Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/26 18:33:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781849.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_SRR1781849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781849_1.fastq.gz SRR1781849_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 26 18:33:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781849.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	157,371,624
Mapped reads	153,893,276 / 97.79%
Unmapped reads	3,478,348 / 2.21%
Mapped paired reads	153,893,276 / 97.79%
Mapped reads, first in pair	77,590,219 / 49.3%
Mapped reads, second in pair	76,303,057 / 48.49%
Mapped reads, both in pair	152,154,314 / 96.68%
Mapped reads, singletons	1,738,962 / 1.11%
Secondary alignments	0
Supplementary alignments	402,256 / 0.26%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	10,574,612 / 6.72%
Duplication rate	6.6%
Clipped reads	5,927,815 / 3.77%

2.2. ACGT Content

Number/percentage of A's	4,552,455,316 / 29.76%
Number/percentage of C's	3,081,534,061 / 20.15%
Number/percentage of T's	4,539,910,195 / 29.68%
Number/percentage of G's	3,120,010,808 / 20.4%
Number/percentage of N's	1,731,369 / 0.01%

GC Percentage	40.54%

2.3. Coverage

Mean	4.9419
Standard Deviation	6.6281

2.4. Mapping Quality

Mean Mapping Quality	54.01

2.5. Insert size

Mean	24,433.85
Standard Deviation	1,487,048.3
P25/Median/P75	173 / 210 / 254

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	57,557,774
Insertions	1,701,187
Mapped reads with at least one insertion	1.09%
Deletions	1,382,660
Mapped reads with at least one deletion	0.88%
Homopolymer indels	47.2%

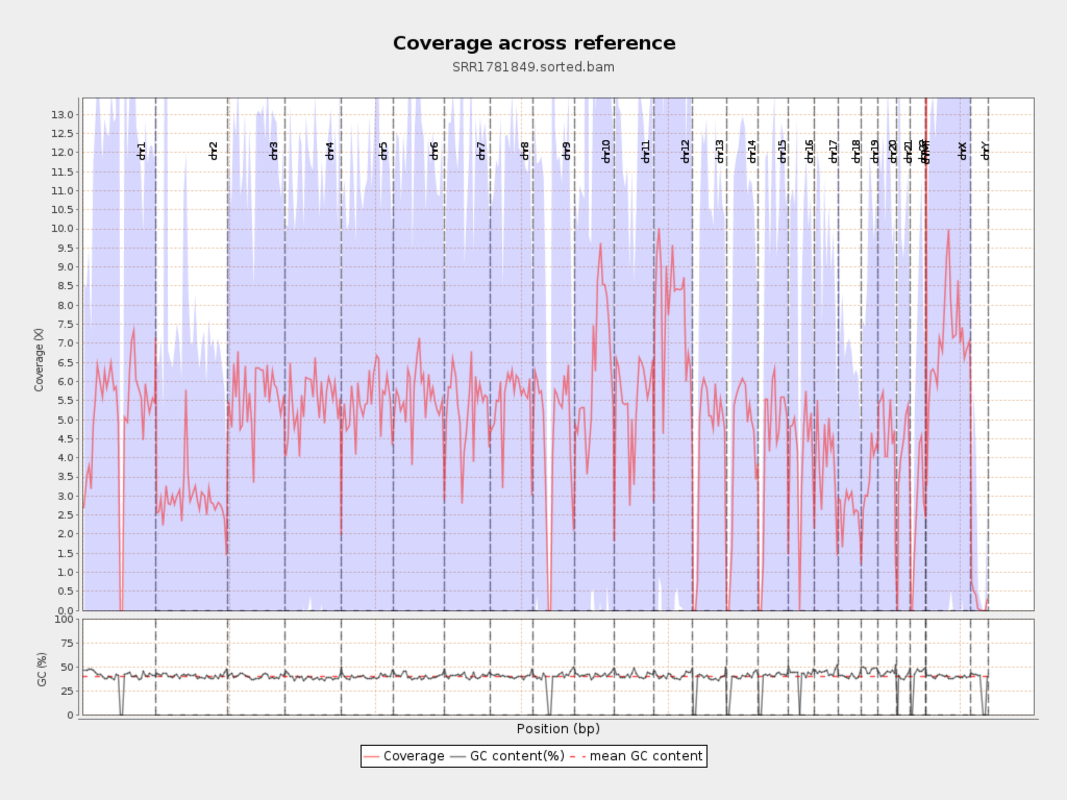
2.7. Chromosome stats

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

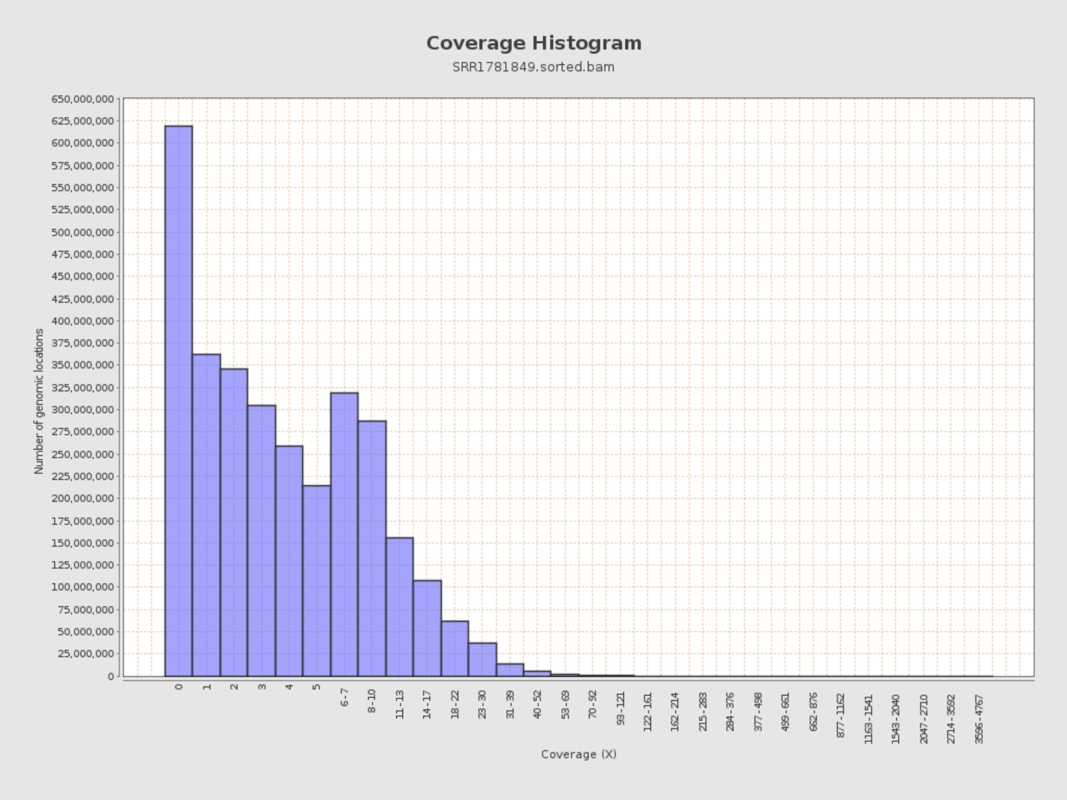
		bases	**coverage**	**deviation**
chr1	249250621	1274073667	5.1116	7.9277
chr2	243199373	712510966	2.9297	5.8783
chr3	198022430	1112263098	5.6169	6.049
chr4	191154276	1050814926	5.4972	5.9612
chr5	180915260	983492094	5.4362	5.7122
chr6	171115067	965121602	5.6402	6.3206
chr7	159138663	835419519	5.2496	6.6671
chr8	146364022	801878941	5.4787	5.878
chr9	141213431	650376917	4.6056	6.6349
chr10	135534747	869110395	6.4125	9.2548
chr11	135006516	741503382	5.4924	6.2943
chr12	133851895	1067918604	7.9784	8.3784
chr13	115169878	504981305	4.3847	5.4094
chr14	107349540	467116646	4.3514	5.5426
chr15	102531392	434886927	4.2415	5.68
chr16	90354753	360553353	3.9904	5.5166
chr17	81195210	323413980	3.9832	5.3741
chr18	78077248	207059404	2.652	4.4401
chr19	59128983	207297192	3.5058	5.8506
chr20	63025520	297479031	4.72	6.345
chr21	48129895	187860458	3.9032	7.0985
chr22	51304566	131855649	2.5701	4.516
chrMT	16571	848071	51.178	17.5595
chrX	155270560	1097086803	7.0656	7.7374

chrY	59373566	13809345	0.2326	2.5773

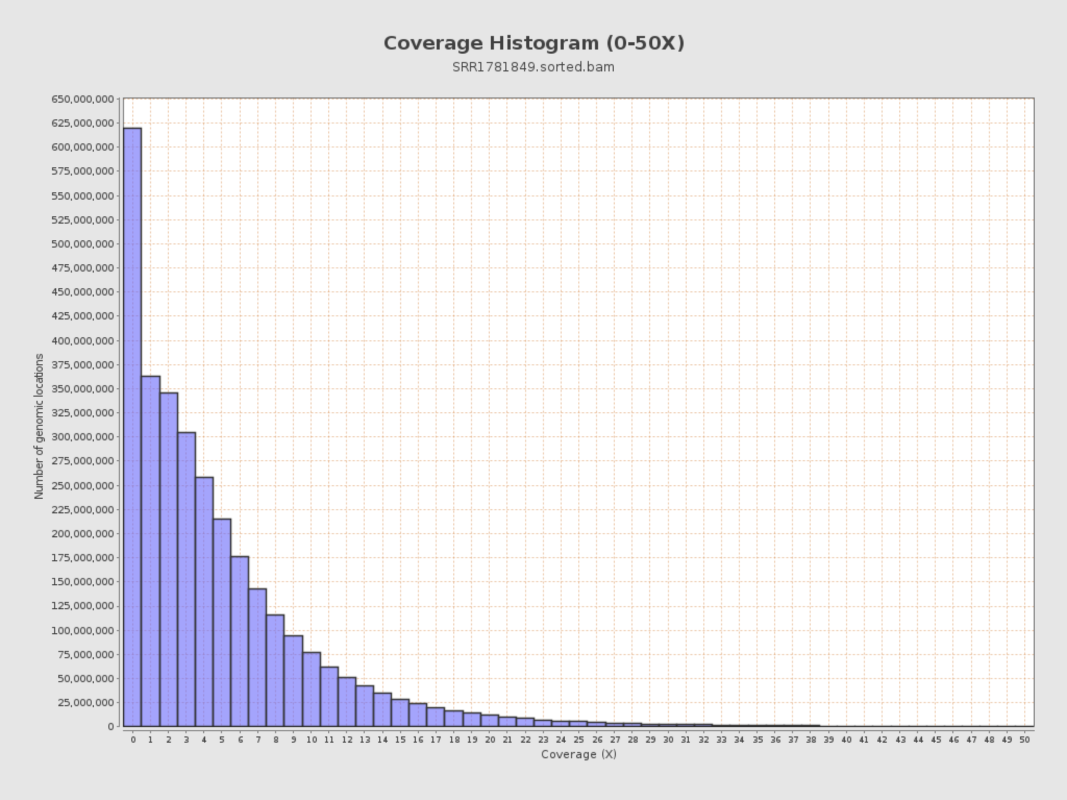
3. Results : Coverage across reference



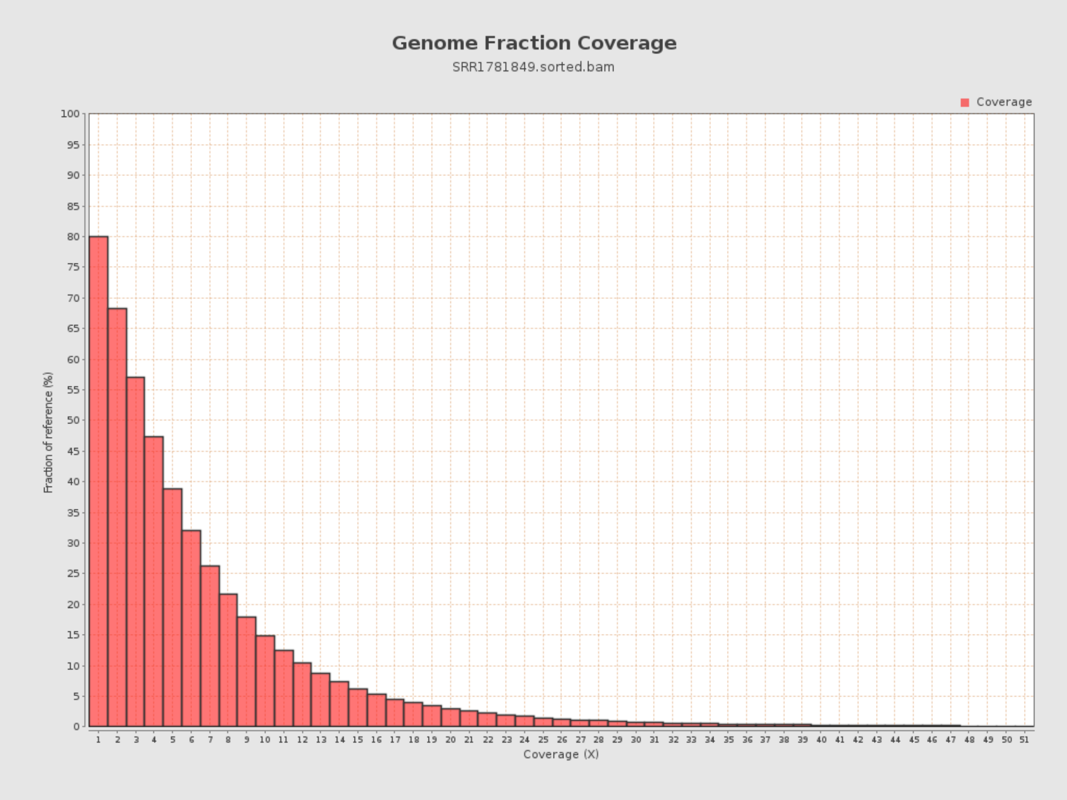
4. Results : Coverage Histogram



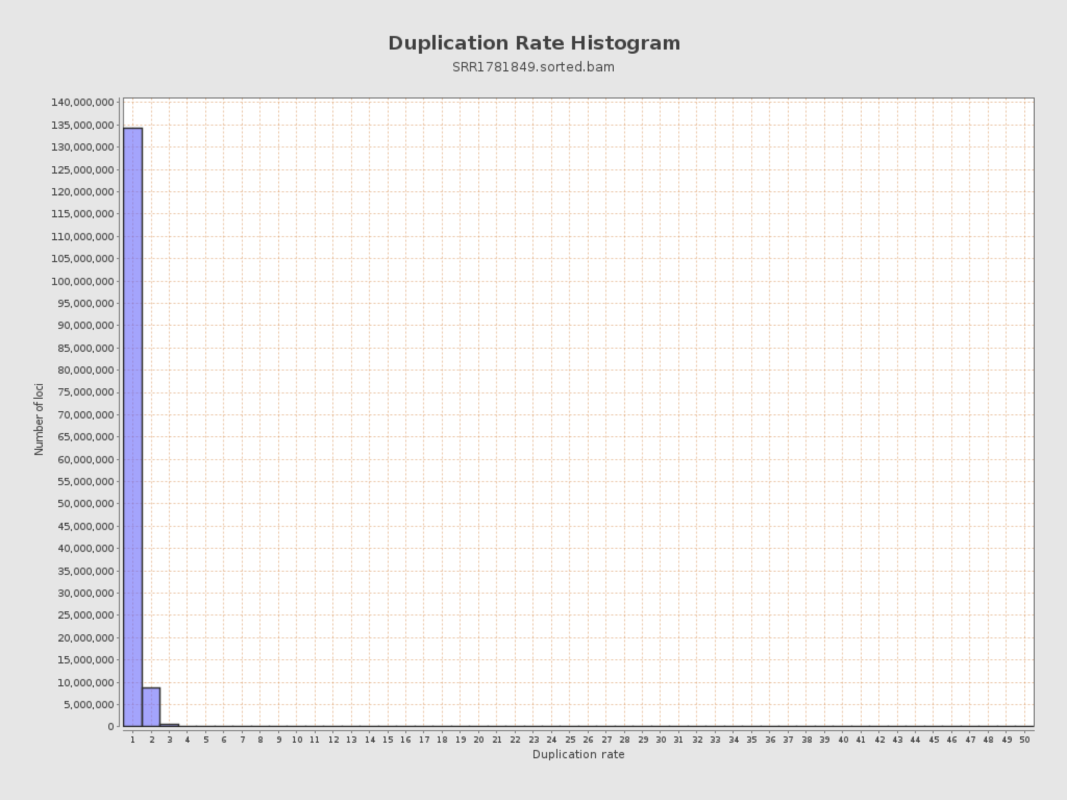
5. Results : Coverage Histogram (0-50X)



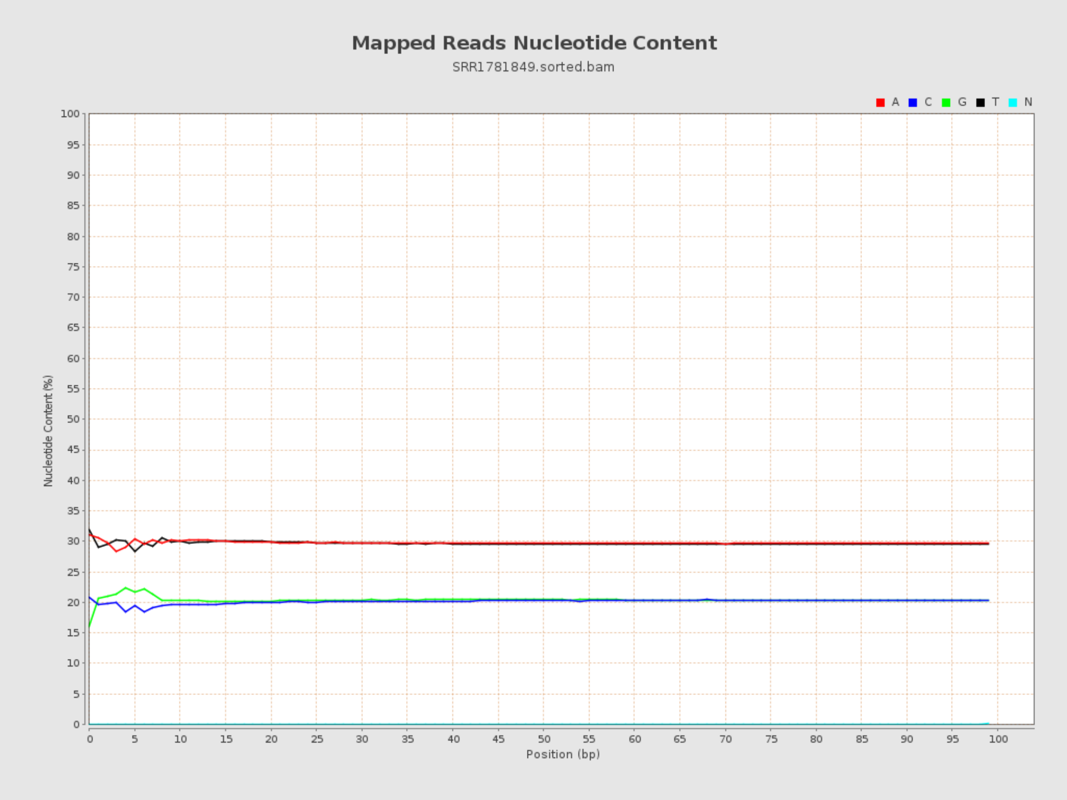
6. Results : Genome Fraction Coverage



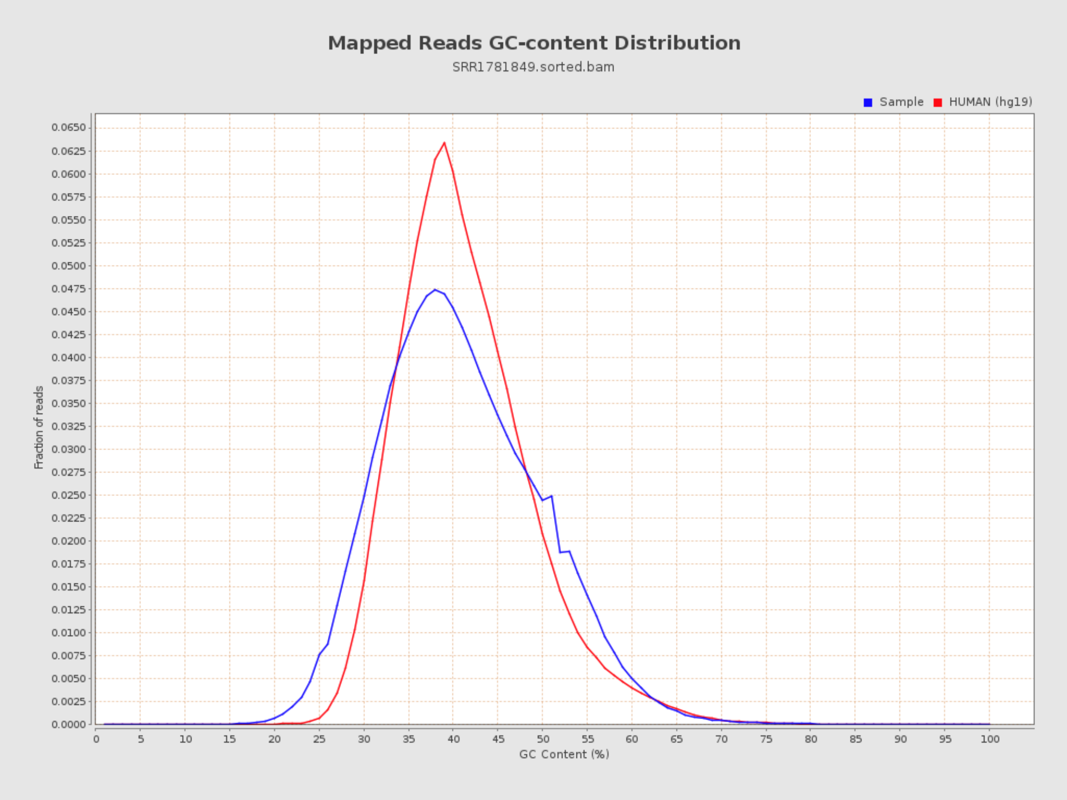
7. Results : Duplication Rate Histogram



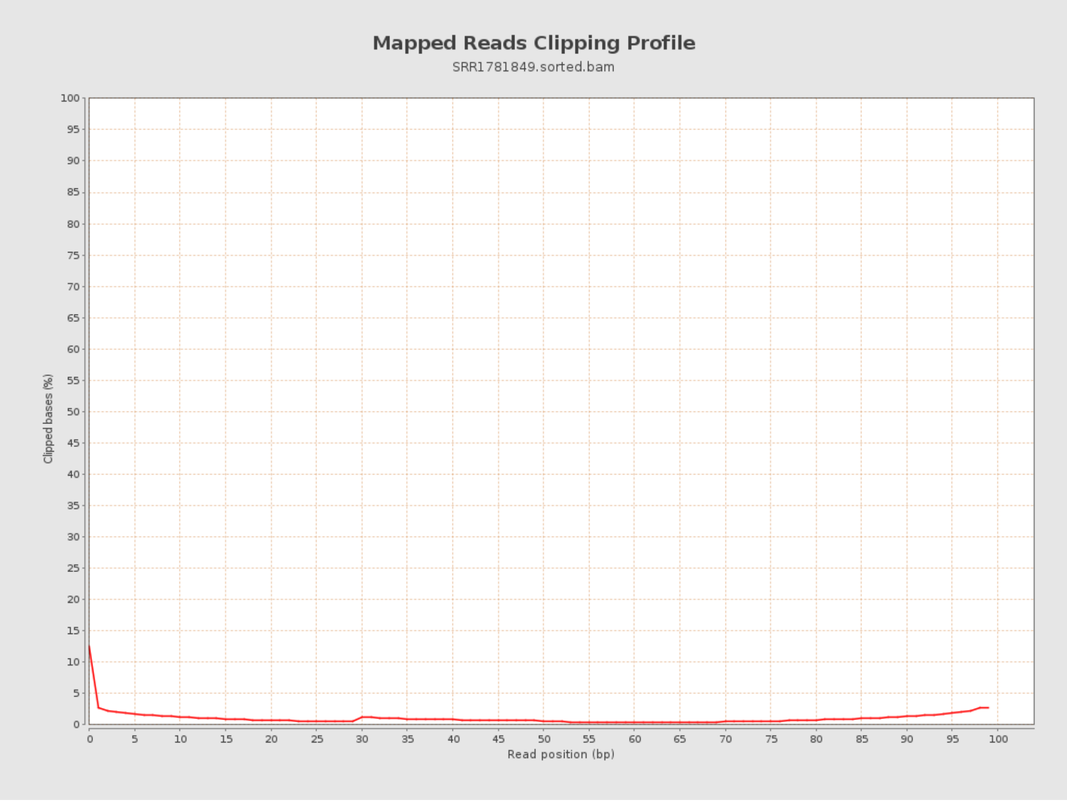
8. Results : Mapped Reads Nucleotide Content



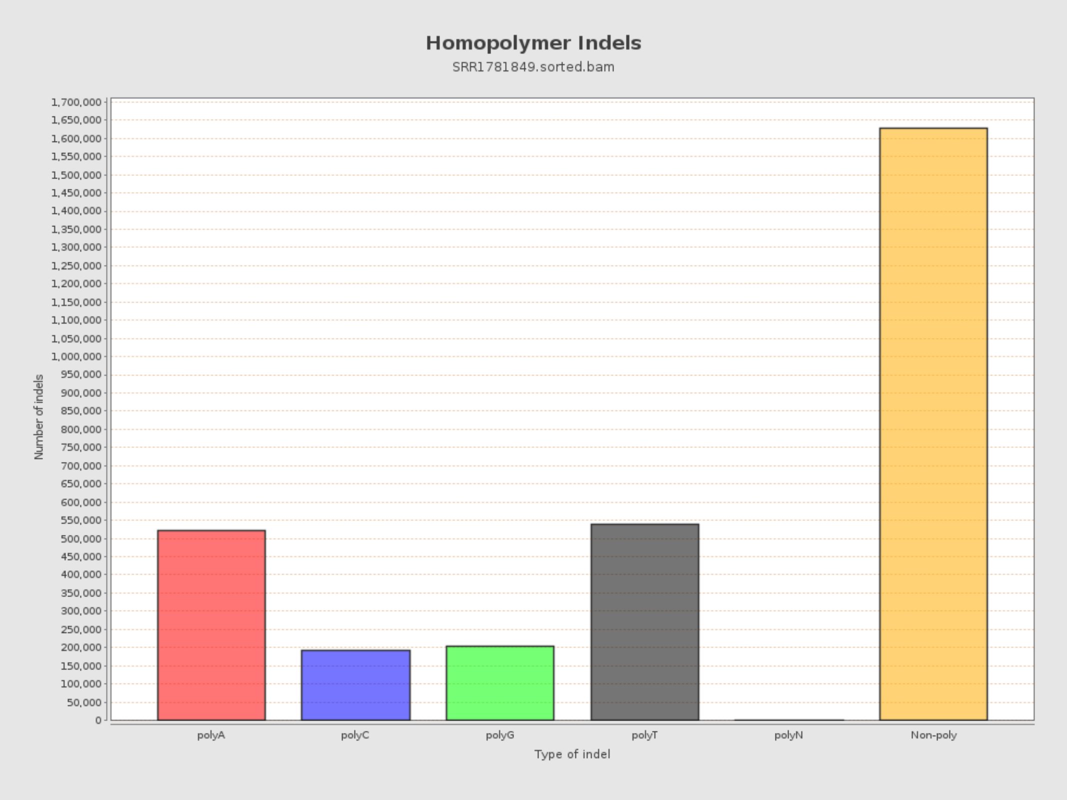
9. Results : Mapped Reads GC-content Distribution



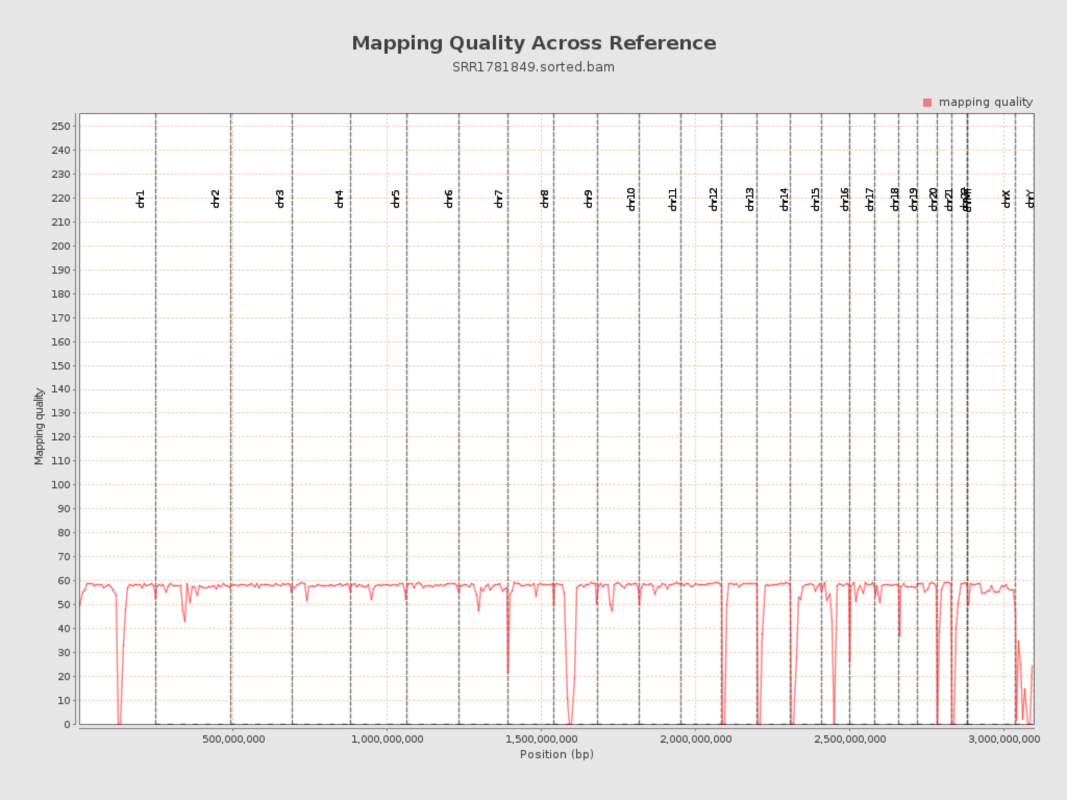
10. Results : Mapped Reads Clipping Profile



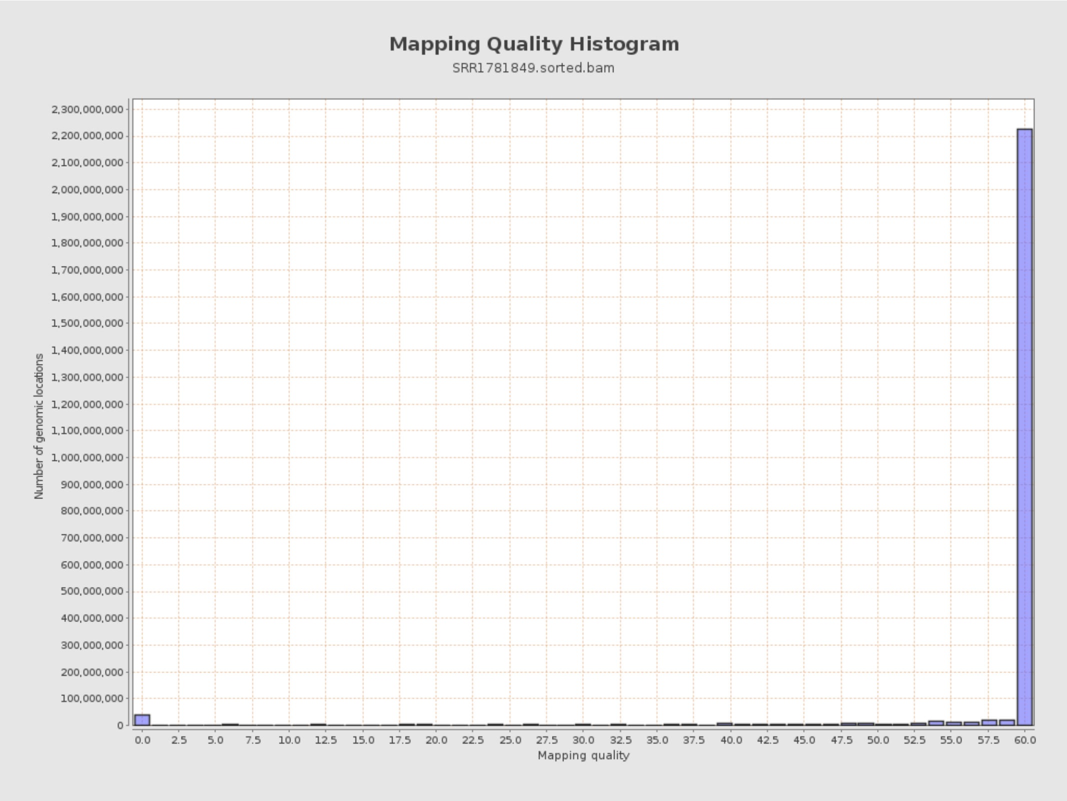
11. Results : Homopolymer Indels



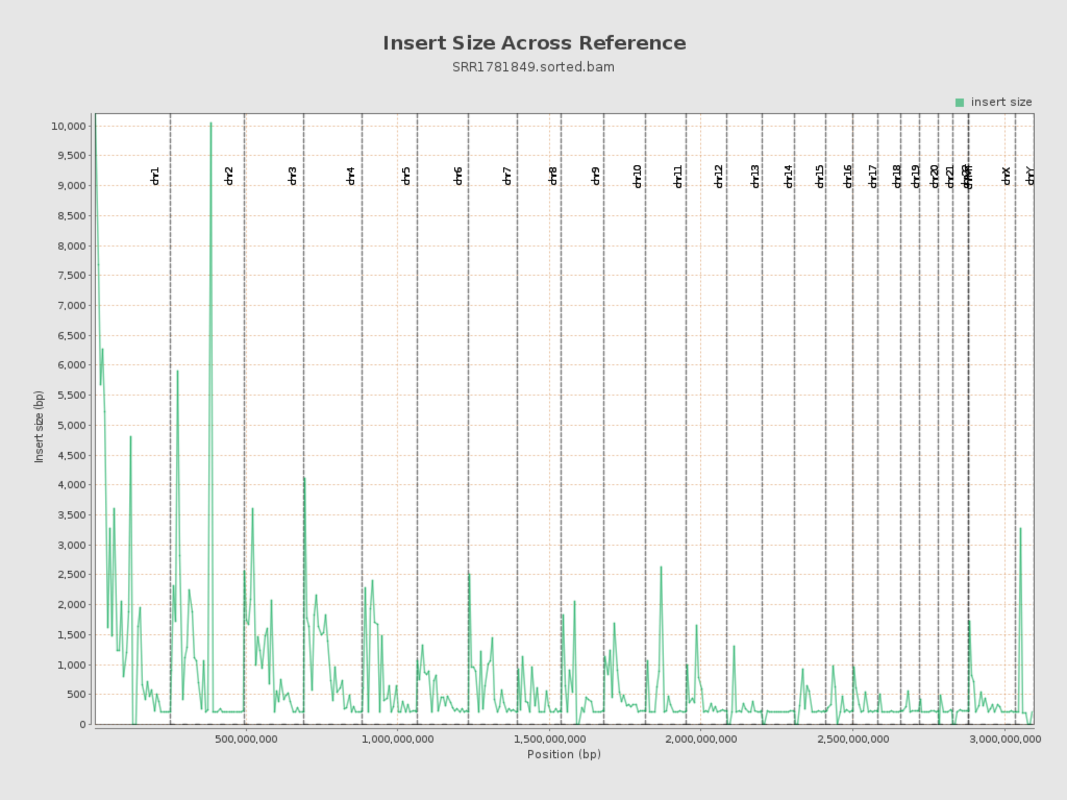
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram