Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/26 15:35:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781848.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_SRR1781848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781848_1.fastq.gz SRR1781848_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 26 15:35:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781848.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	189,366,380
Mapped reads	184,519,441 / 97.44%
Unmapped reads	4,846,939 / 2.56%
Mapped paired reads	184,519,441 / 97.44%
Mapped reads, first in pair	93,016,007 / 49.12%
Mapped reads, second in pair	91,503,434 / 48.32%
Mapped reads, both in pair	182,331,266 / 96.28%
Mapped reads, singletons	2,188,175 / 1.16%
Secondary alignments	0
Supplementary alignments	601,123 / 0.32%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	13,662,892 / 7.22%
Duplication rate	7.14%
Clipped reads	8,563,541 / 4.52%

2.2. ACGT Content

Number/percentage of A's	5,449,449,271 / 29.75%
Number/percentage of C's	3,696,490,711 / 20.18%
Number/percentage of T's	5,434,448,615 / 29.67%
Number/percentage of G's	3,735,617,523 / 20.39%
Number/percentage of N's	2,082,344 / 0.01%

GC Percentage	40.57%

2.3. Coverage

Mean	5.9185
Standard Deviation	7.2693

2.4. Mapping Quality

Mean Mapping Quality	53.9

2.5. Insert size

Mean	36,069.8
Standard Deviation	1,838,394.07
P25/Median/P75	158 / 193 / 237

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	72,854,594
Insertions	1,990,116
Mapped reads with at least one insertion	1.06%
Deletions	1,651,006
Mapped reads with at least one deletion	0.88%
Homopolymer indels	46.86%

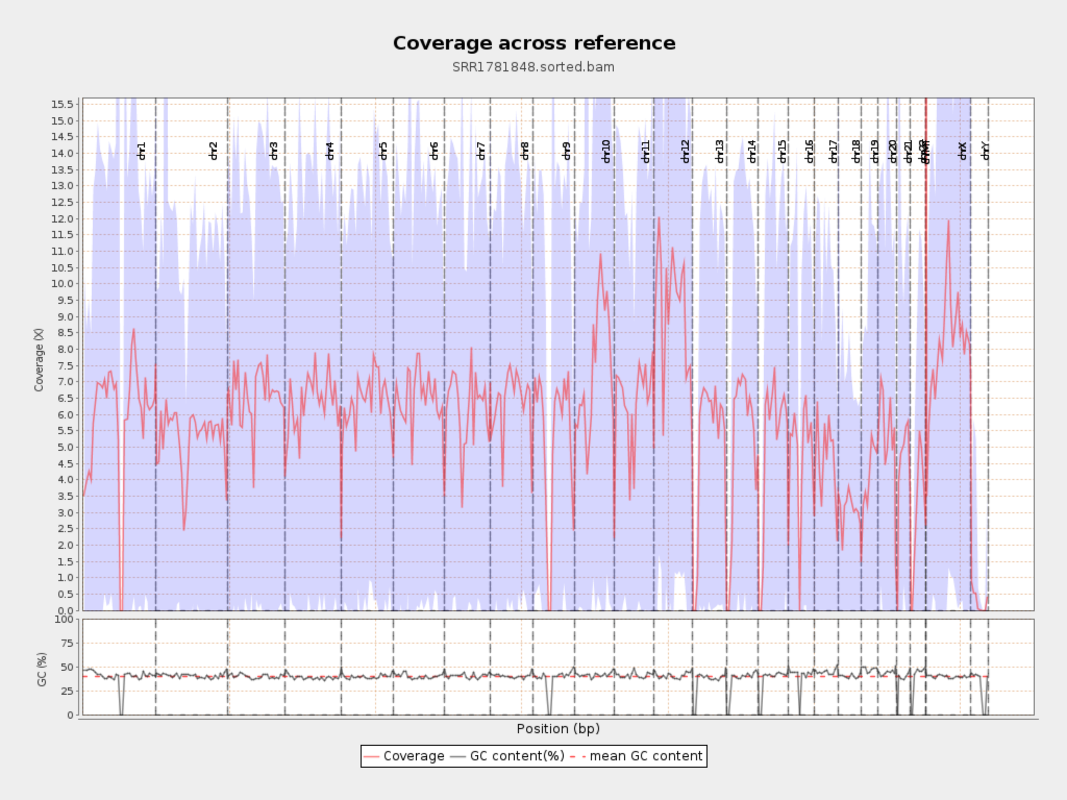
2.7. Chromosome stats

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

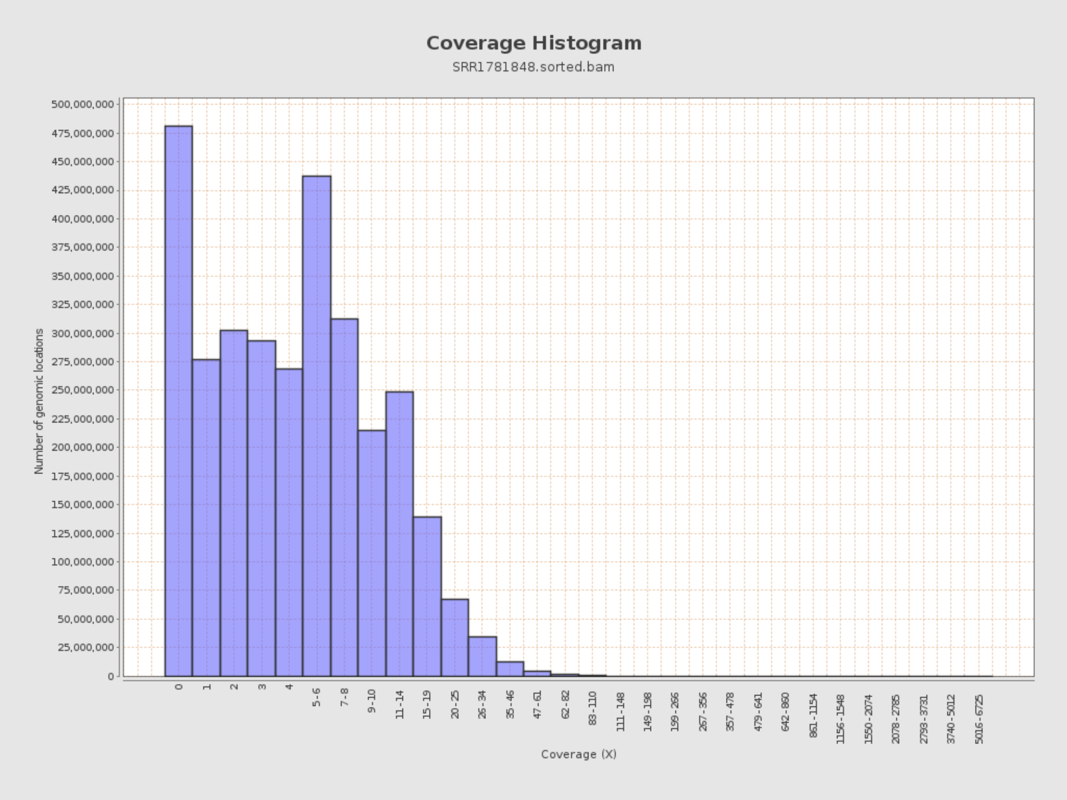
		bases	coverage	deviation
chr1	249250621	1475418315	5.9194	8.8022
chr2	243199373	1282260542	5.2725	8.2243
chr3	198022430	1304413683	6.5872	6.3833
chr4	191154276	1228606884	6.4273	6.4825
chr5	180915260	1156175137	6.3907	6.0423
chr6	171115067	1118767859	6.5381	6.5757
chr7	159138663	976326824	6.1351	6.9014
chr8	146364022	933600994	6.3786	6.2585
chr9	141213431	755098410	5.3472	7.1881
chr10	135534747	1012645071	7.4715	9.8654
chr11	135006516	862100946	6.3856	6.6125
chr12	133851895	1249385107	9.3341	8.9693
chr13	115169878	591405543	5.1351	5.7263
chr14	107349540	556921014	5.1879	6.1463
chr15	102531392	513786296	5.011	6.1324
chr16	90354753	422967003	4.6812	5.9548
chr17	81195210	385675106	4.75	5.7488
chr18	78077248	241768647	3.0965	4.8246
chr19	59128983	244046677	4.1274	6.3956
chr20	63025520	348900900	5.5359	7.1817
chr21	48129895	214012236	4.4466	8.0732
chr22	51304566	157564135	3.0712	4.8817
chrMT	16571	685934	41.3936	13.2329
chrX	155270560	1272635366	8.1962	8.2096

chrY	59373566	16624356	0.28	2.8846

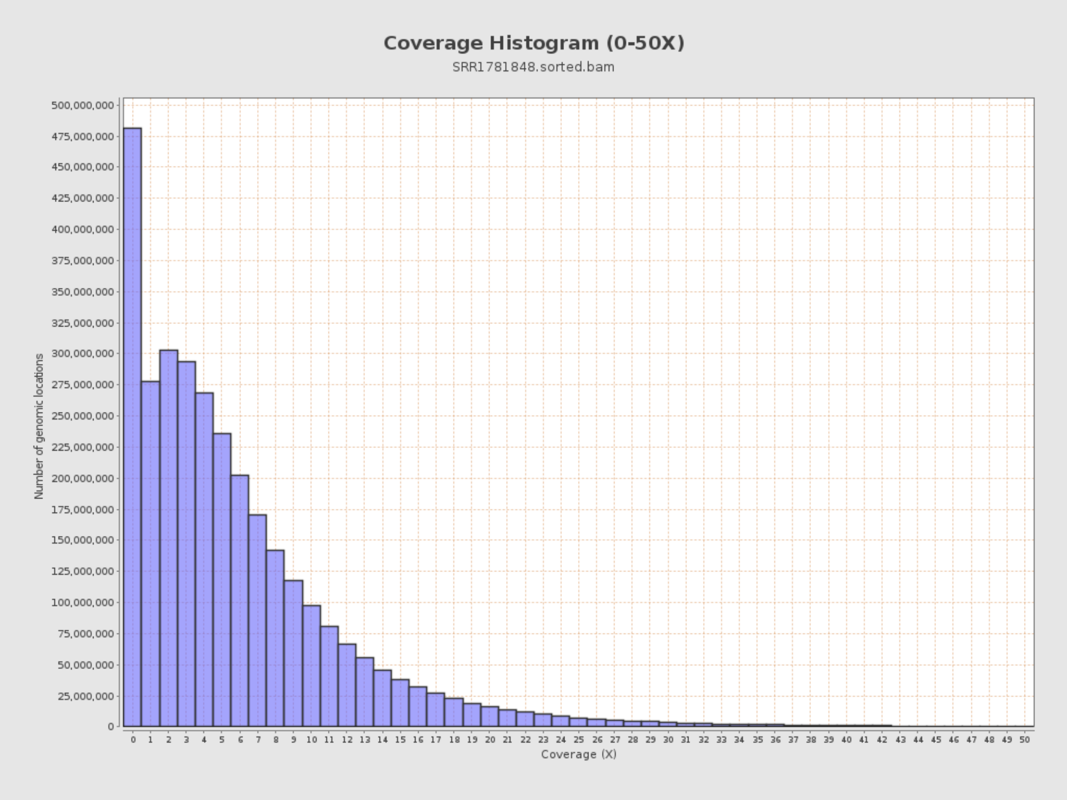
3. Results : Coverage across reference



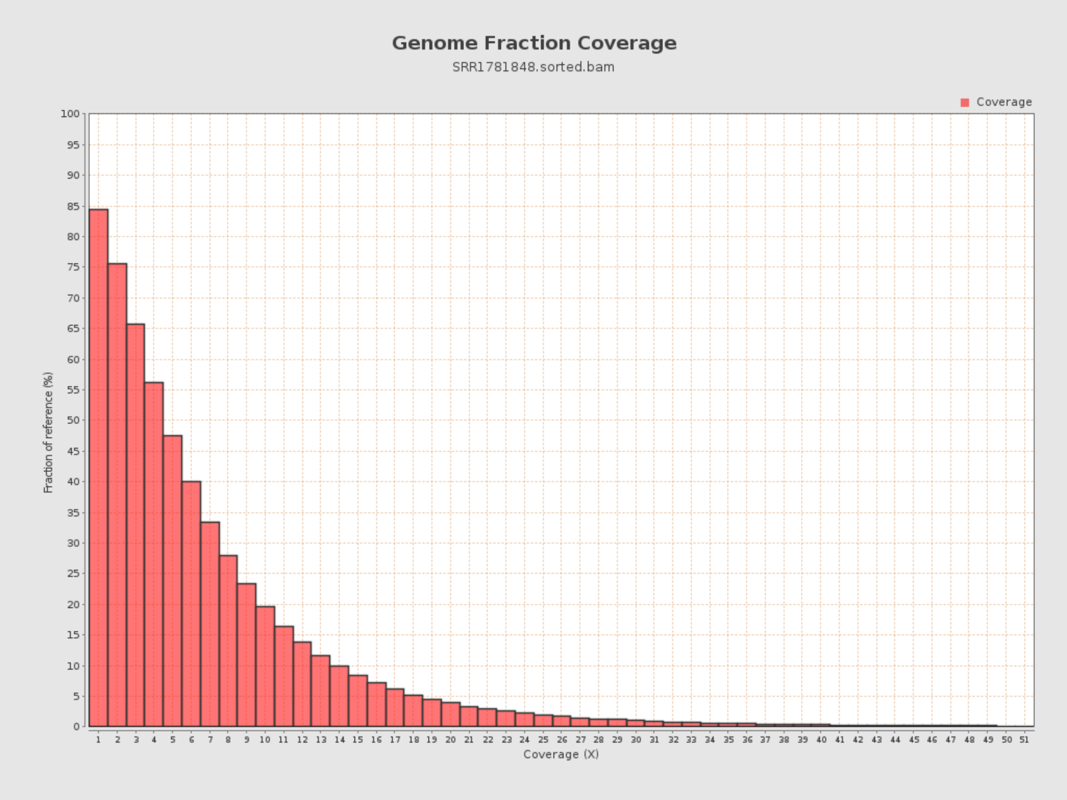
4. Results : Coverage Histogram



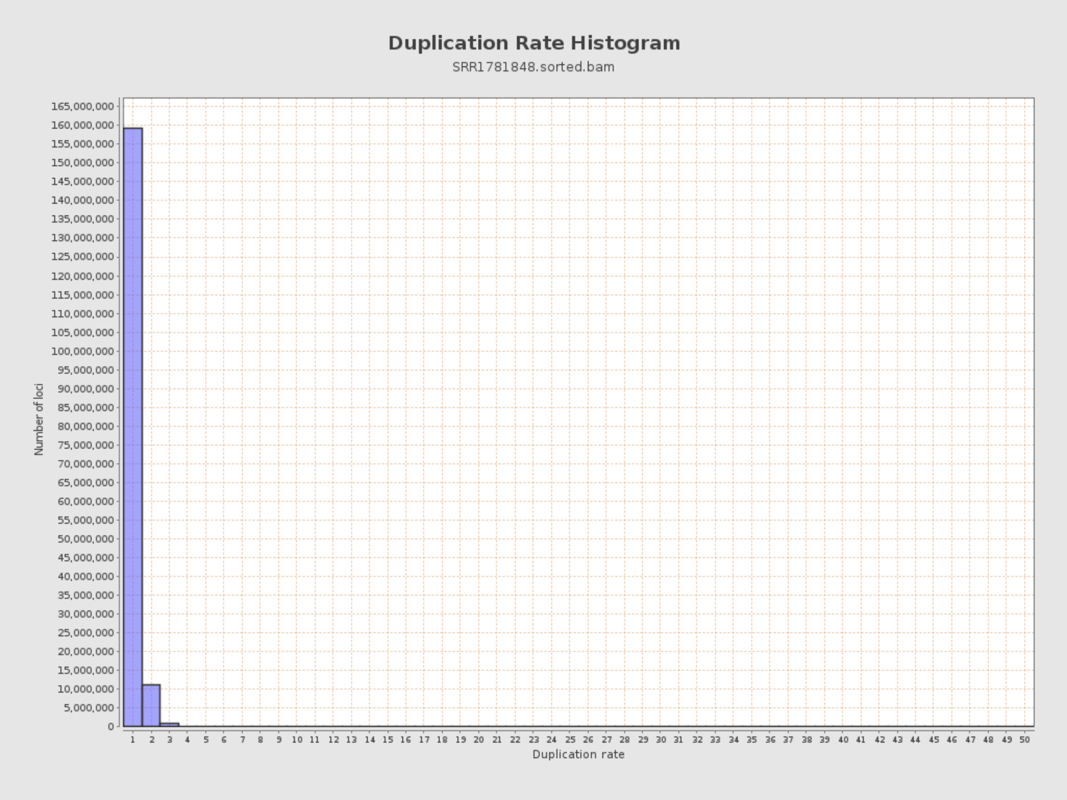
5. Results : Coverage Histogram (0-50X)



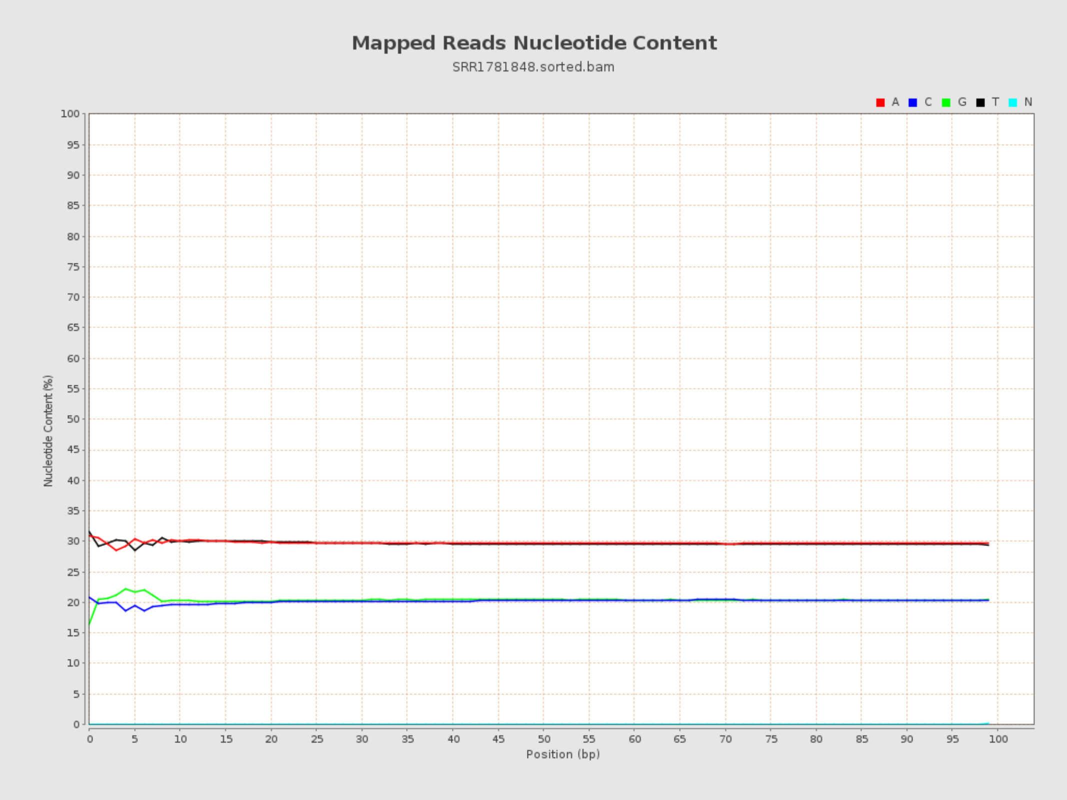
6. Results : Genome Fraction Coverage



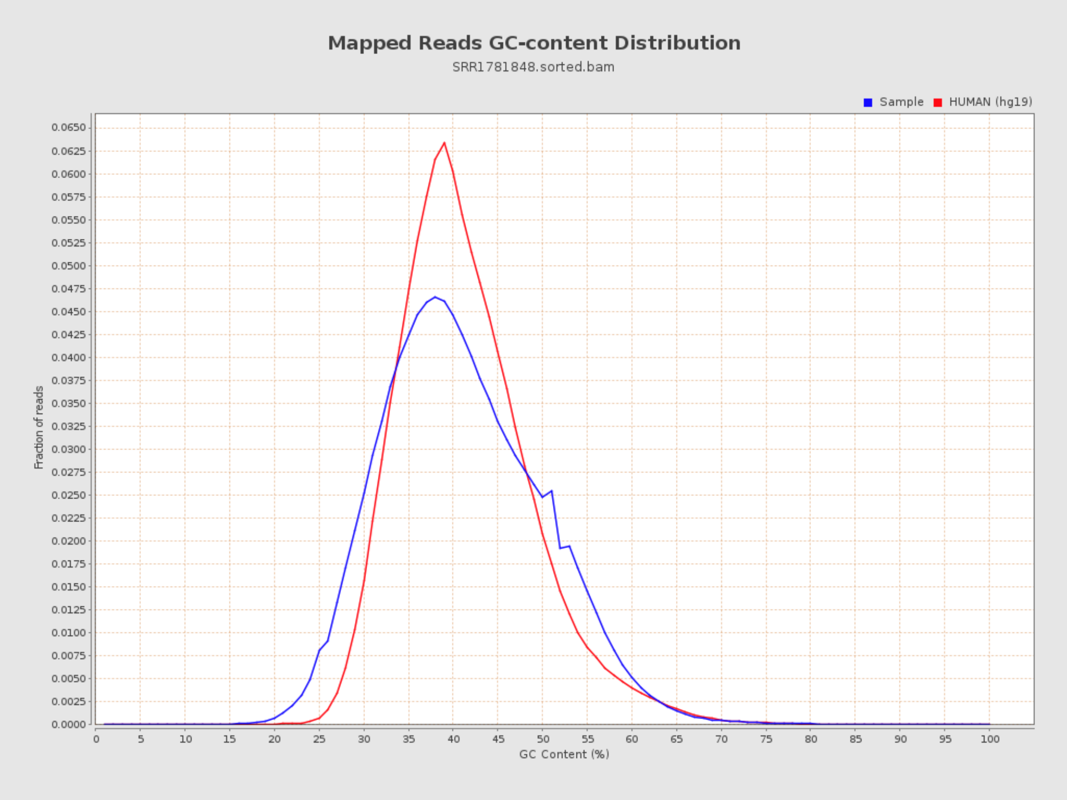
7. Results : Duplication Rate Histogram



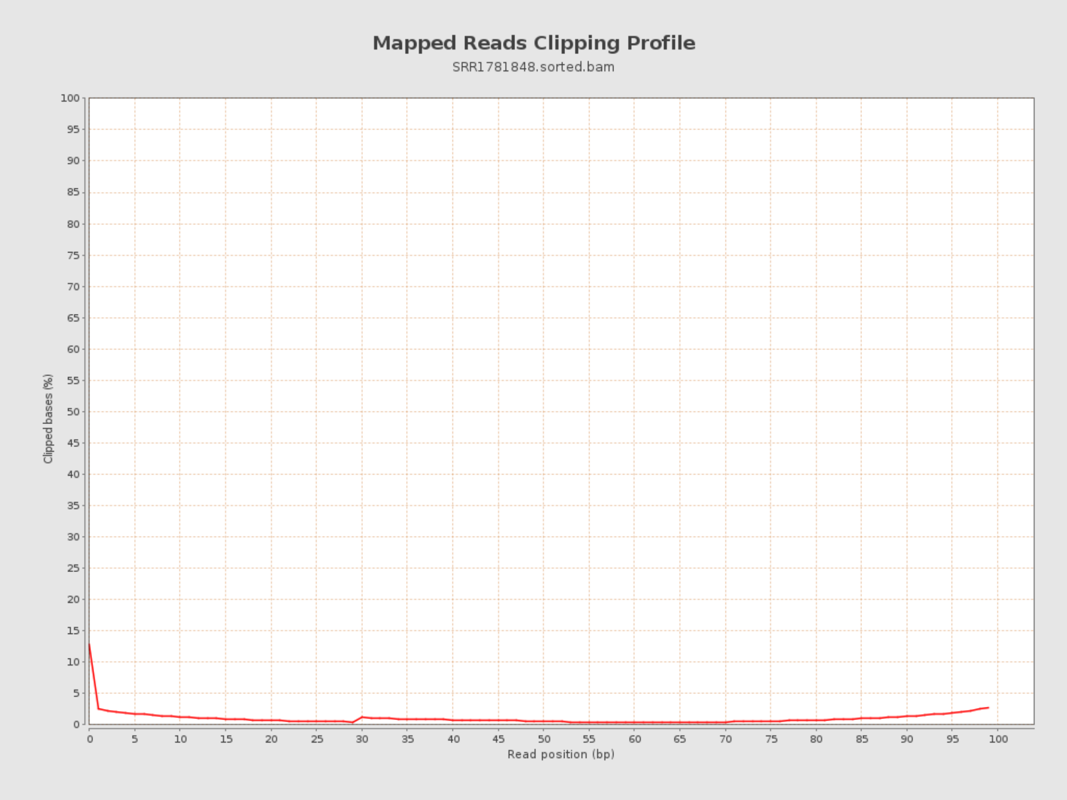
8. Results : Mapped Reads Nucleotide Content



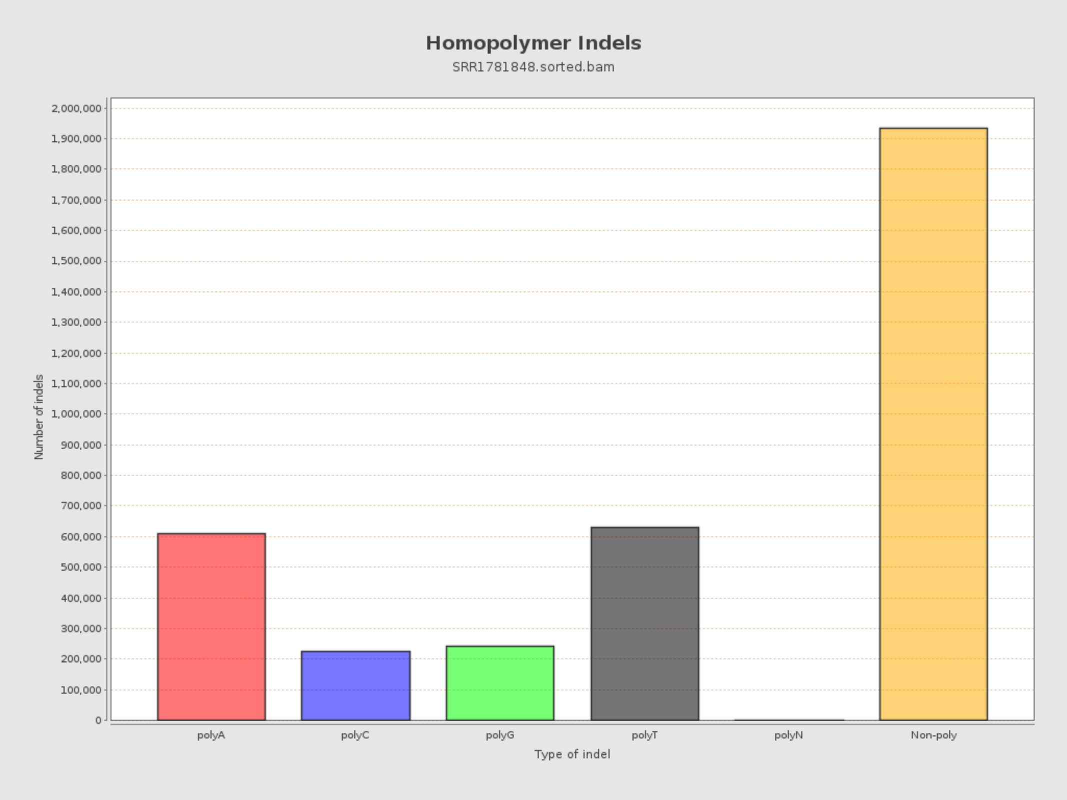
9. Results : Mapped Reads GC-content Distribution



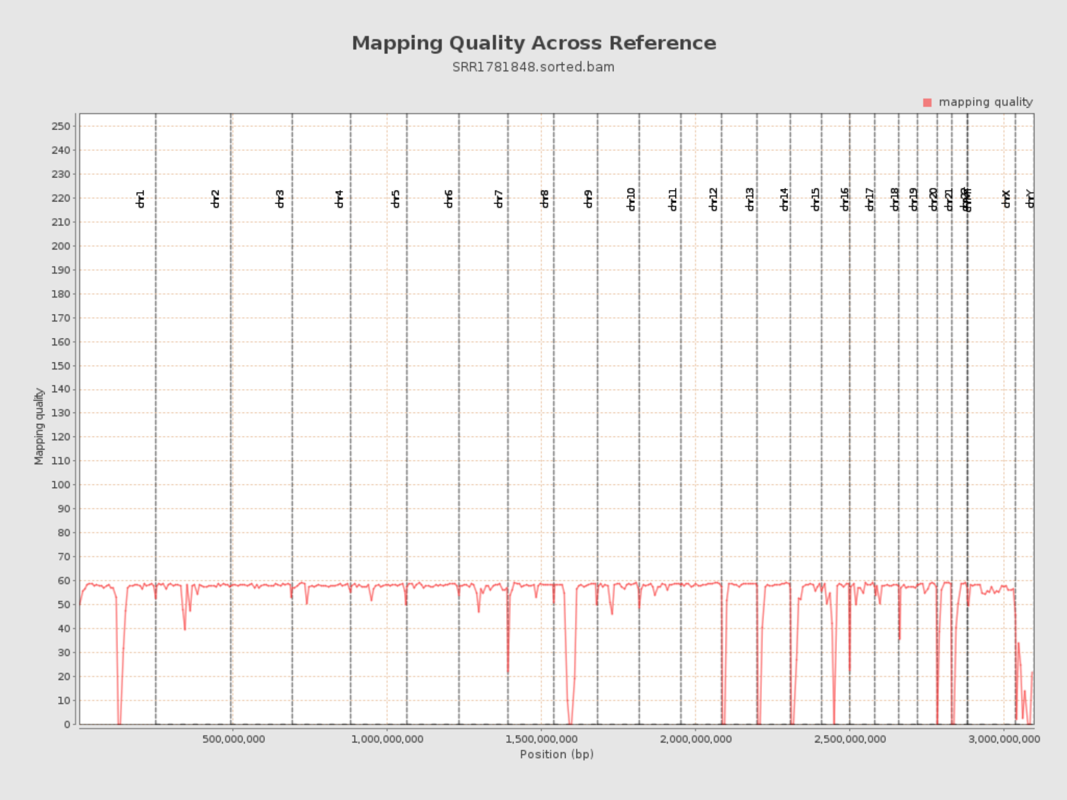
10. Results : Mapped Reads Clipping Profile



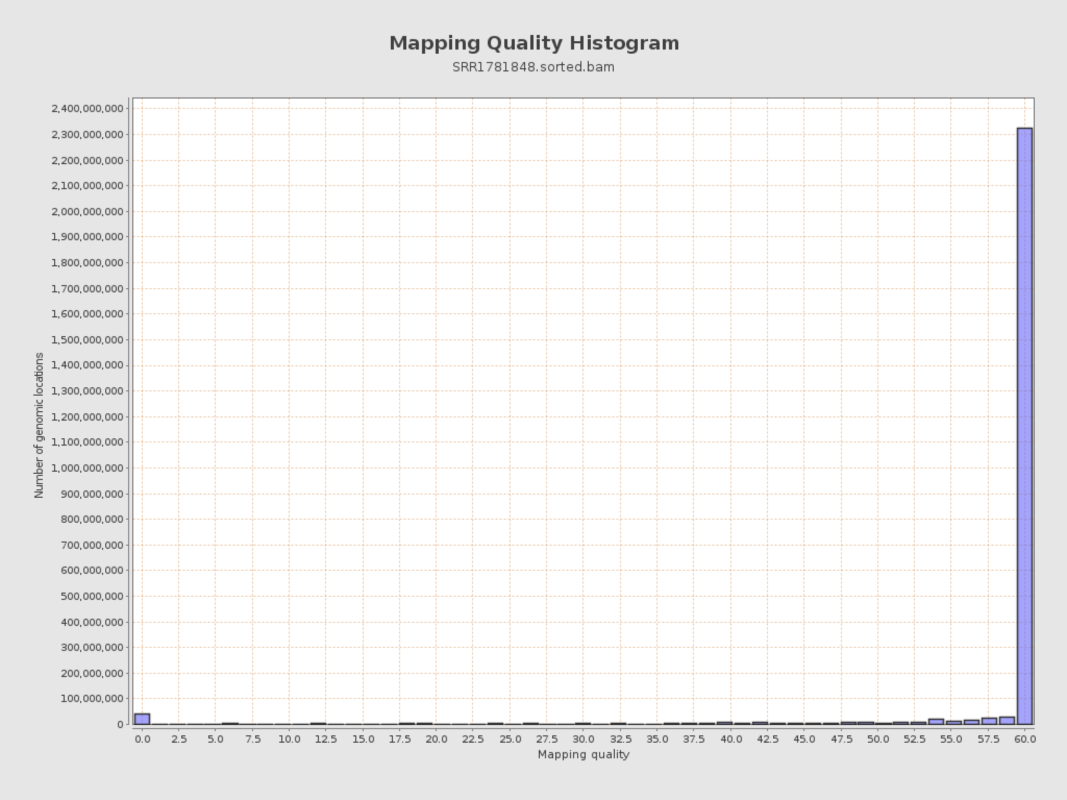
11. Results : Homopolymer Indels



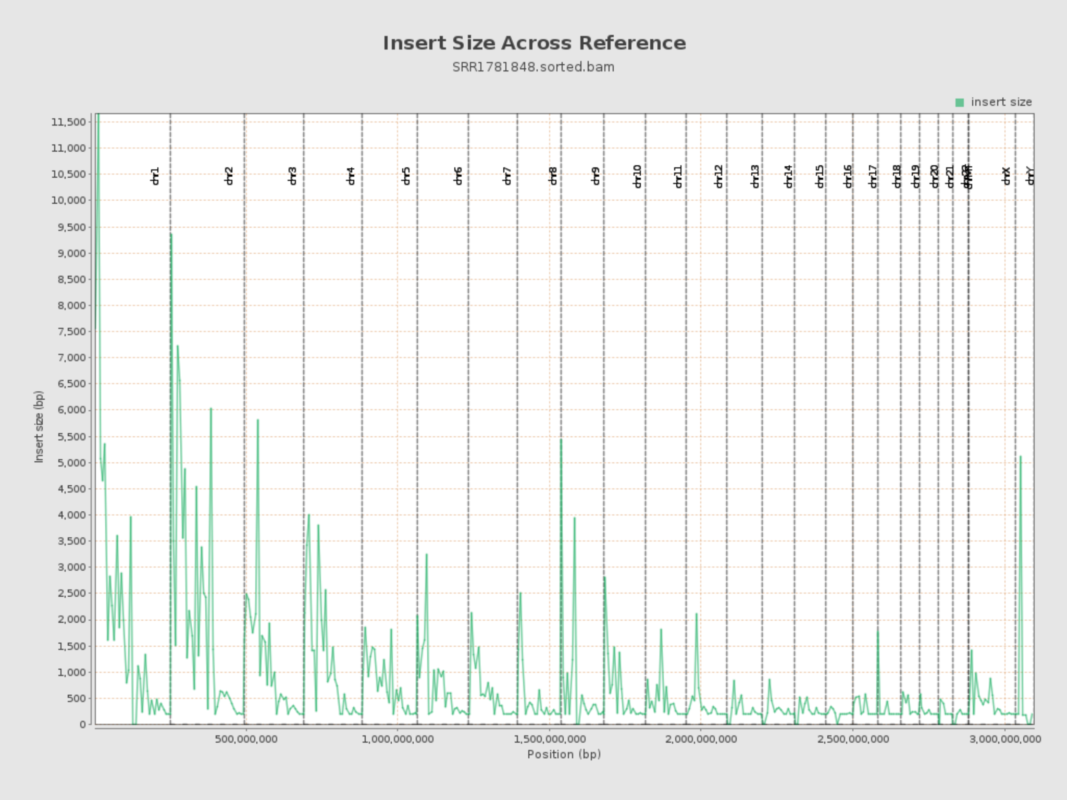
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram