Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/24 07:48:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781807.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_SRR1781807 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781807_1.fastq.gz SRR1781807_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Mar 24 07:48:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781807.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	145,286,944
Mapped reads	142,058,080 / 97.78%
Unmapped reads	3,228,864 / 2.22%
Mapped paired reads	142,058,080 / 97.78%
Mapped reads, first in pair	71,767,216 / 49.4%
Mapped reads, second in pair	70,290,864 / 48.38%
Mapped reads, both in pair	140,099,332 / 96.43%
Mapped reads, singletons	1,958,748 / 1.35%
Secondary alignments	0
Supplementary alignments	500,554 / 0.34%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	8,301,481 / 5.71%
Duplication rate	5.59%
Clipped reads	6,111,943 / 4.21%

2.2. ACGT Content

Number/percentage of A's	4,158,365,980 / 29.49%
Number/percentage of C's	2,878,698,071 / 20.41%
Number/percentage of T's	4,145,656,020 / 29.4%
Number/percentage of G's	2,918,845,963 / 20.7%
Number/percentage of N's	1,334,904 / 0.01%

GC Percentage	41.11%

2.3. Coverage

Mean	4.5566
Standard Deviation	5.9076

2.4. Mapping Quality

Mean Mapping Quality	53.97

2.5. Insert size

Mean	35,483.52
Standard Deviation	1,828,768.57
P25/Median/P75	161 / 197 / 243

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	65,762,177
Insertions	1,311,907
Mapped reads with at least one insertion	0.91%
Deletions	1,304,346
Mapped reads with at least one deletion	0.9%
Homopolymer indels	46.25%

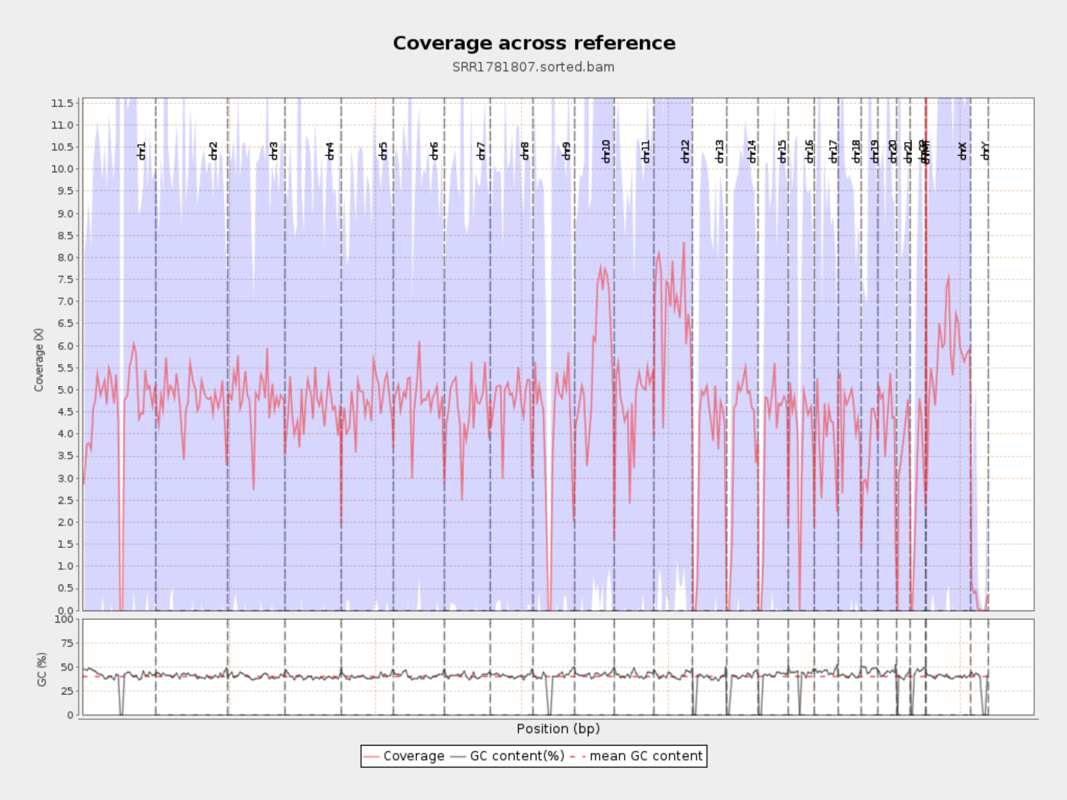
2.7. Chromosome stats

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

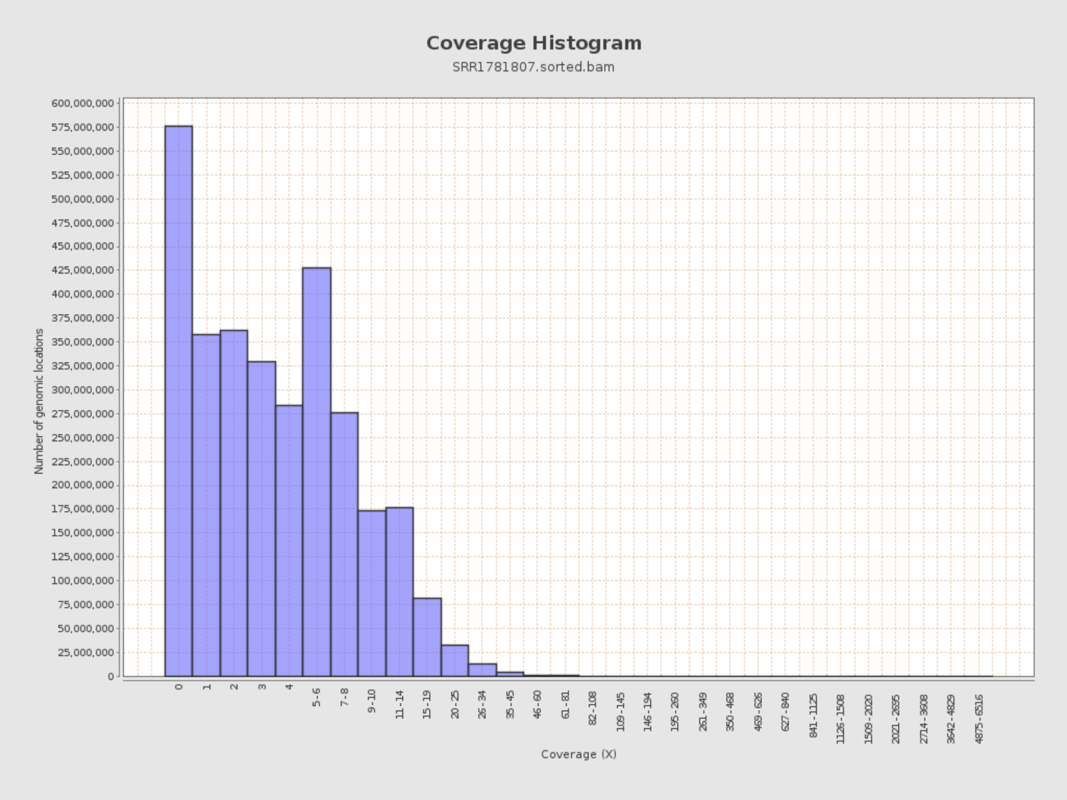
		bases	coverage	deviation
chr1	249250621	1131168057	4.5383	8.7394
chr2	243199373	1157828596	4.7608	5.5421
chr3	198022430	955728153	4.8264	4.7628
chr4	191154276	880984648	4.6088	5.4128
chr5	180915260	846402757	4.6784	4.5783
chr6	171115067	824496024	4.8184	5.354
chr7	159138663	719362789	4.5204	5.3873
chr8	146364022	691953763	4.7276	4.8444
chr9	141213431	577520566	4.0897	5.8098
chr10	135534747	784332092	5.7869	8.9408
chr11	135006516	634574198	4.7003	4.9782
chr12	133851895	937534107	7.0043	6.5753
chr13	115169878	430733764	3.74	4.3072
chr14	107349540	420607831	3.9181	4.6229
chr15	102531392	391211978	3.8155	4.6126
chr16	90354753	349929948	3.8728	4.8204
chr17	81195210	321749489	3.9627	5.1394
chr18	78077248	349276098	4.4735	6.0261
chr19	59128983	209706782	3.5466	6.0297
chr20	63025520	277658221	4.4055	5.4125
chr21	48129895	166050693	3.4501	7.6366
chr22	51304566	136973505	2.6698	4.274
chrMT	16571	467226	28.1954	8.13
chrX	155270560	896788811	5.7757	5.7687

chrY	59373566	12800037	0.2156	2.4657

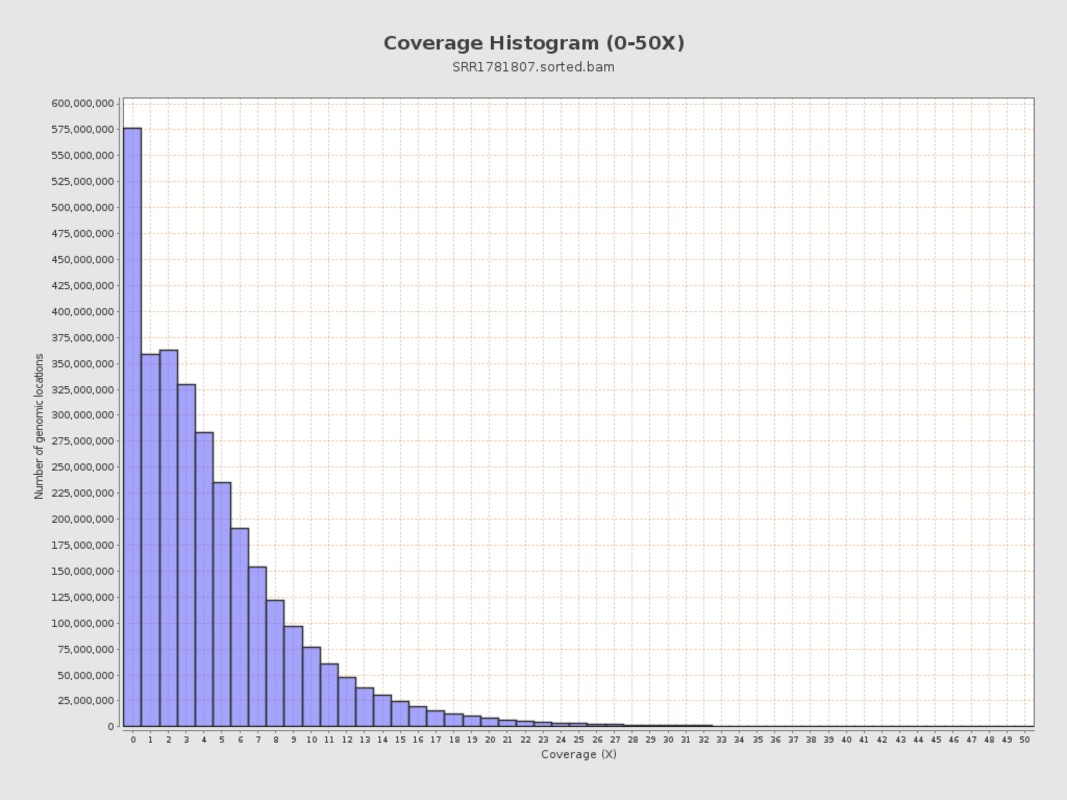
3. Results : Coverage across reference



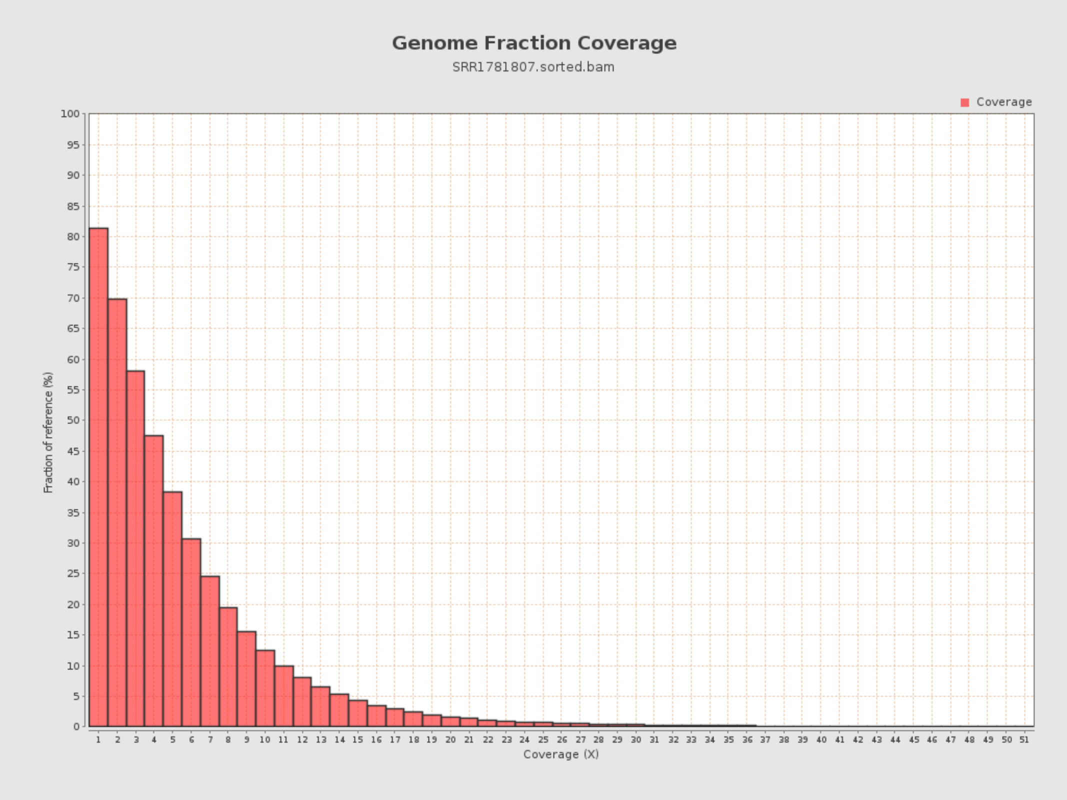
4. Results : Coverage Histogram



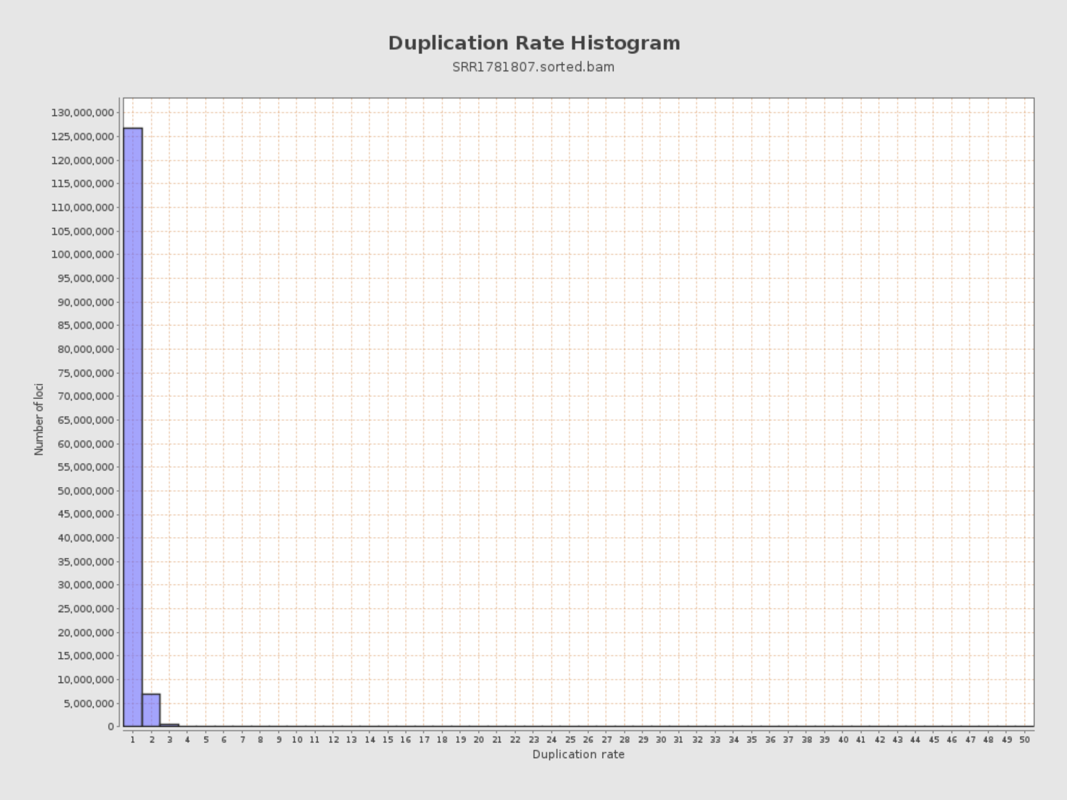
5. Results : Coverage Histogram (0-50X)



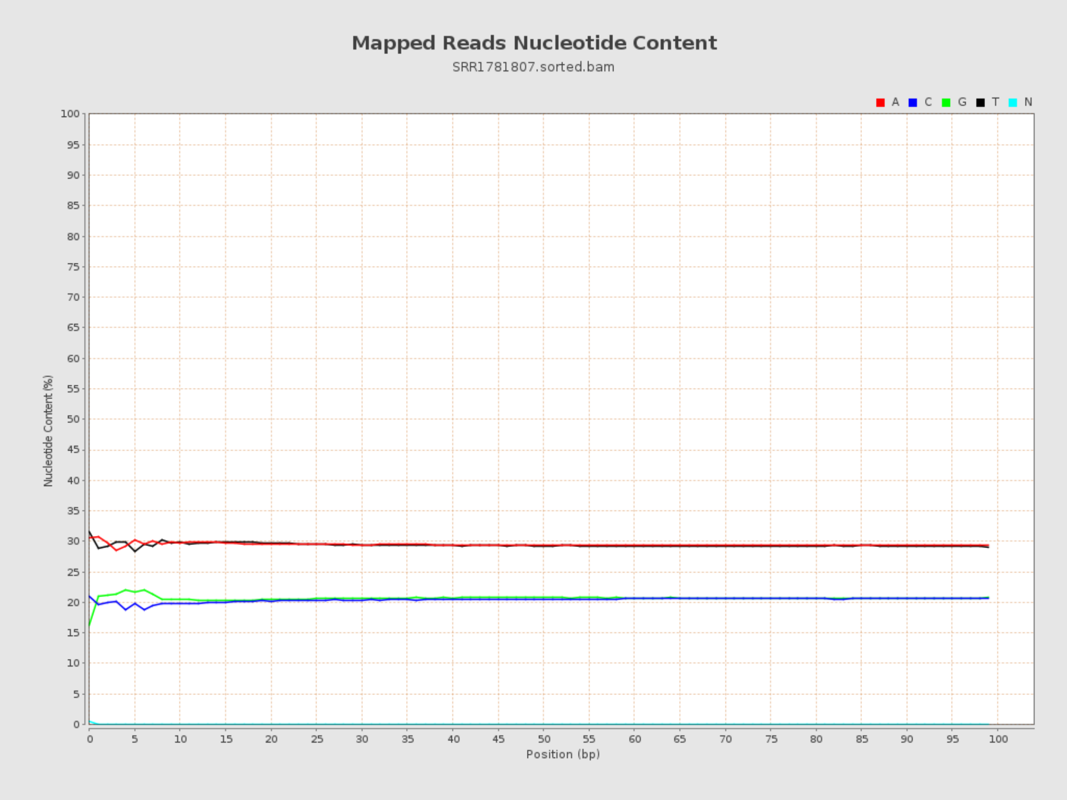
6. Results : Genome Fraction Coverage



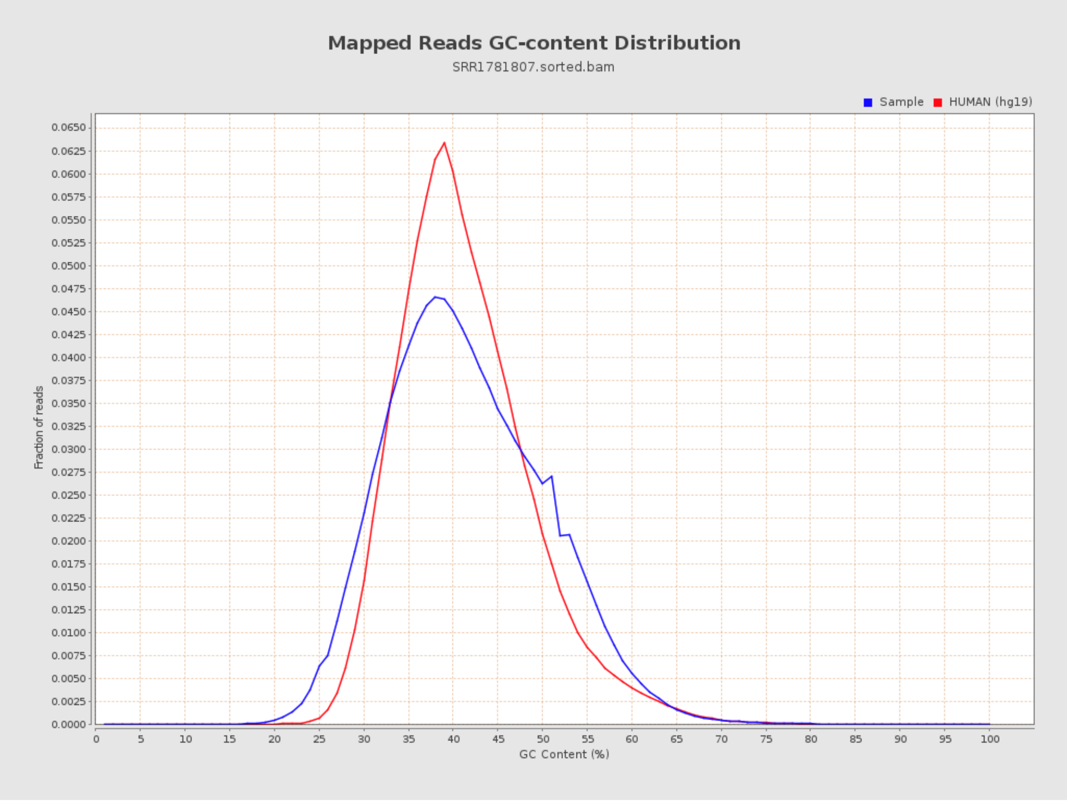
7. Results : Duplication Rate Histogram



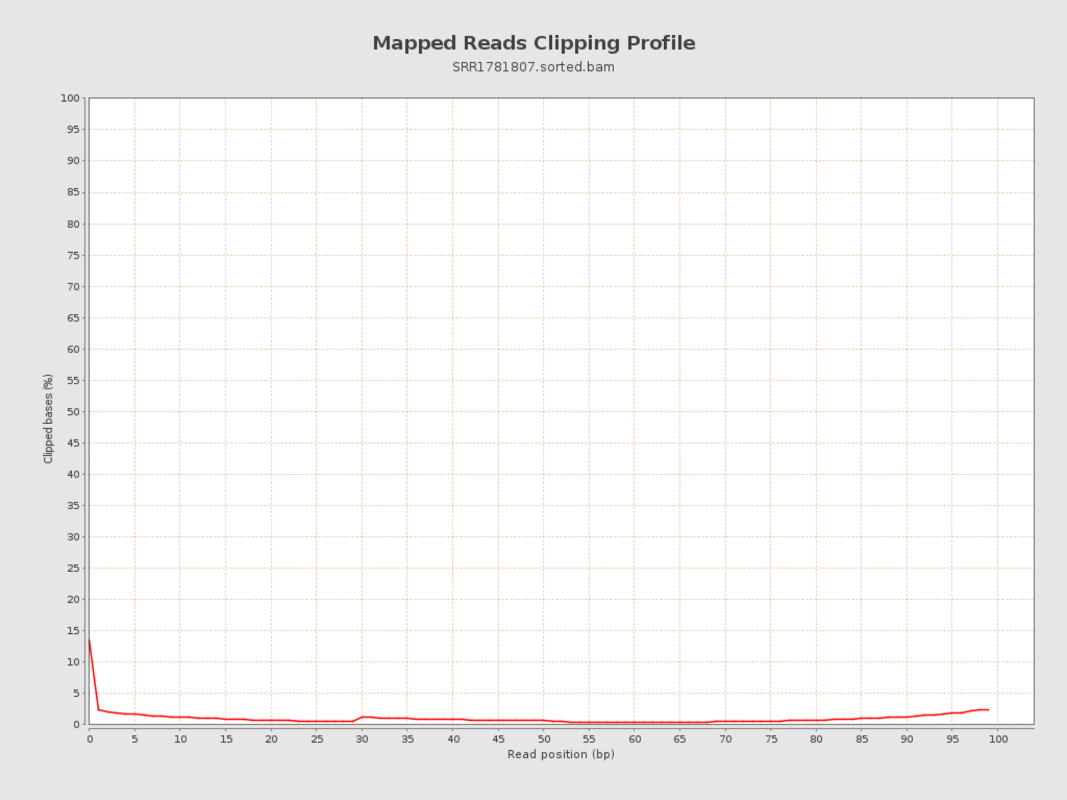
8. Results : Mapped Reads Nucleotide Content



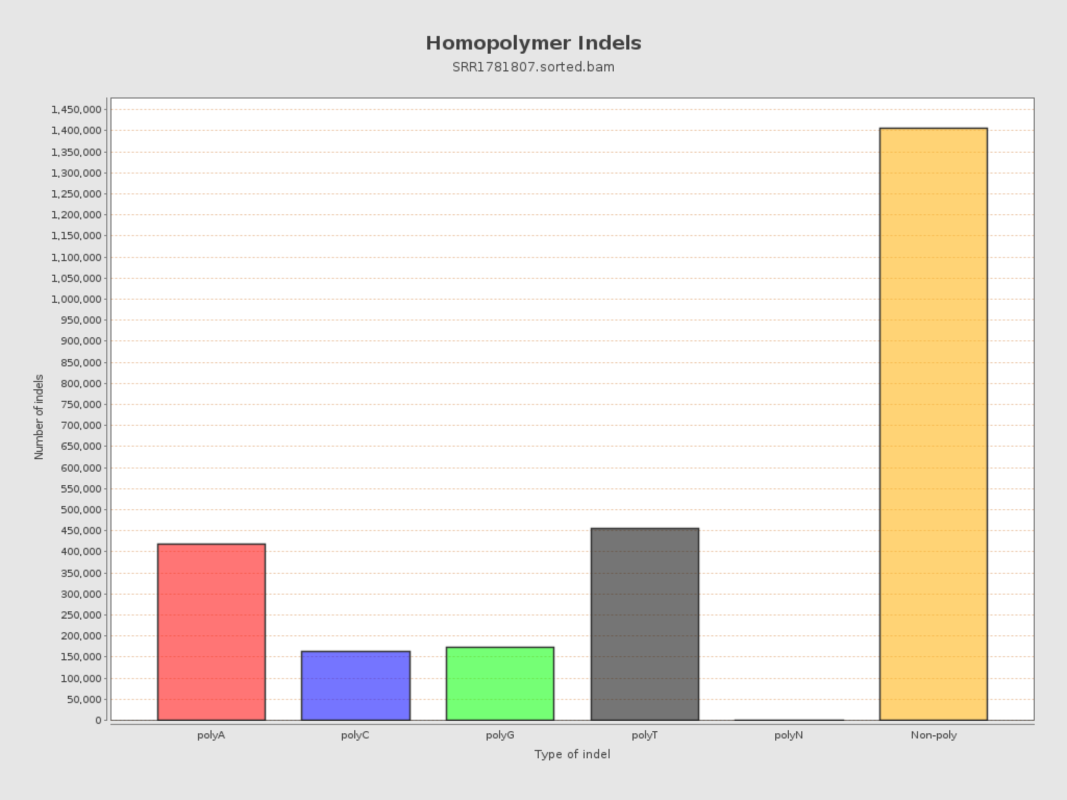
9. Results : Mapped Reads GC-content Distribution



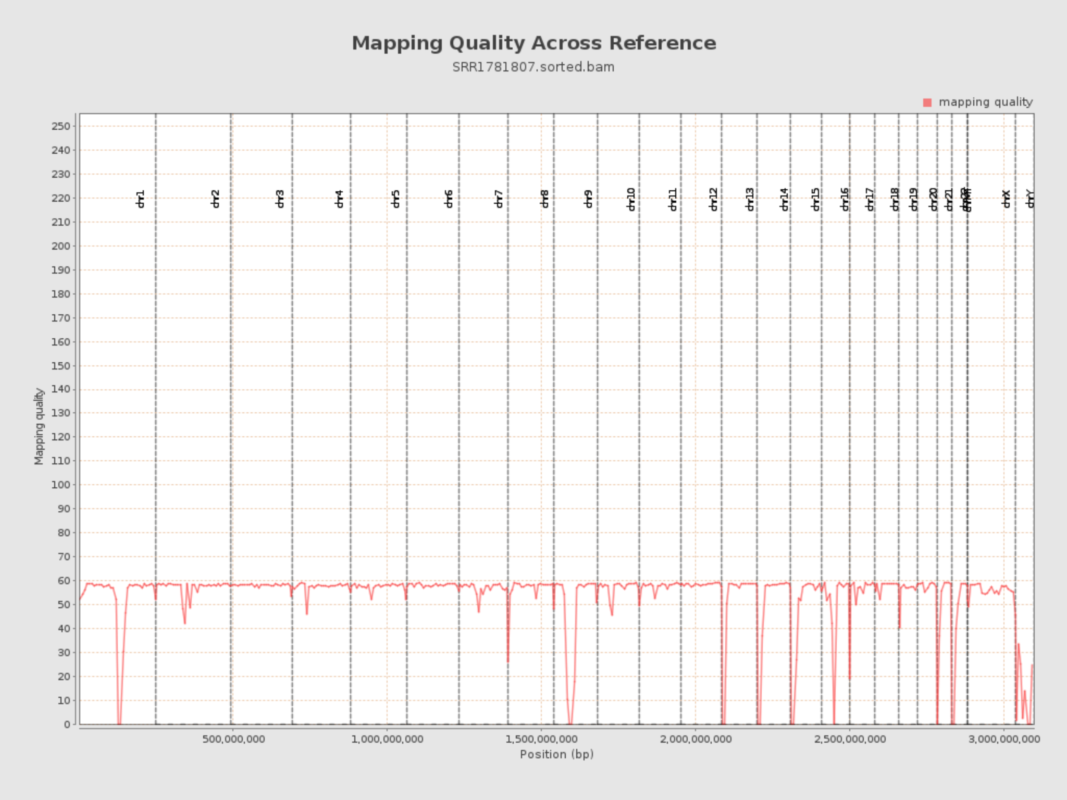
10. Results : Mapped Reads Clipping Profile



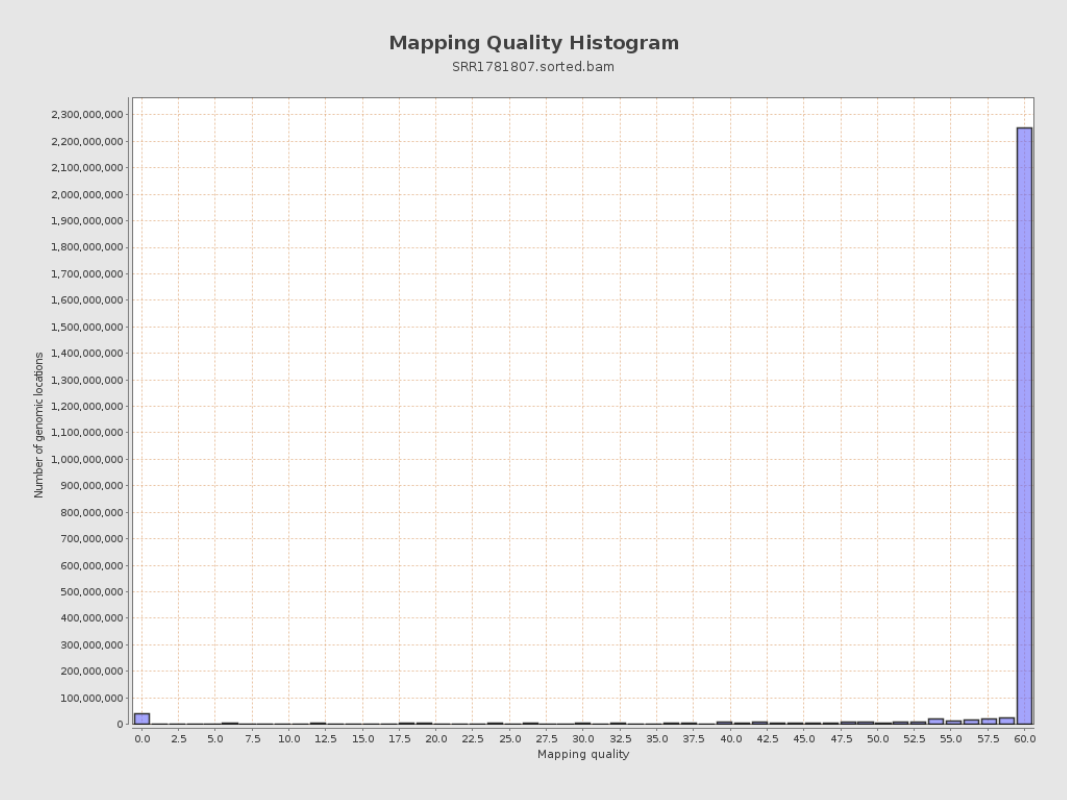
11. Results : Homopolymer Indels



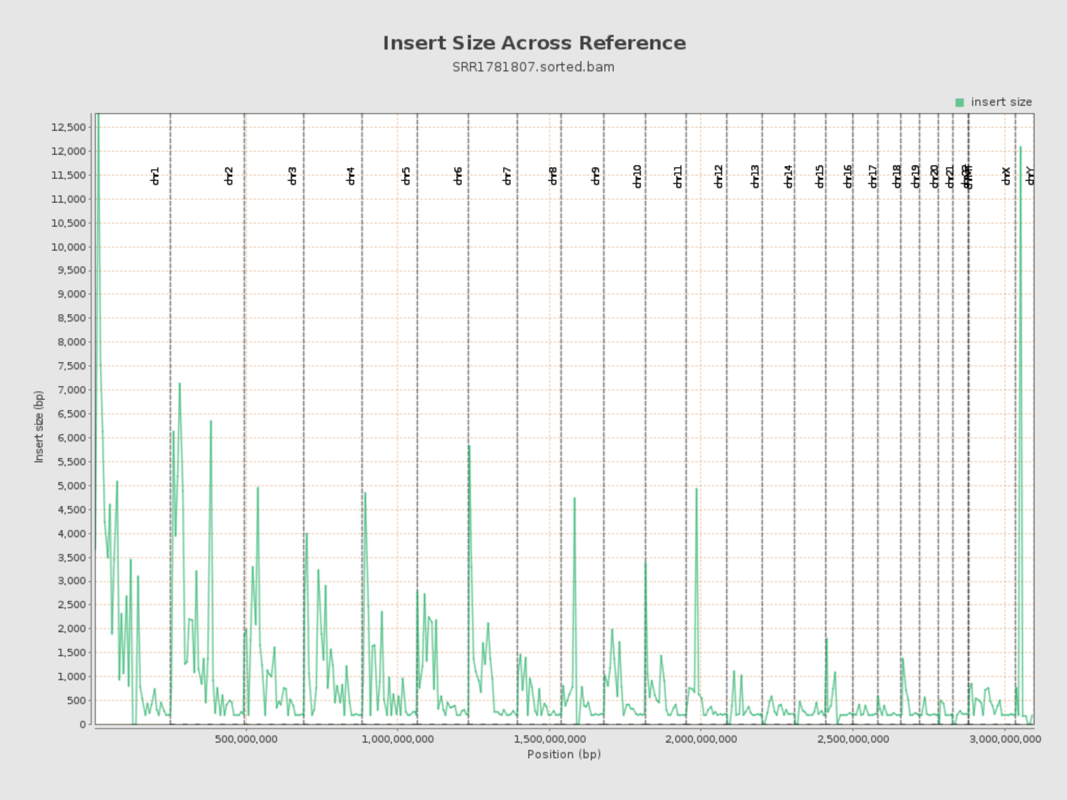
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram