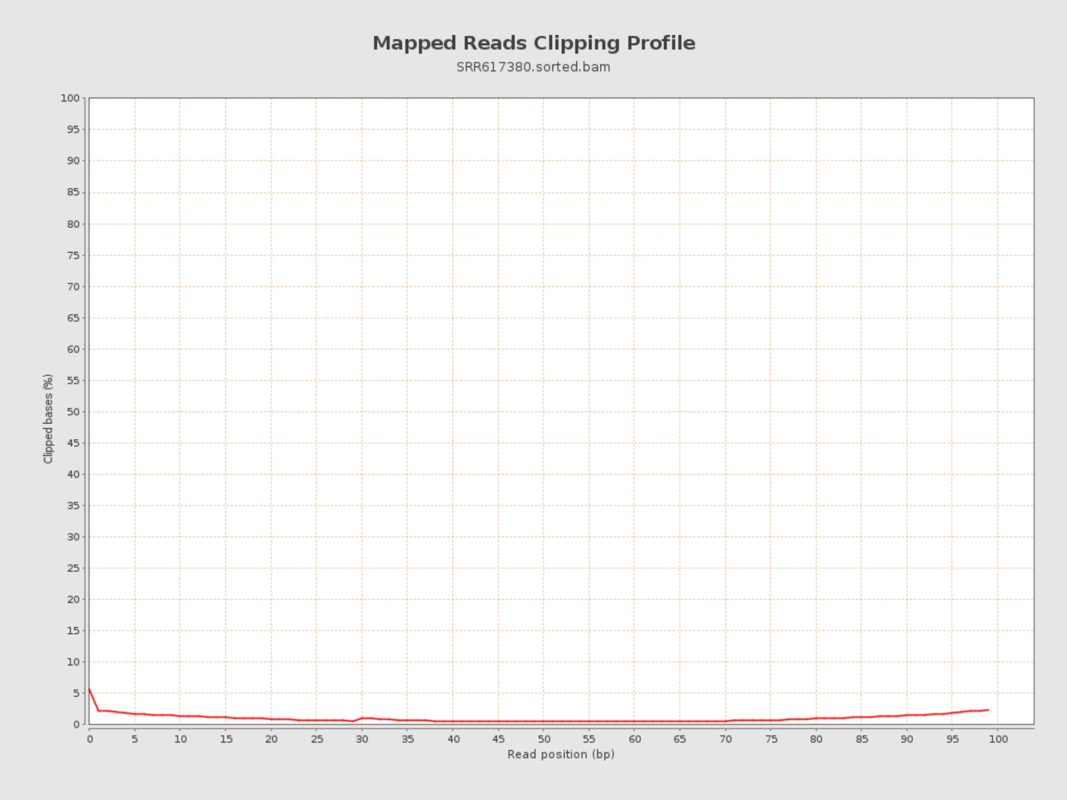
8. Results : Mapped Reads Nucleotide Content



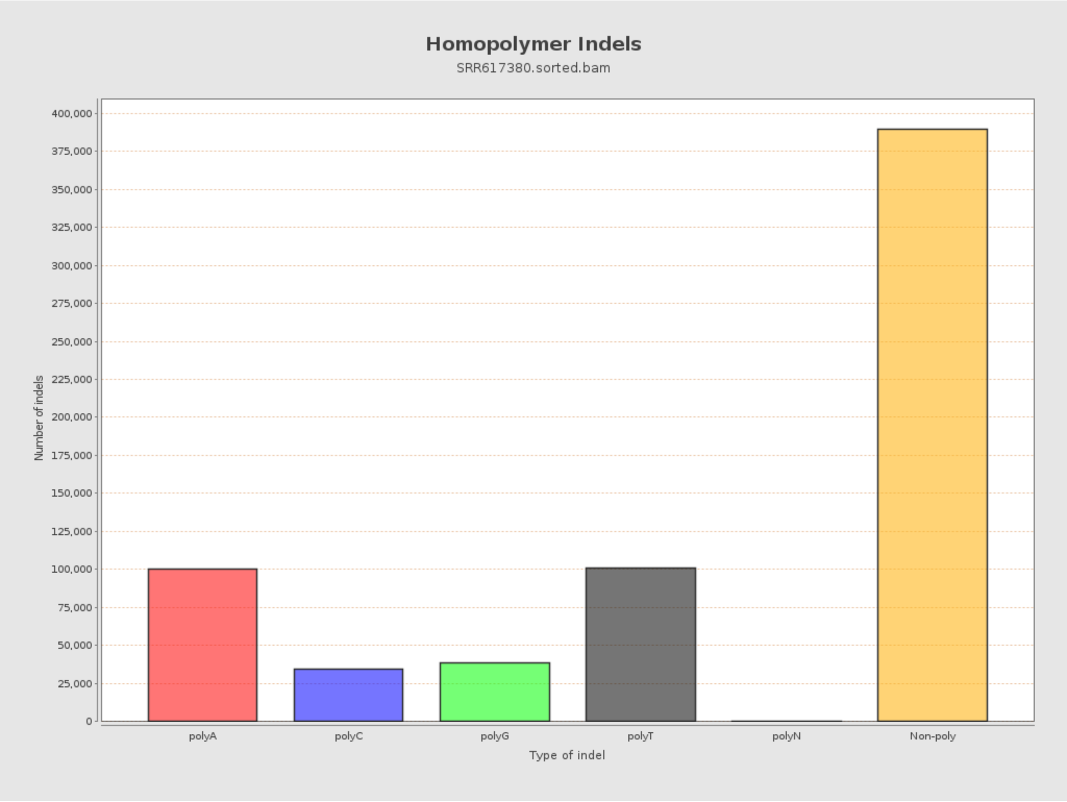
9. Results : Mapped Reads GC-content Distribution



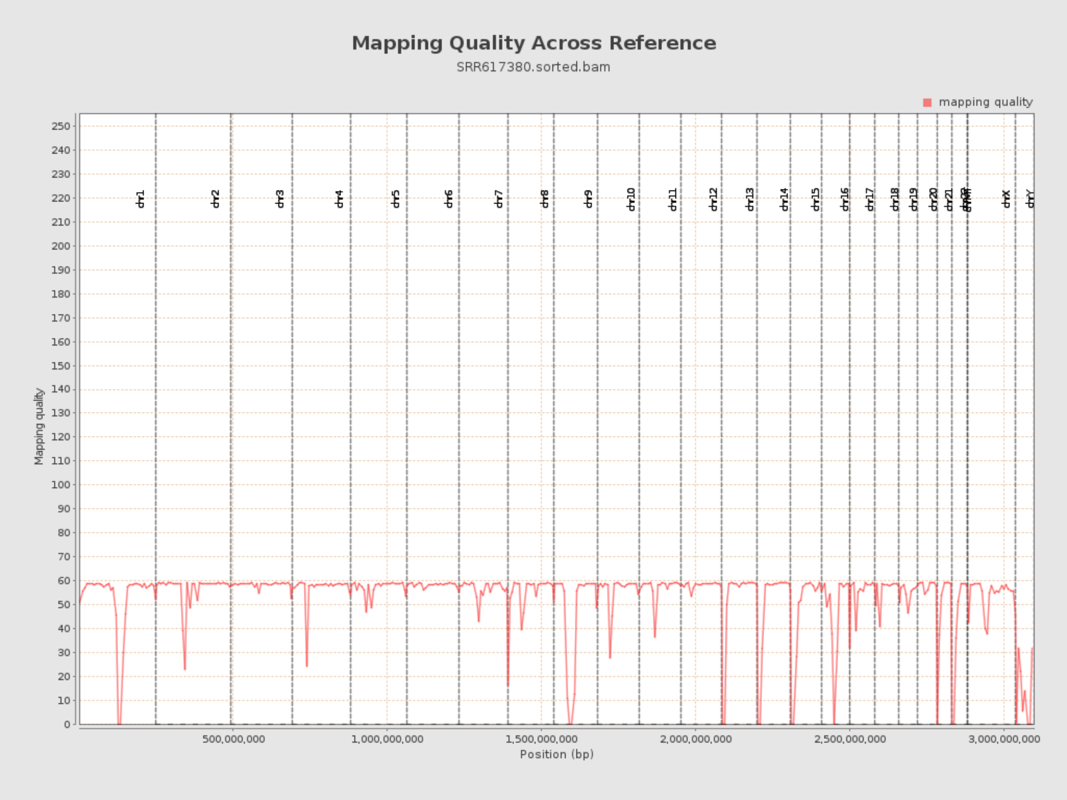
10. Results : Mapped Reads Clipping Profile



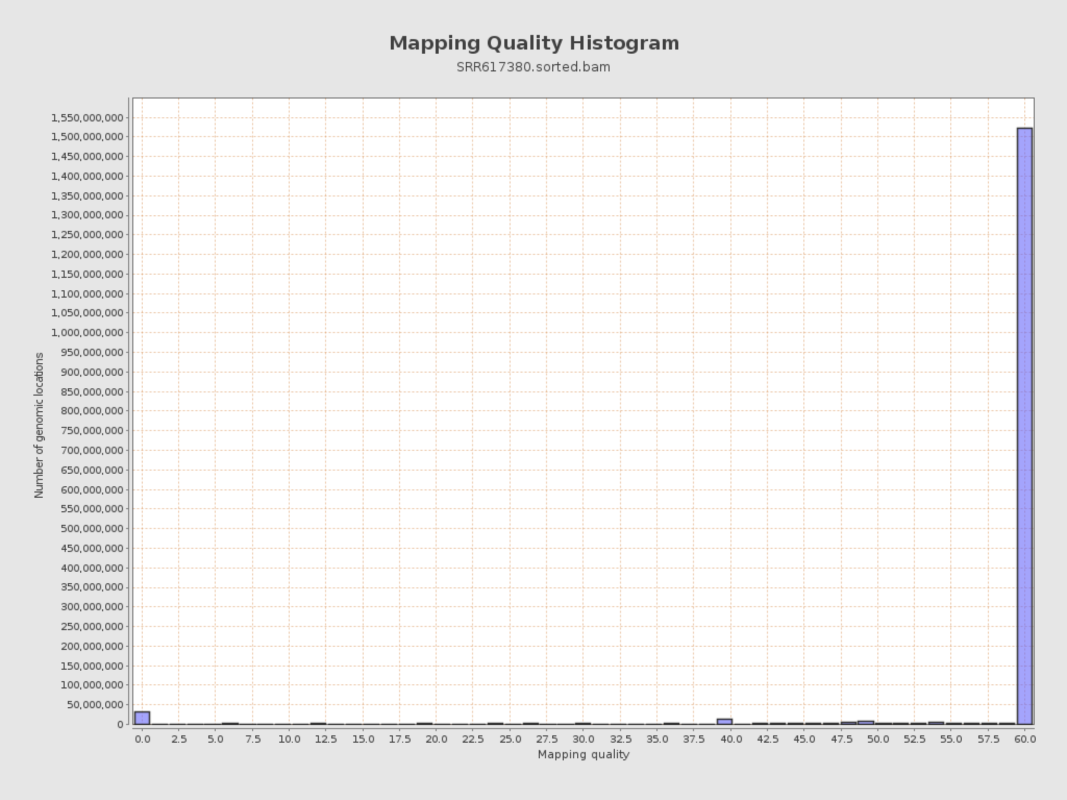
11. Results : Homopolymer Indels



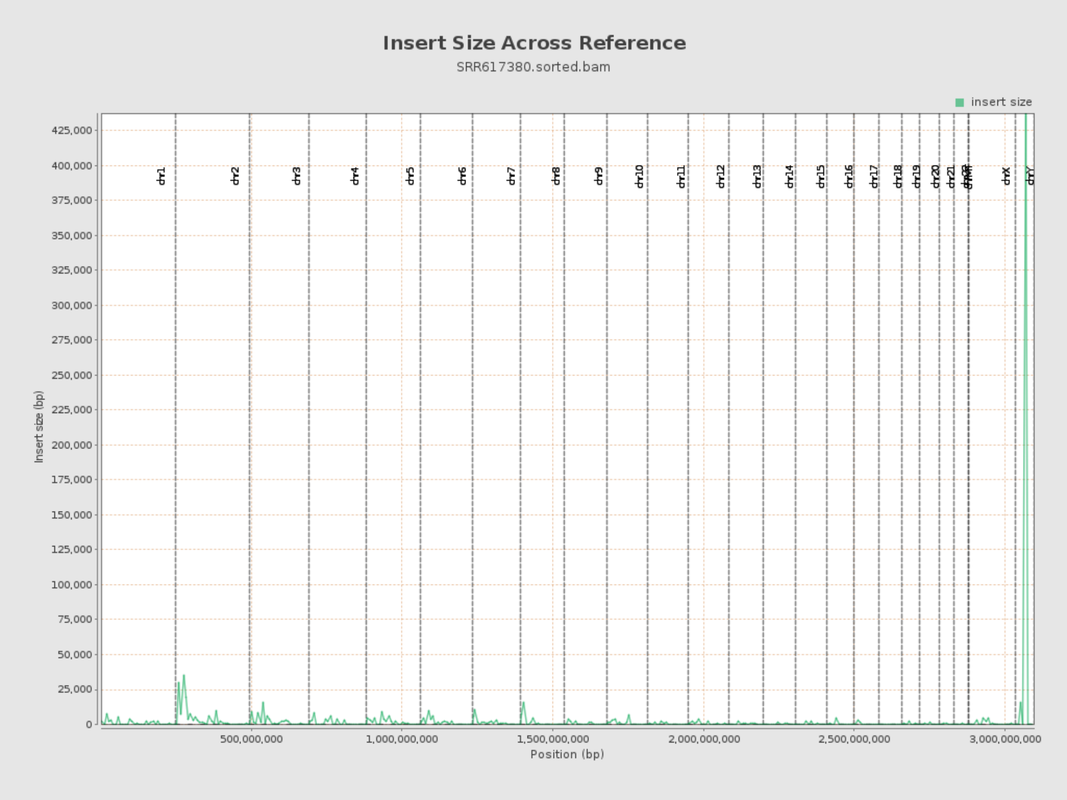
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram