Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:21:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173845.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_SRR10173845 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173845_1.fastq.gz SRR10173845_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:21:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173845.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,587,812
Mapped reads	3,488,248 / 97.22%
Unmapped reads	99,564 / 2.78%
Mapped paired reads	3,488,248 / 97.22%
Mapped reads, first in pair	1,750,037 / 48.78%
Mapped reads, second in pair	1,738,211 / 48.45%
Mapped reads, both in pair	3,419,852 / 95.32%
Mapped reads, singletons	68,396 / 1.91%
Secondary alignments	0
Supplementary alignments	359,279 / 10.01%
Read min/max/mean length	30 / 133 / 128.18
Duplicated reads (estimated)	2,667,086 / 74.34%
Duplication rate	63.9%
Clipped reads	1,550,162 / 43.21%

2.2. ACGT Content

Number/percentage of A's	122,572,146 / 29.94%
Number/percentage of C's	80,446,744 / 19.65%
Number/percentage of T's	122,586,976 / 29.94%
Number/percentage of G's	83,812,763 / 20.47%
Number/percentage of N's	4,946 / 0%

GC Percentage	40.12%

2.3. Coverage

Mean	0.1323
Standard Deviation	2.0541

2.4. Mapping Quality

Mean Mapping Quality	52.69

2.5. Insert size

Mean	1,063,072.78
Standard Deviation	9,789,703.66
P25/Median/P75	142 / 201 / 284

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	4,377,034
Insertions	43,341
Mapped reads with at least one insertion	1.2%
Deletions	116,016
Mapped reads with at least one deletion	3.25%
Homopolymer indels	41.6%

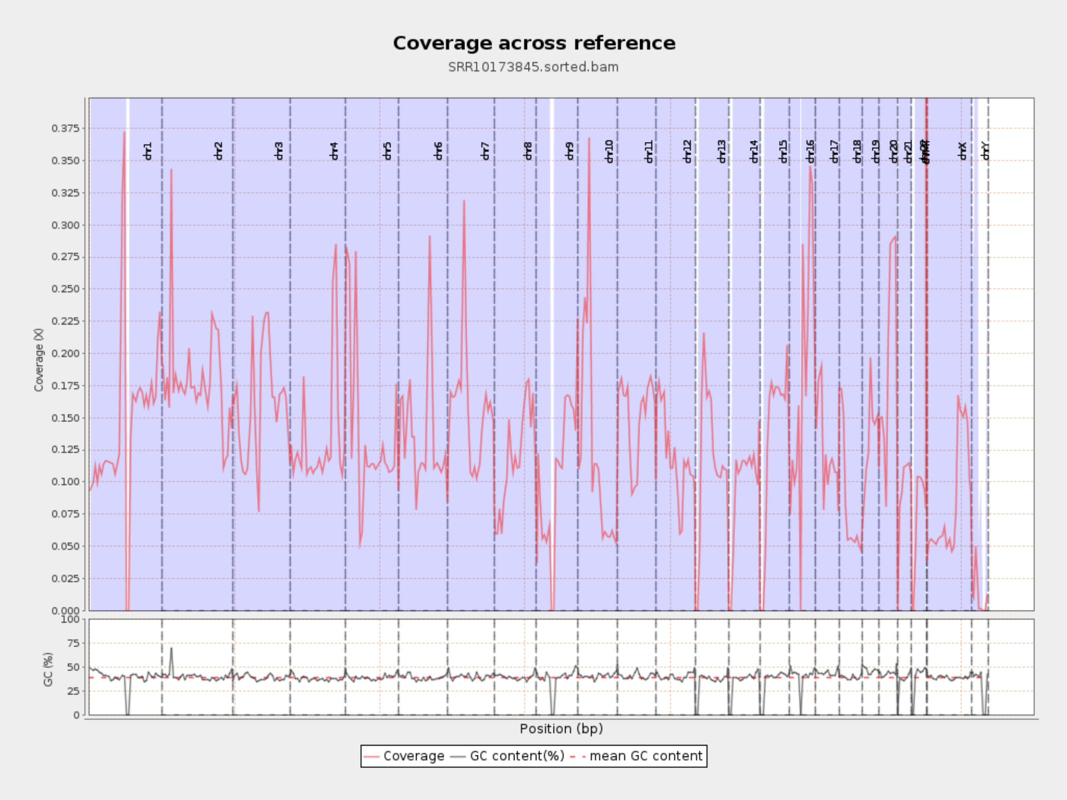
2.7. Chromosome stats

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

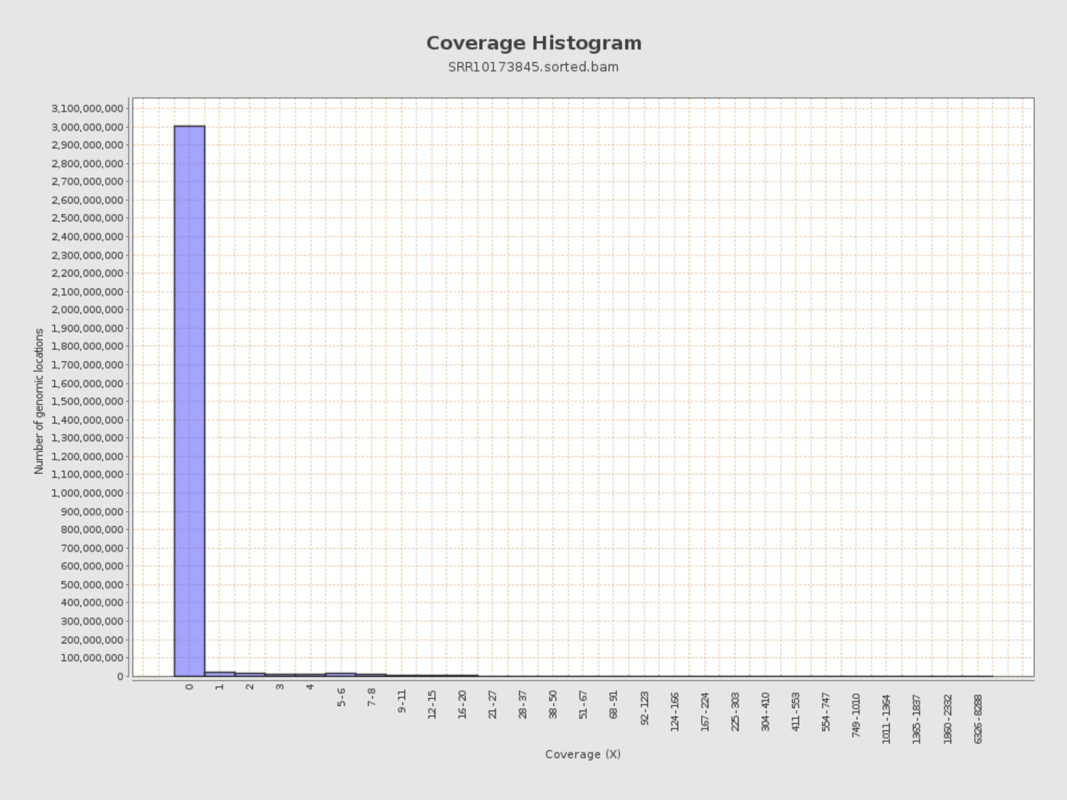
		bases	coverage	deviation
chr1	249250621	36316612	0.1457	1.7045
chr2	243199373	43555780	0.1791	5.8735
chr3	198022430	31767823	0.1604	1.1273
chr4	191154276	25125550	0.1314	1.2094
chr5	180915260	25175313	0.1392	1.0416
chr6	171115067	23706569	0.1385	1.0955
chr7	159138663	25150145	0.158	1.6281
chr8	146364022	17505790	0.1196	1.1072
chr9	141213431	14610843	0.1035	1.0736
chr10	135534747	16778465	0.1238	2.1396
chr11	135006516	20418363	0.1512	1.1205
chr12	133851895	16057966	0.12	0.9631
chr13	115169878	13342628	0.1159	0.9538
chr14	107349540	10033297	0.0935	0.8607
chr15	102531392	13759971	0.1342	1.0047
chr16	90354753	16442196	0.182	1.5076
chr17	81195210	9978358	0.1229	1.0358
chr18	78077248	6544245	0.0838	1.4504
chr19	59128983	7865432	0.133	1.6296
chr20	63025520	12626794	0.2003	1.2714
chr21	48129895	4490968	0.0933	0.8959
chr22	51304566	3571414	0.0696	0.6922
chrMT	16571	1288841	77.7769	55.299
chrX	155270560	12922589	0.0832	0.8075

chrY	59373566	656015	0.011	0.495

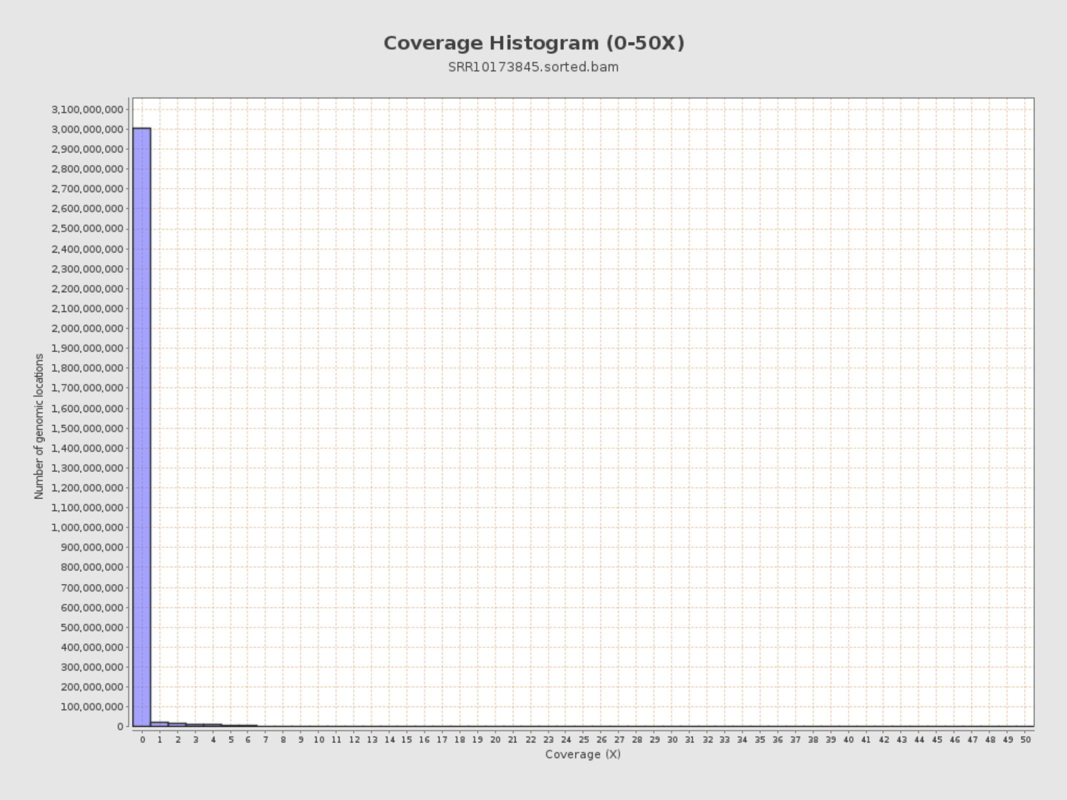
3. Results : Coverage across reference



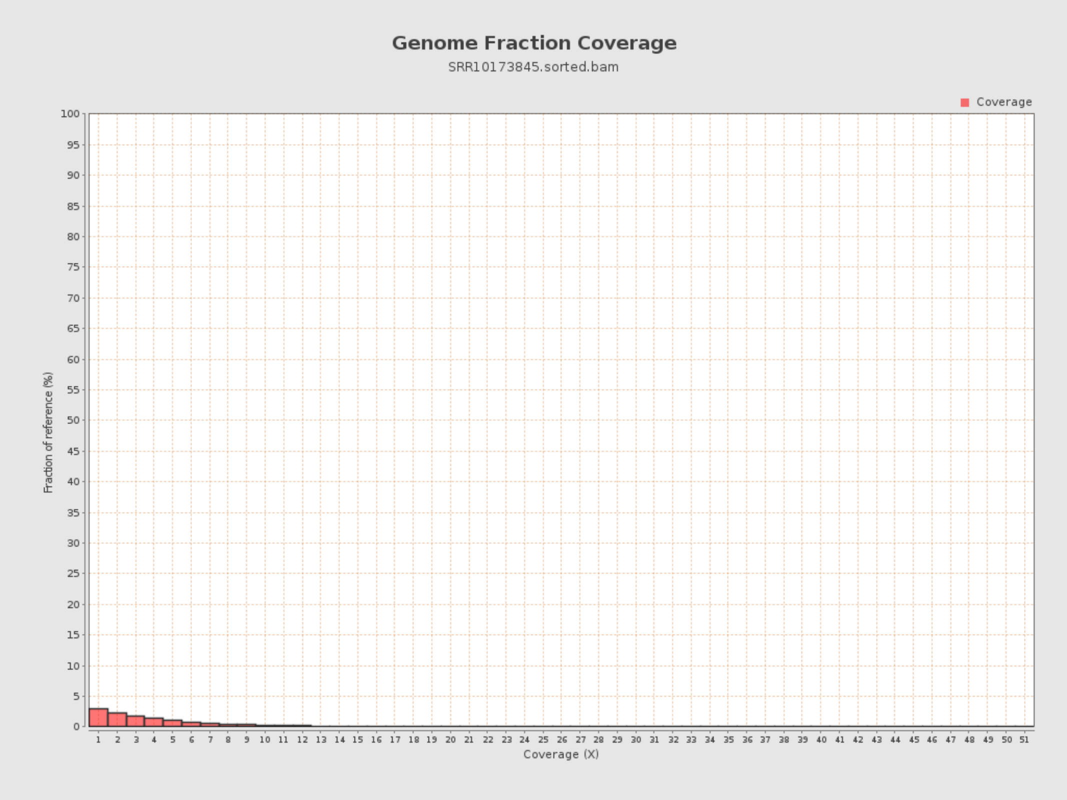
4. Results : Coverage Histogram



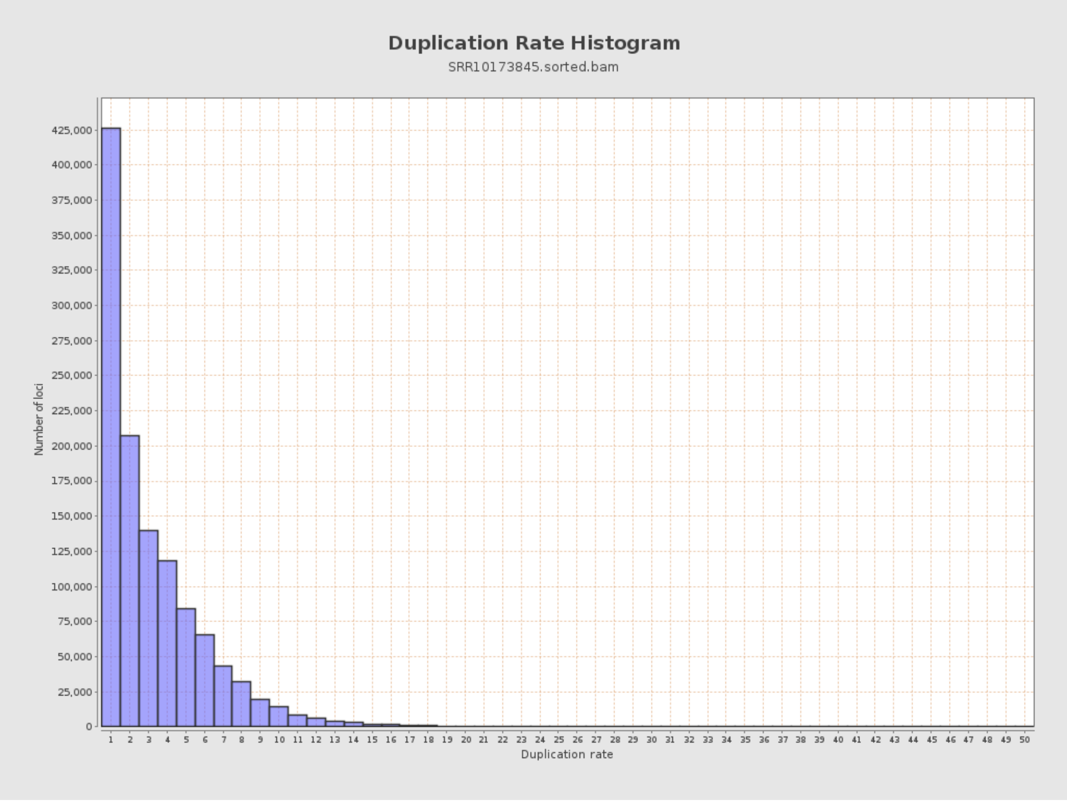
5. Results : Coverage Histogram (0-50X)



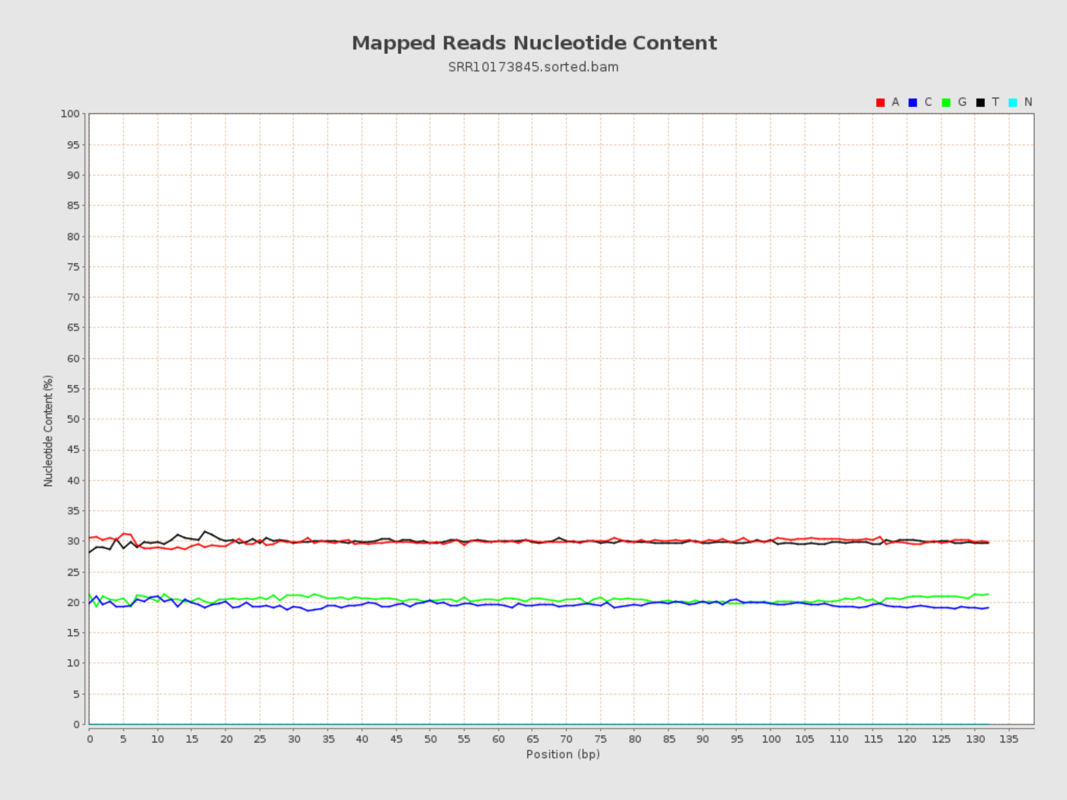
6. Results : Genome Fraction Coverage



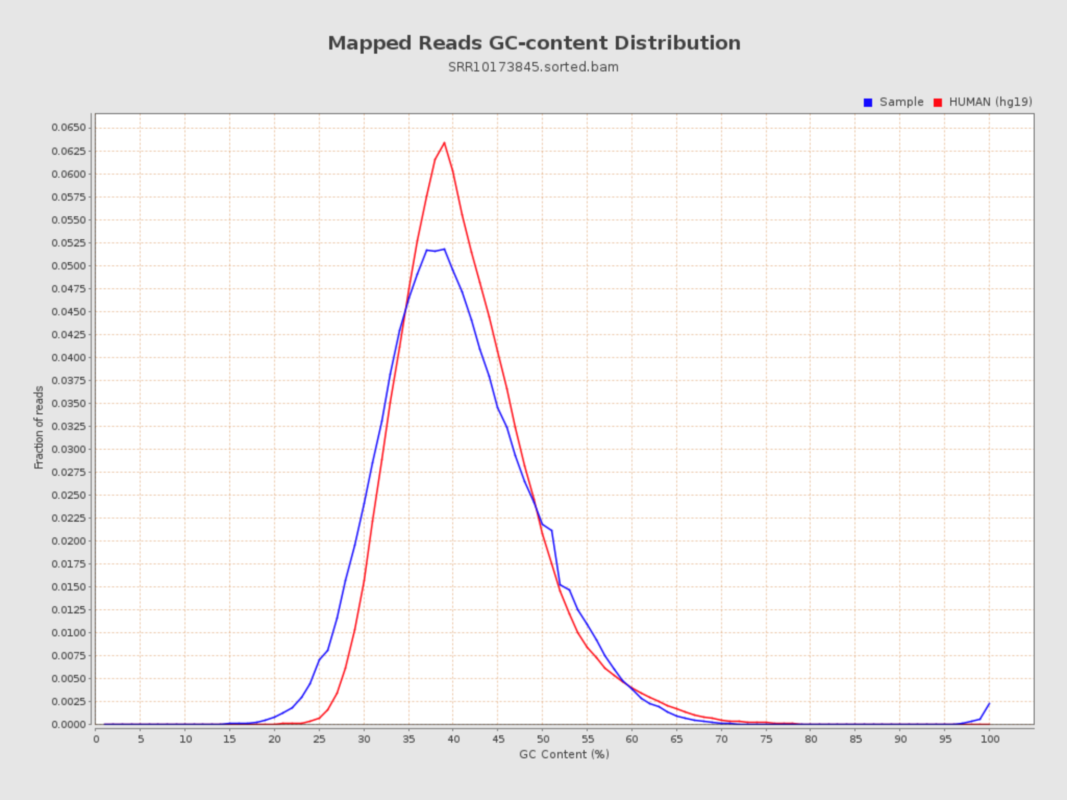
7. Results : Duplication Rate Histogram



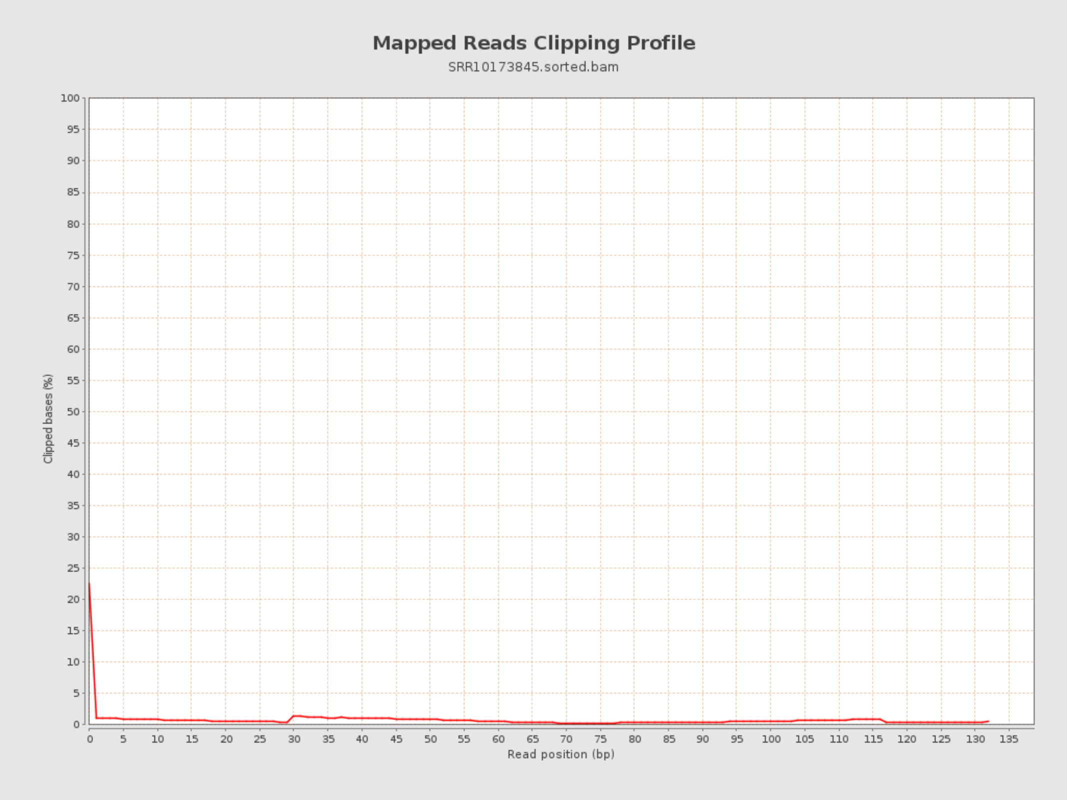
8. Results : Mapped Reads Nucleotide Content



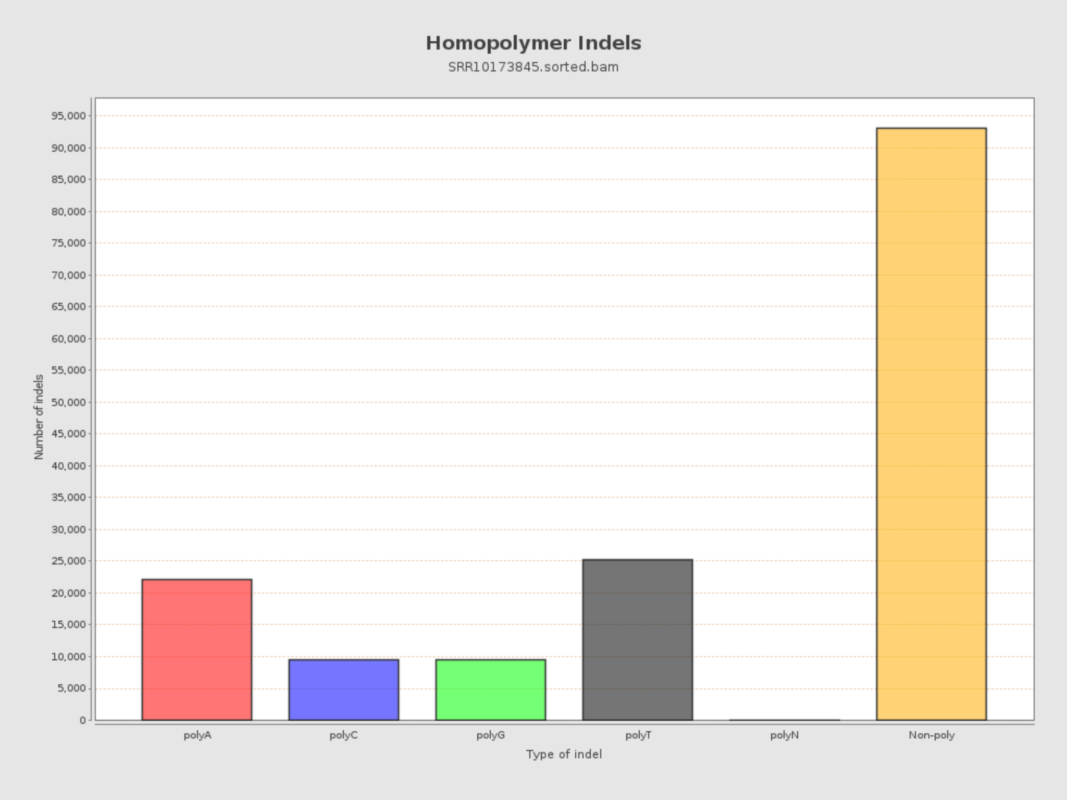
9. Results : Mapped Reads GC-content Distribution



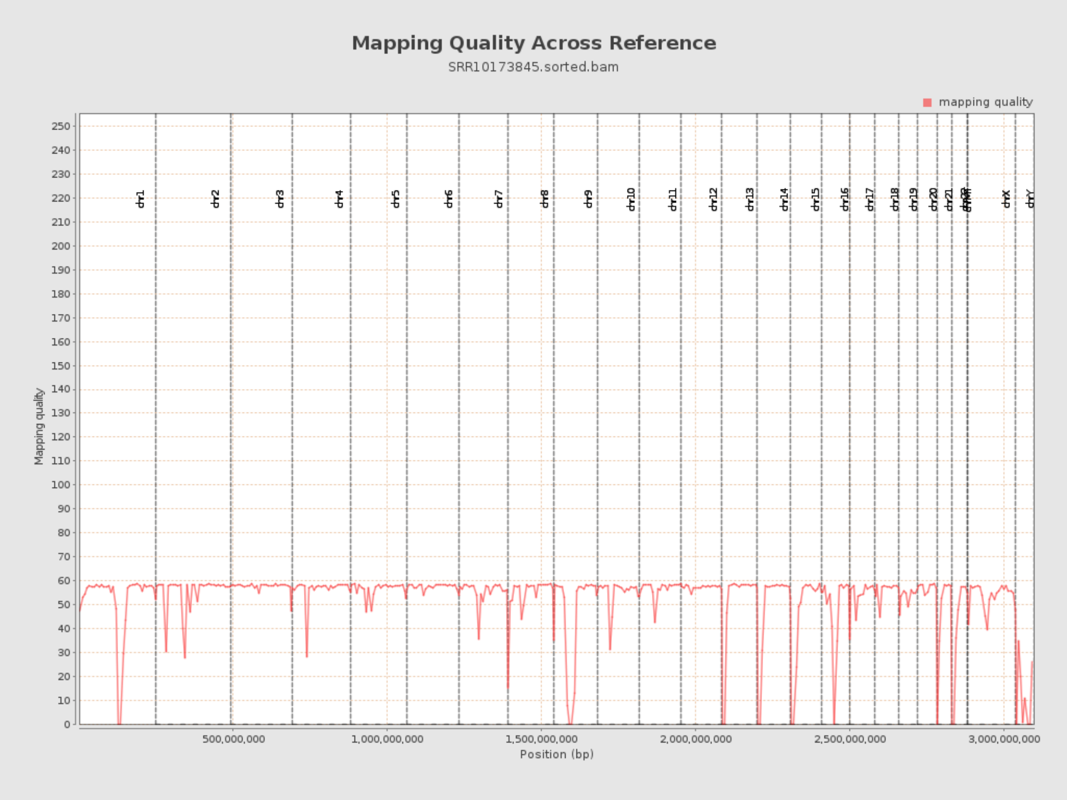
10. Results : Mapped Reads Clipping Profile



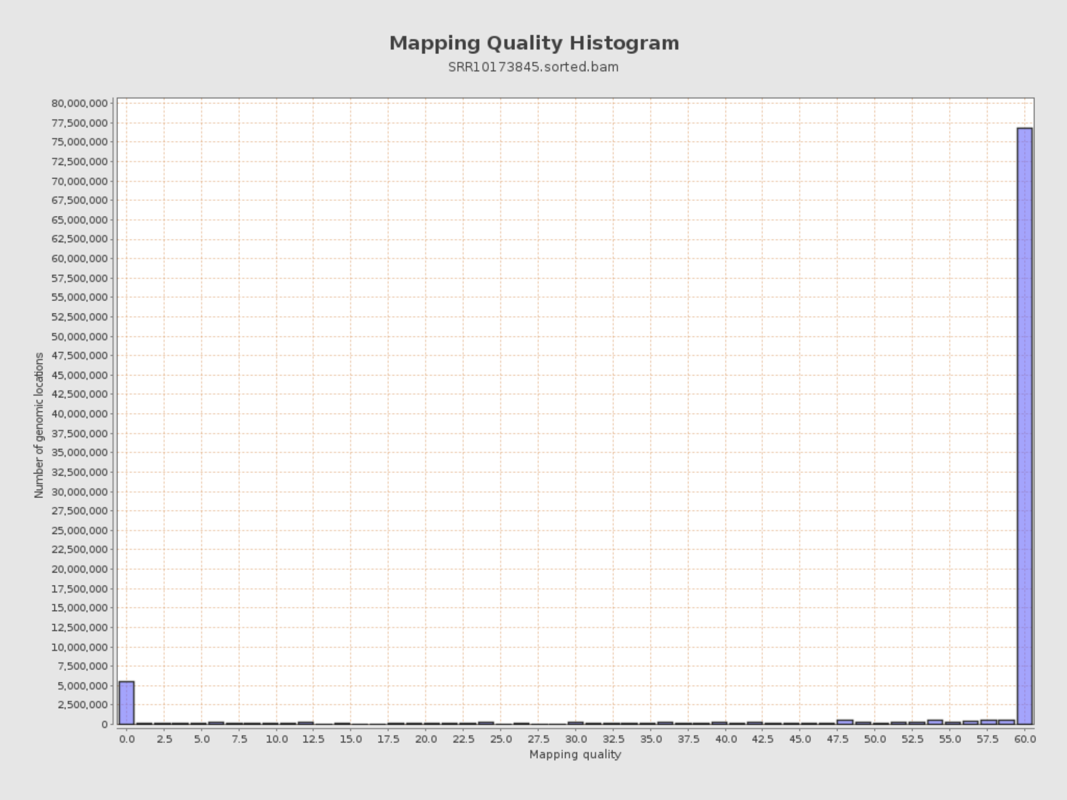
11. Results : Homopolymer Indels



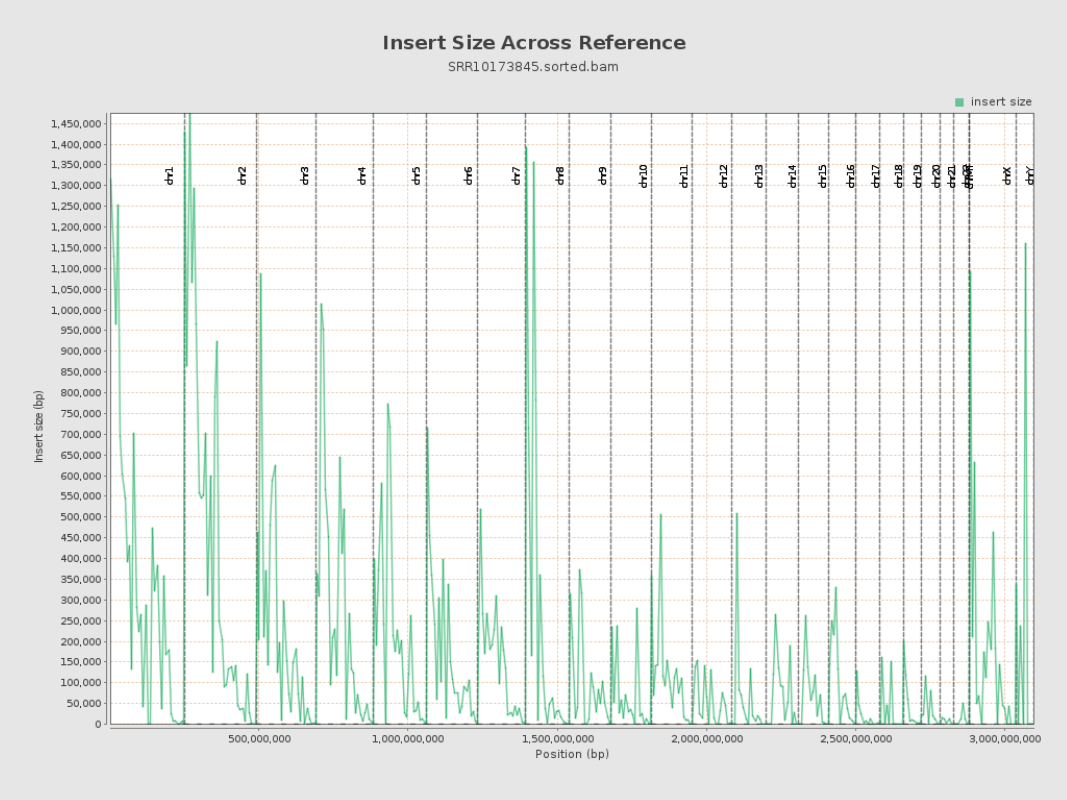
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram