Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 11:41:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038441.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_SRR5038441 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038441_1.fastq.gz SRR5038441_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 11:41:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038441.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	81,756,652
Mapped reads	81,395,387 / 99.56%
Unmapped reads	361,265 / 0.44%
Mapped paired reads	81,395,387 / 99.56%
Mapped reads, first in pair	40,799,622 / 49.9%
Mapped reads, second in pair	40,595,765 / 49.65%
Mapped reads, both in pair	81,153,570 / 99.26%
Mapped reads, singletons	241,817 / 0.3%
Secondary alignments	0
Supplementary alignments	137,914 / 0.17%
Read min/max/mean length	30 / 150 / 150.08
Duplicated reads (estimated)	33,502,066 / 40.98%
Duplication rate	38.54%
Clipped reads	5,669,289 / 6.93%

2.2. ACGT Content

Number/percentage of A's	3,019,250,815 / 24.98%
Number/percentage of C's	3,024,189,056 / 25.02%
Number/percentage of T's	3,037,610,480 / 25.13%
Number/percentage of G's	3,004,173,051 / 24.86%
Number/percentage of N's	1,244,863 / 0.01%

GC Percentage	49.88%

2.3. Coverage

Mean	3.9049
Standard Deviation	25.7834

2.4. Mapping Quality

Mean Mapping Quality	55.87

2.5. Insert size

Mean	21,607.76
Standard Deviation	1,549,011.15
P25/Median/P75	197 / 230 / 268

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	62,652,754
Insertions	591,450
Mapped reads with at least one insertion	0.7%
Deletions	704,279
Mapped reads with at least one deletion	0.84%
Homopolymer indels	46.12%

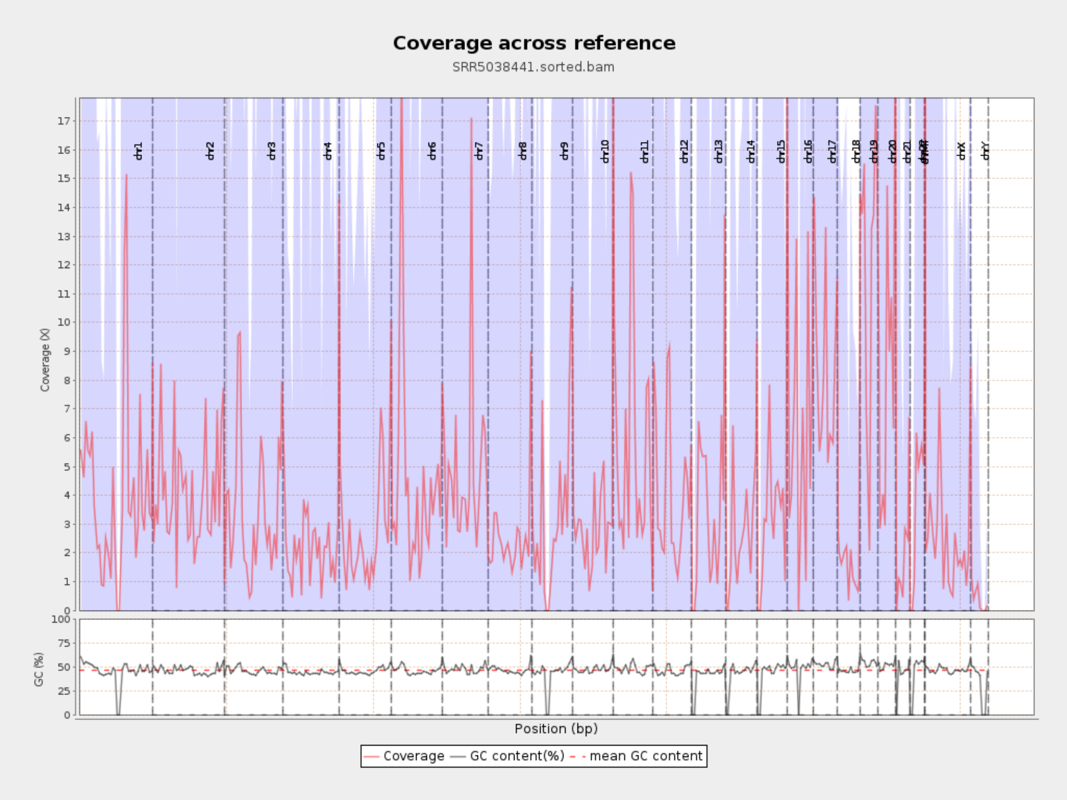
2.7. Chromosome stats

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

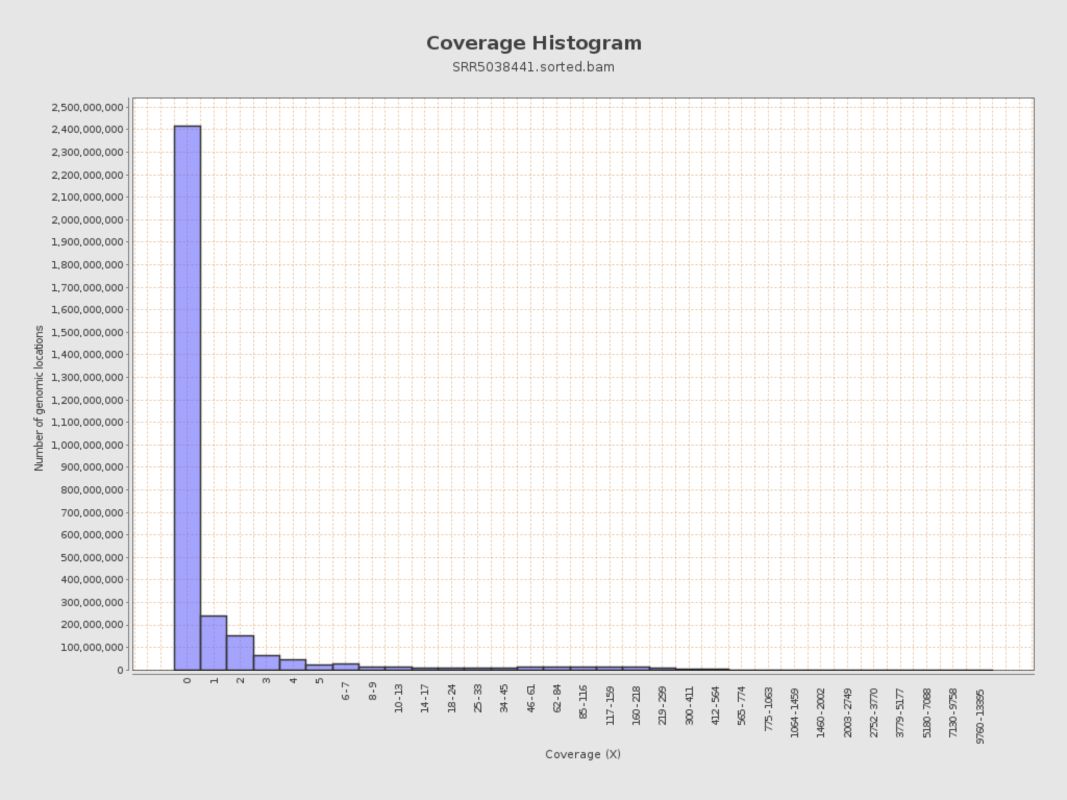
		bases	**coverage**	**deviation**
chr1	249250621	1015333456	4.0735	24.5894
chr2	243199373	1010246401	4.154	27.8519
chr3	198022430	688819709	3.4785	22.8655
chr4	191154276	413494802	2.1631	16.6738
chr5	180915260	518405415	2.8655	21.5015
chr6	171115067	739846197	4.3237	28.8911
chr7	159138663	791829417	4.9757	34.3144
chr8	146364022	371619320	2.539	18.0998
chr9	141213431	466586026	3.3041	22.0666
chr10	135534747	372132973	2.7457	17.406
chr11	135006516	832068855	6.1632	35.7096
chr12	133851895	554347559	4.1415	23.2755
chr13	115169878	389177366	3.3792	28.6036
chr14	107349540	283257732	2.6386	17.0603
chr15	102531392	311474097	3.0378	18.204
chr16	90354753	594005496	6.5741	34.775
chr17	81195210	688154920	8.4753	36.8852
chr18	78077248	116735967	1.4951	11.4252
chr19	59128983	716045954	12.1099	43.4572
chr20	63025520	519746164	8.2466	46.6257
chr21	48129895	93550915	1.9437	20.2299
chr22	51304566	197490574	3.8494	20.5693
chrMT	16571	1178248	71.103	29.2055
chrX	155270560	379604541	2.4448	18.3985

chrY	59373566	23261403	0.3918	5.4815

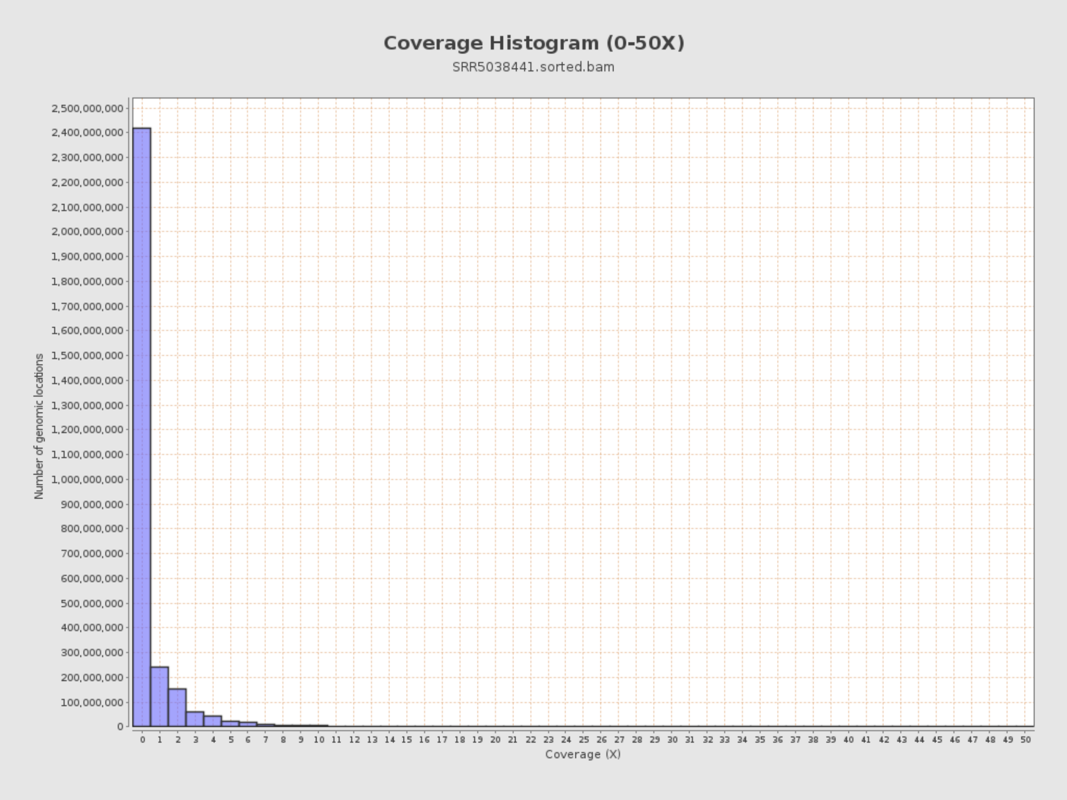
3. Results : Coverage across reference



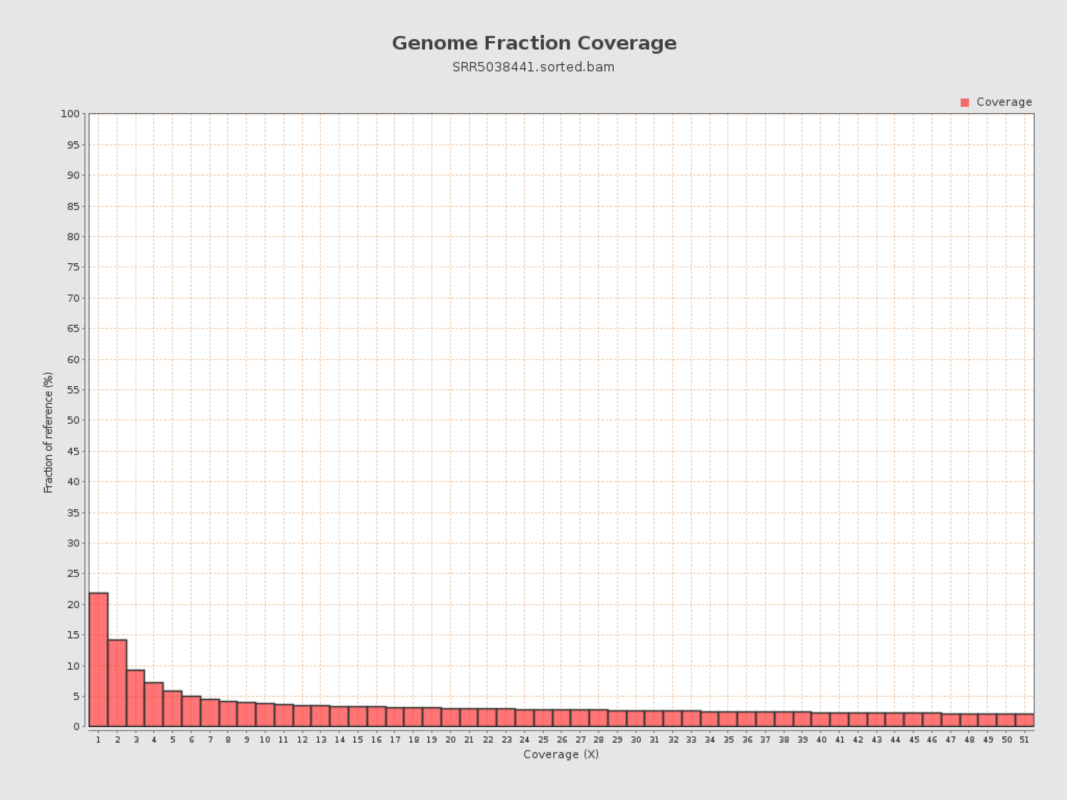
4. Results : Coverage Histogram



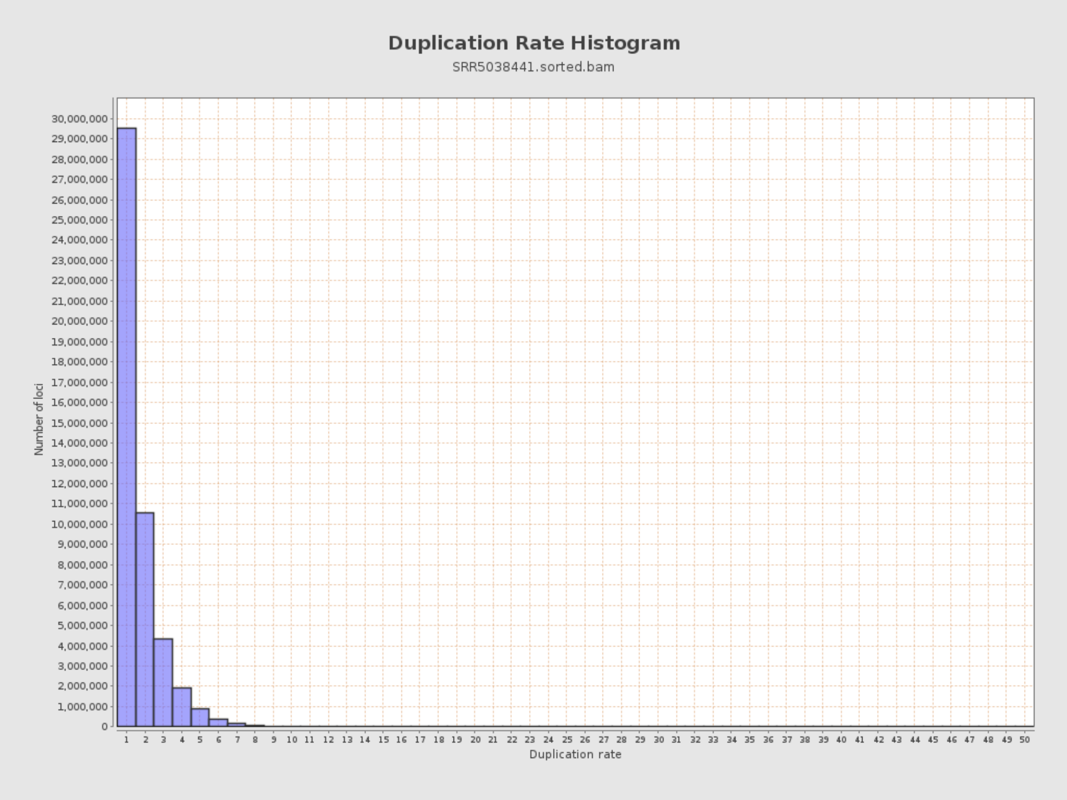
5. Results : Coverage Histogram (0-50X)



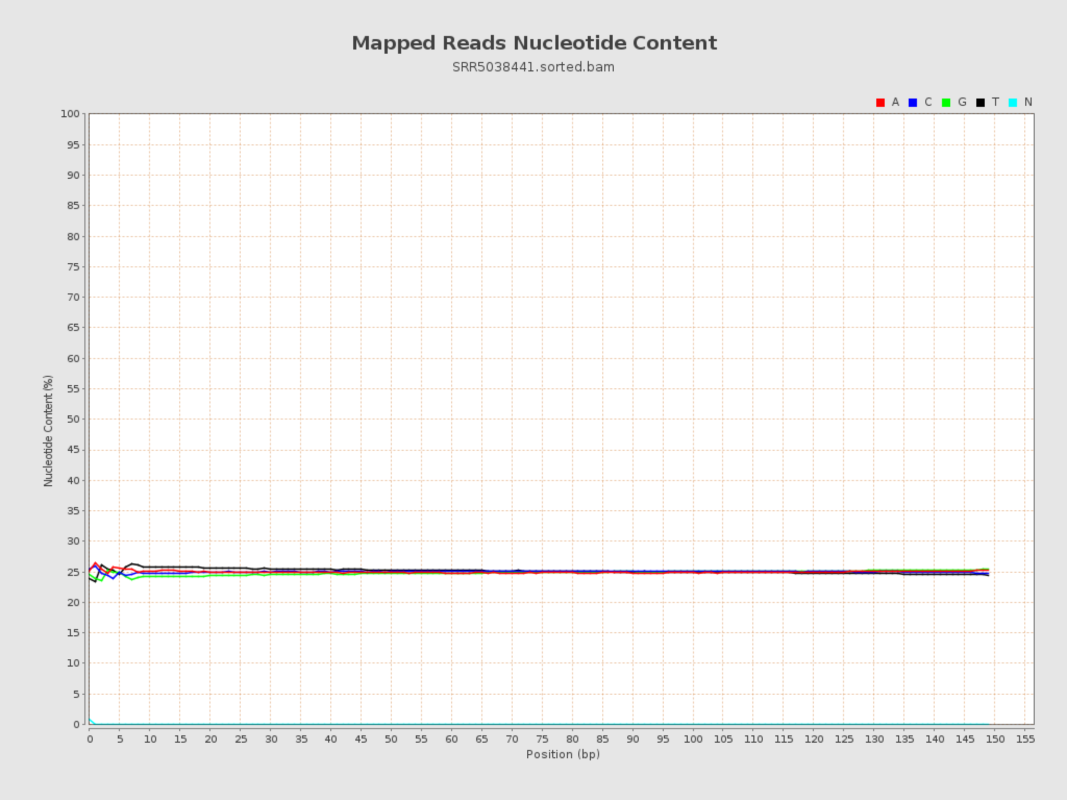
6. Results : Genome Fraction Coverage



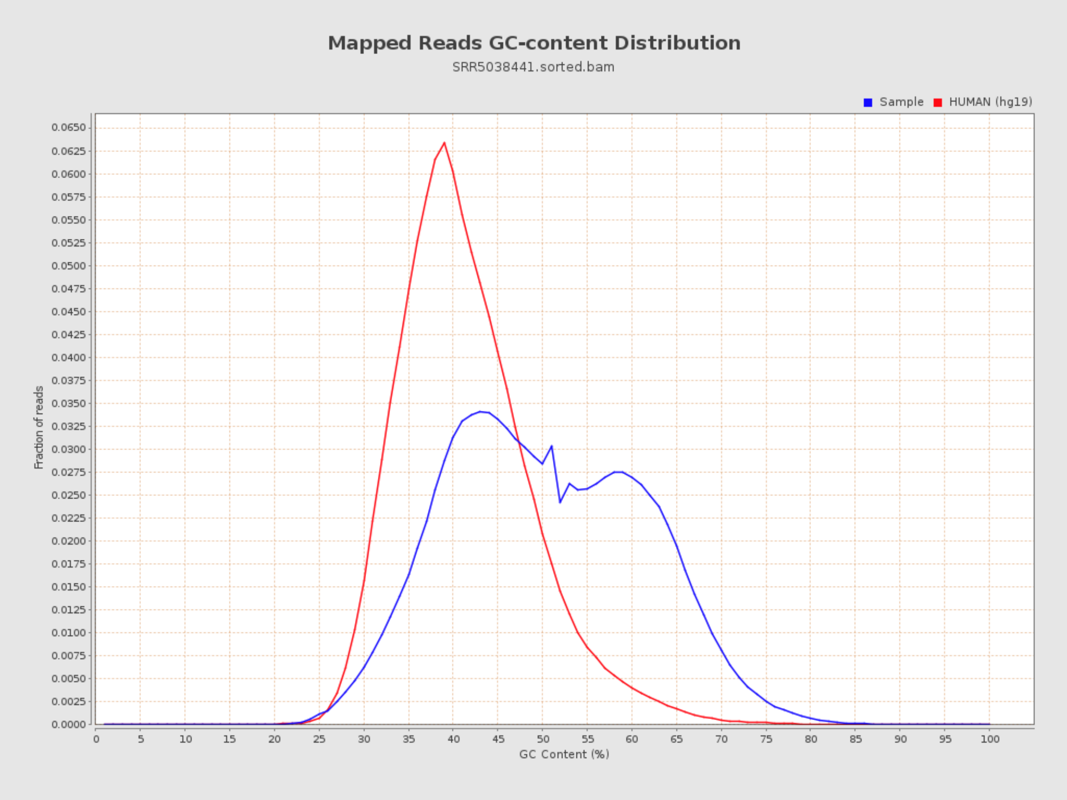
7. Results : Duplication Rate Histogram



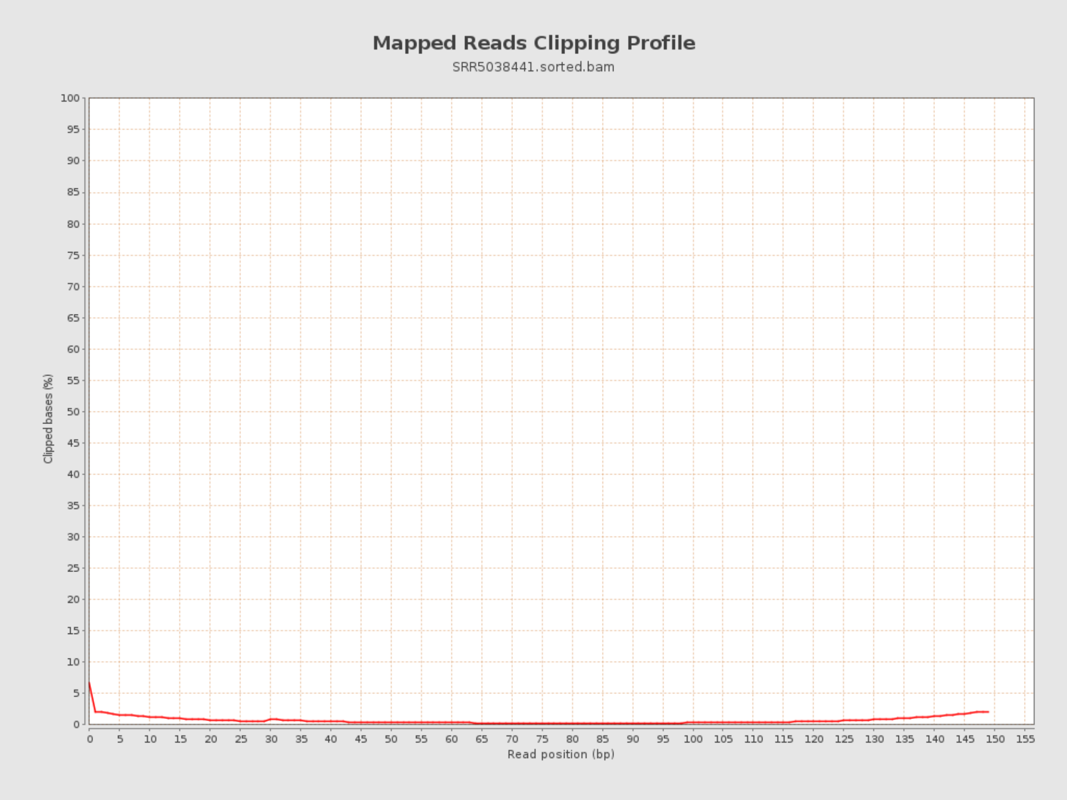
8. Results : Mapped Reads Nucleotide Content



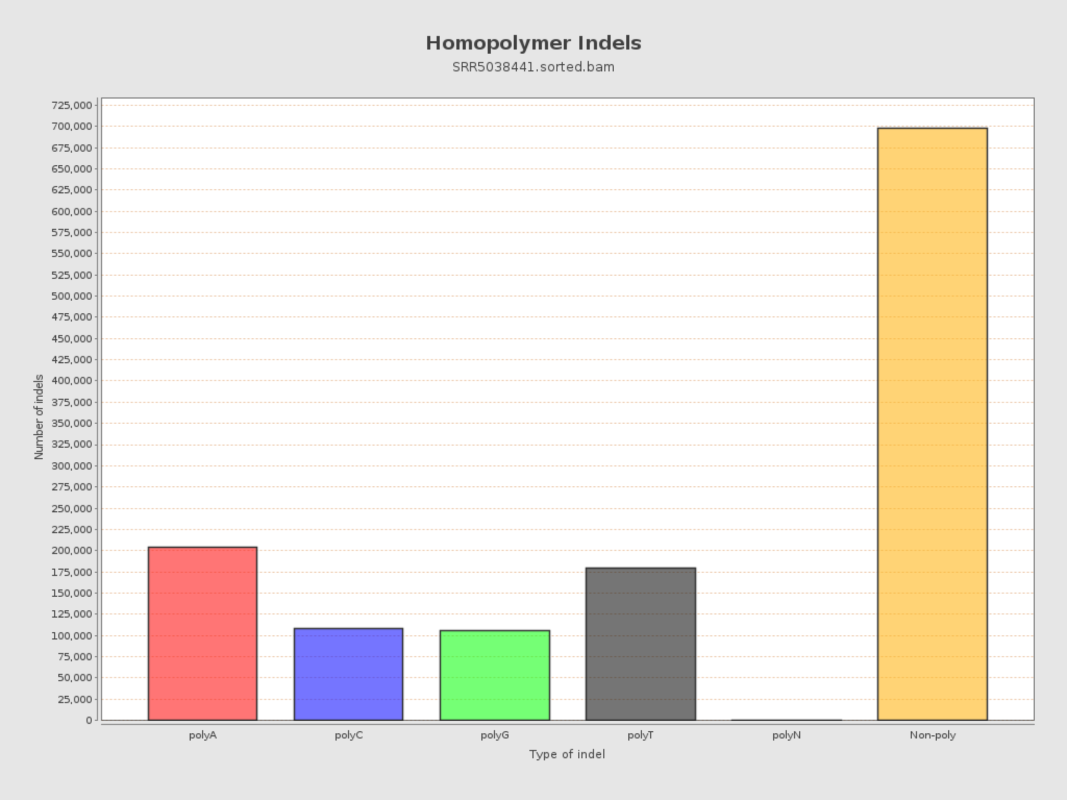
9. Results : Mapped Reads GC-content Distribution



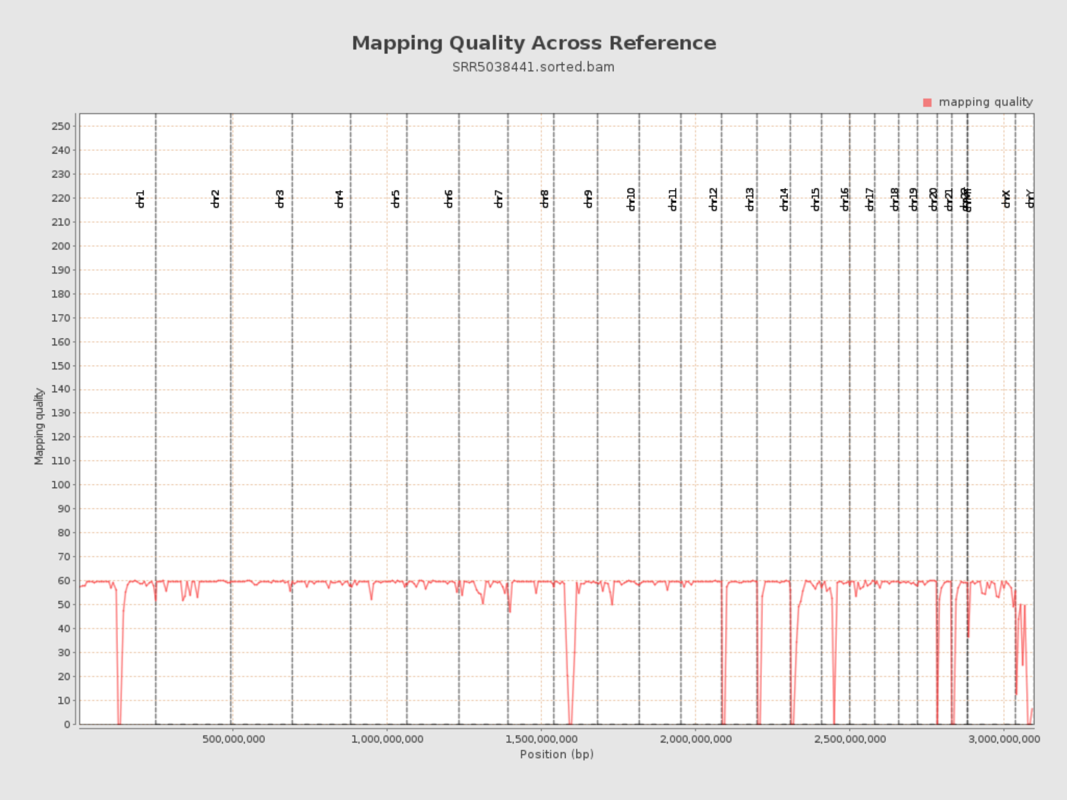
10. Results : Mapped Reads Clipping Profile



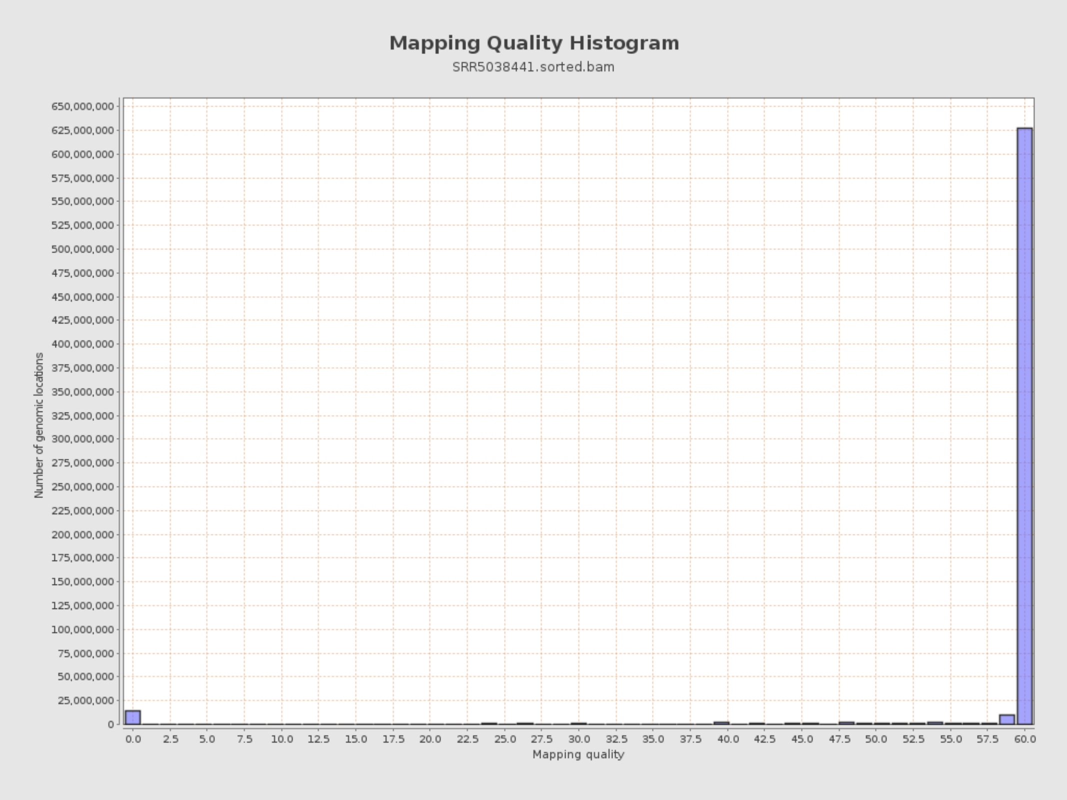
11. Results : Homopolymer Indels



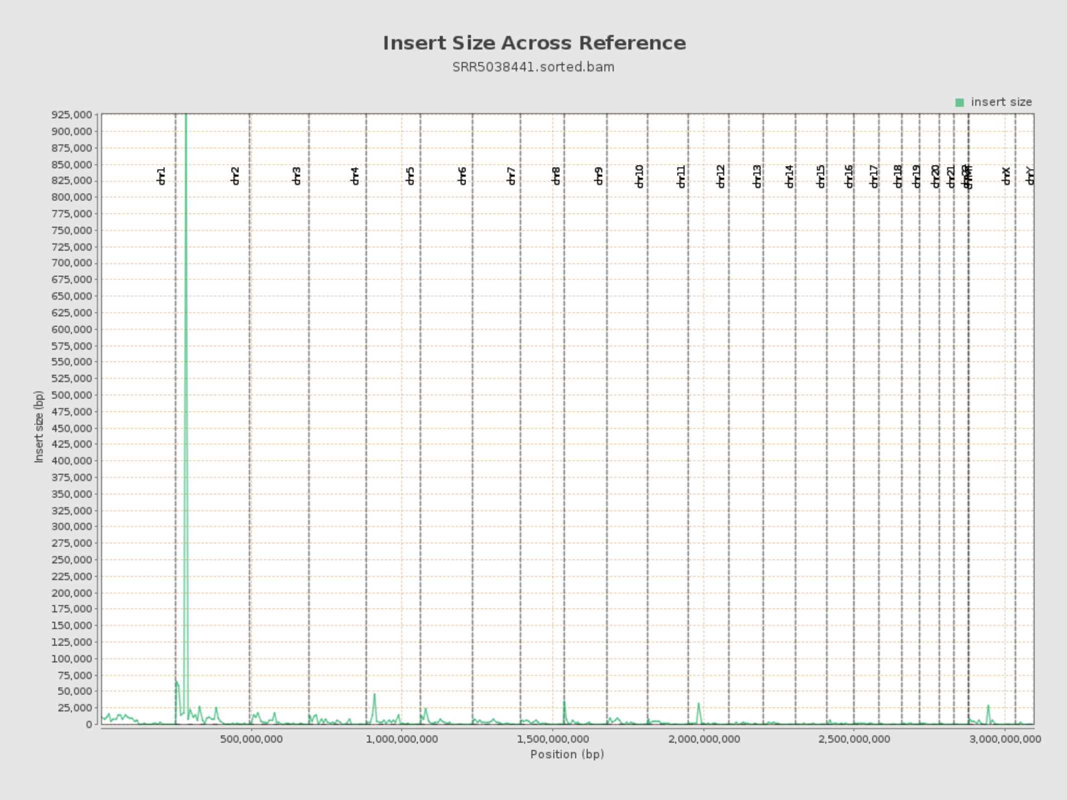
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram