Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 12:58:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438270.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_SRR8438270 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438270_1.fastq.gz SRR8438270_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 12:58:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438270.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	509,406,144
Mapped reads	507,764,857 / 99.68%
Unmapped reads	1,641,287 / 0.32%
Mapped paired reads	507,764,857 / 99.68%
Mapped reads, first in pair	254,054,646 / 49.87%
Mapped reads, second in pair	253,710,211 / 49.81%
Mapped reads, both in pair	506,606,914 / 99.45%
Mapped reads, singletons	1,157,943 / 0.23%
Secondary alignments	0
Supplementary alignments	8,323,769 / 1.63%
Read min/max/mean length	28 / 151 / 144.92
Duplicated reads (estimated)	178,510,011 / 35.04%
Duplication rate	32.6%
Clipped reads	90,280,836 / 17.72%

2.2. ACGT Content

Number/percentage of A's	22,109,625,885 / 30.31%
Number/percentage of C's	14,526,107,440 / 19.92%
Number/percentage of T's	21,088,875,108 / 28.91%
Number/percentage of G's	15,209,083,709 / 20.85%
Number/percentage of N's	549,456 / 0%

GC Percentage	40.77%

2.3. Coverage

Mean	23.5663
Standard Deviation	101.7591

2.4. Mapping Quality

Mean Mapping Quality	54.99

2.5. Insert size

Mean	38,873.41
Standard Deviation	1,920,199.14
P25/Median/P75	190 / 251 / 353

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	372,986,265
Insertions	9,023,374
Mapped reads with at least one insertion	1.75%
Deletions	7,976,483
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.35%

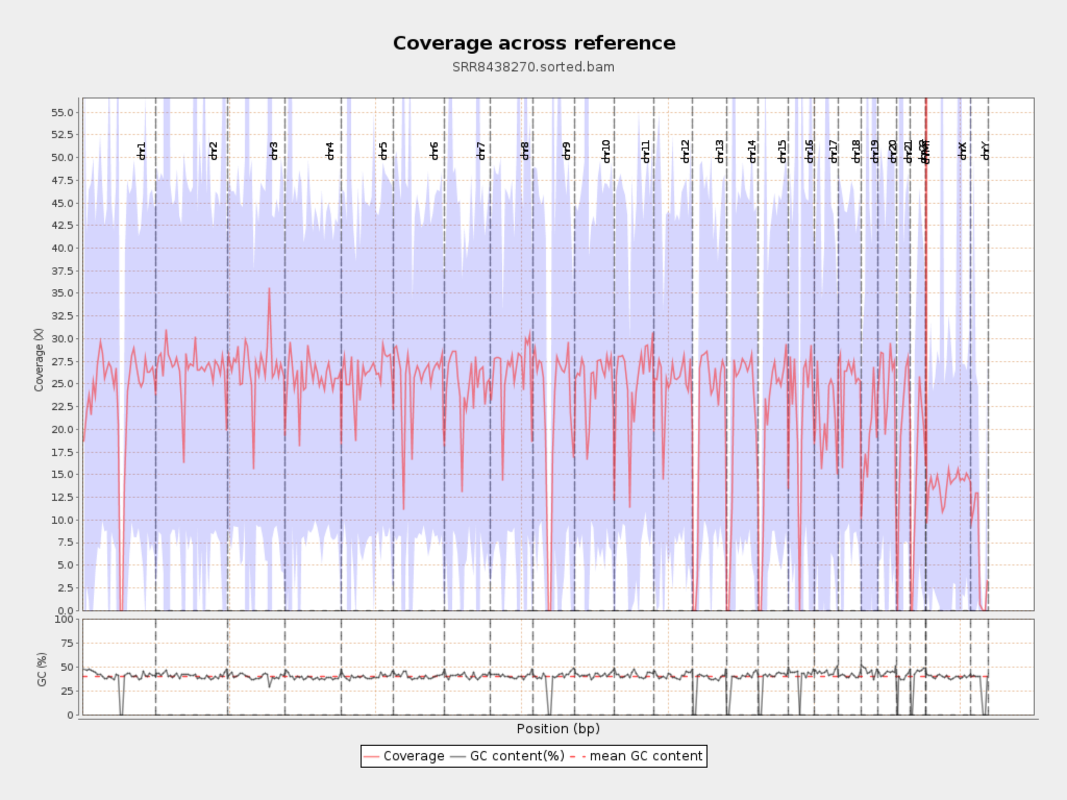
2.7. Chromosome stats

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

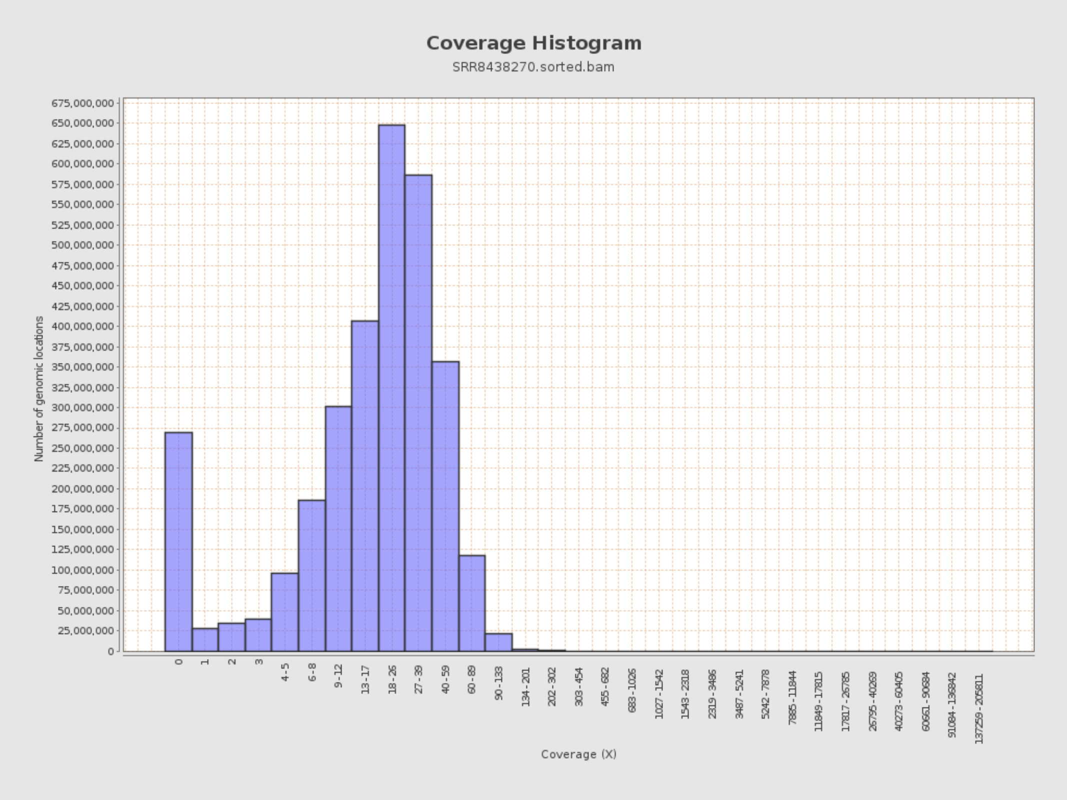
		bases	coverage	deviation
chr1	249250621	5886074440	23.6151	23.5276
chr2	243199373	6481329216	26.6503	93.5178
chr3	198022430	5320495013	26.8681	230.8351
chr4	191154276	4922879683	25.7534	25.8594
chr5	180915260	4717810939	26.0775	35.5209
chr6	171115067	4379626125	25.5946	22.8534
chr7	159138663	3942112115	24.7716	26.9998
chr8	146364022	3840995832	26.2428	23.5585
chr9	141213431	3148008471	22.2926	25.4992
chr10	135534747	3456266678	25.501	37.4923
chr11	135006516	3446310693	25.527	20.3921
chr12	133851895	3386536330	25.3006	20.3589
chr13	115169878	2518128896	21.8645	20.0227
chr14	107349540	2325228784	21.6604	26.3489
chr15	102531392	2106654575	20.5464	22.0165
chr16	90354753	1977308276	21.8838	37.0167
chr17	81195210	1749874715	21.5515	27.4242
chr18	78077248	1990935943	25.4996	19.9259
chr19	59128983	1110456902	18.7802	289.5548
chr20	63025520	1595964715	25.3225	22.5472
chr21	48129895	936989773	19.4679	121.4402
chr22	51304566	774239035	15.091	19.6244
chrMT	16571	413089750	24,928.4744	9,507.6467
chrX	155270560	2158182601	13.8995	40.1058

chrY	59373566	368569933	6.2076	19.1341

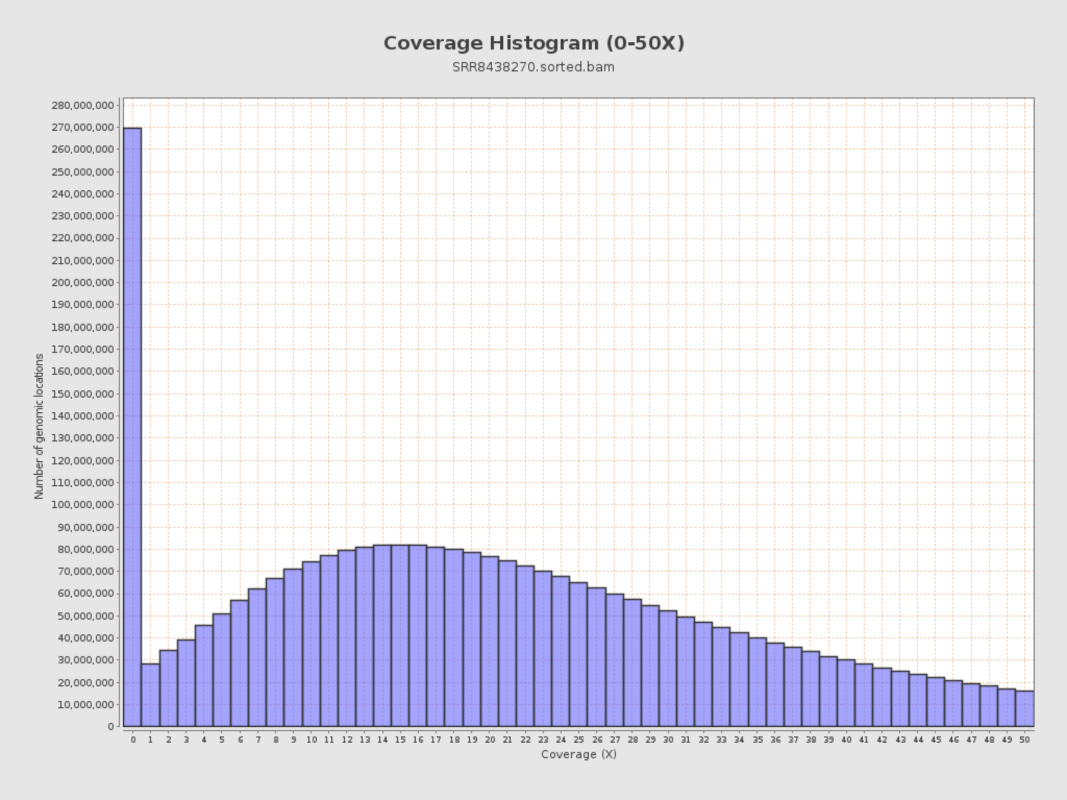
3. Results : Coverage across reference



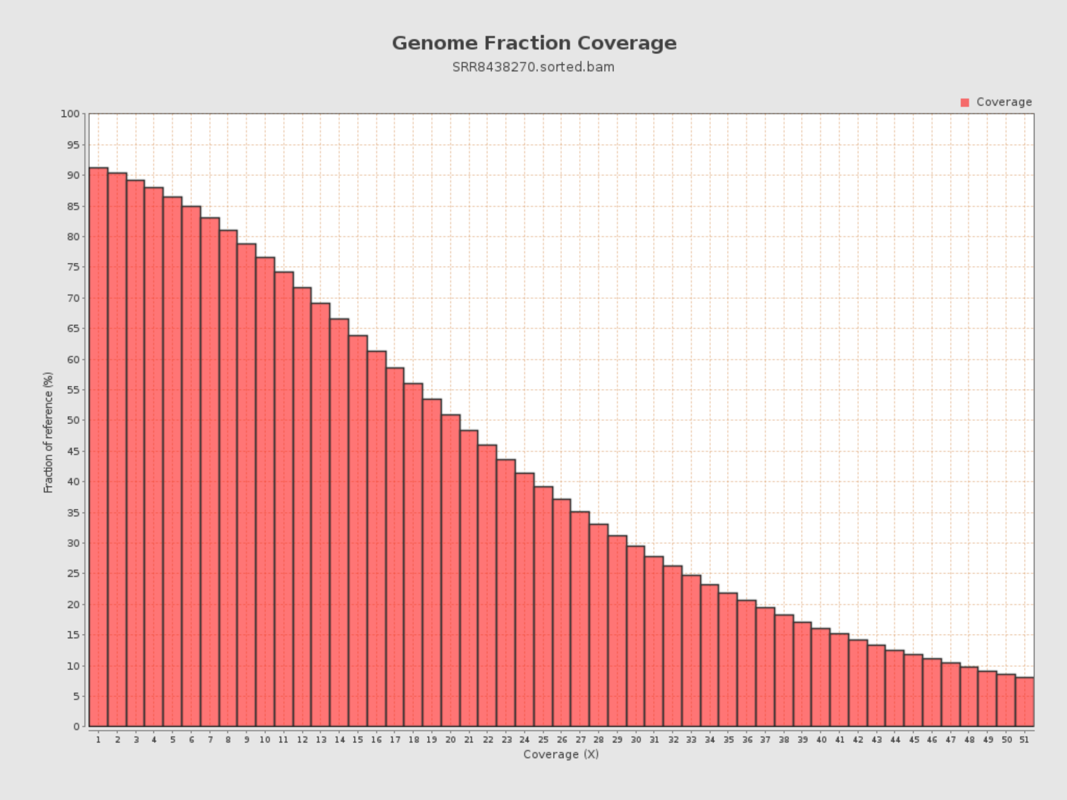
4. Results : Coverage Histogram



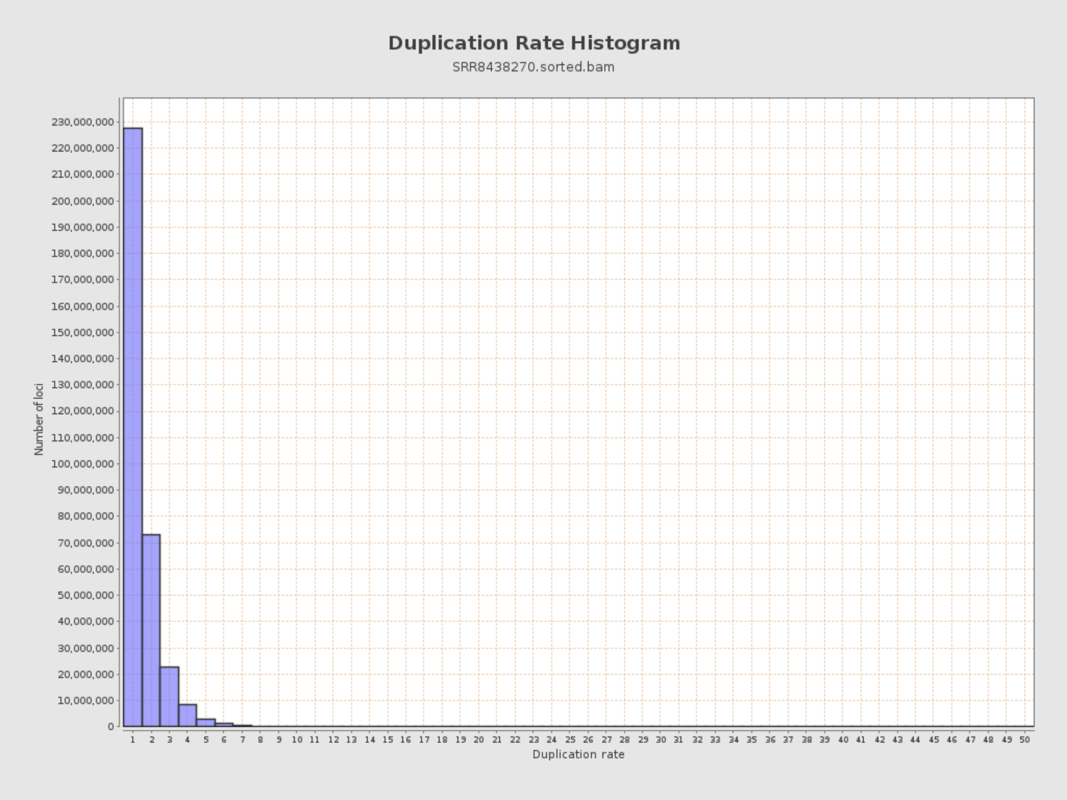
5. Results : Coverage Histogram (0-50X)



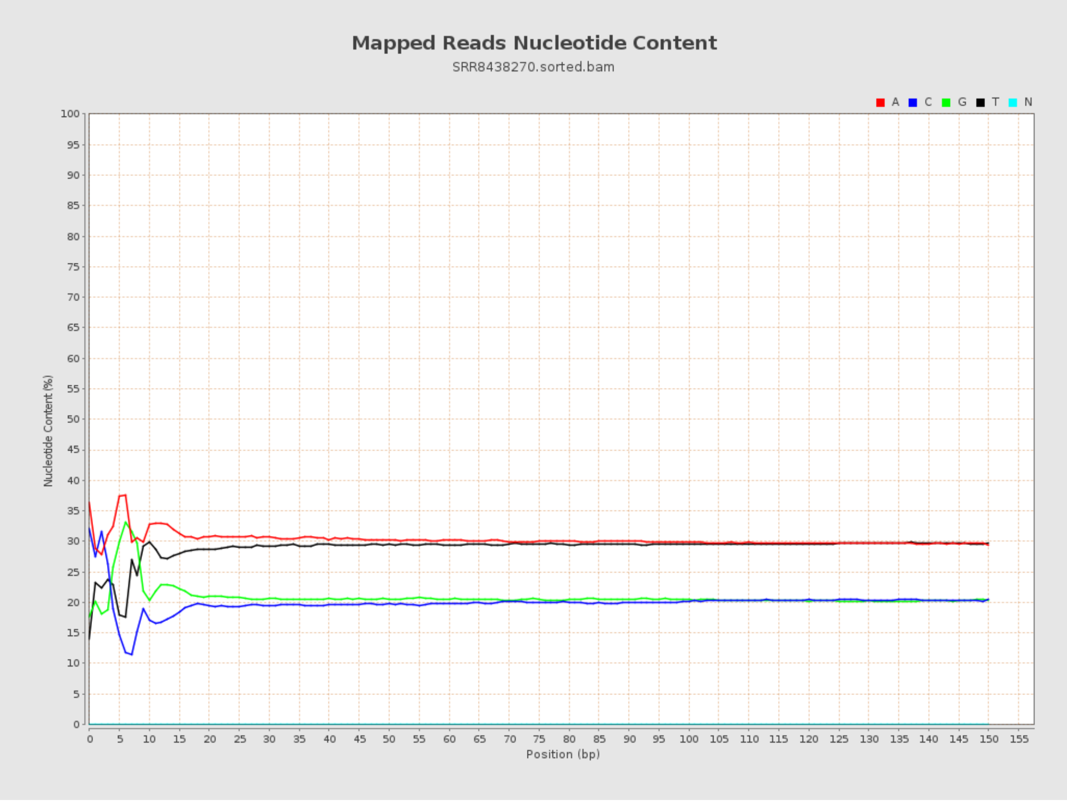
6. Results : Genome Fraction Coverage



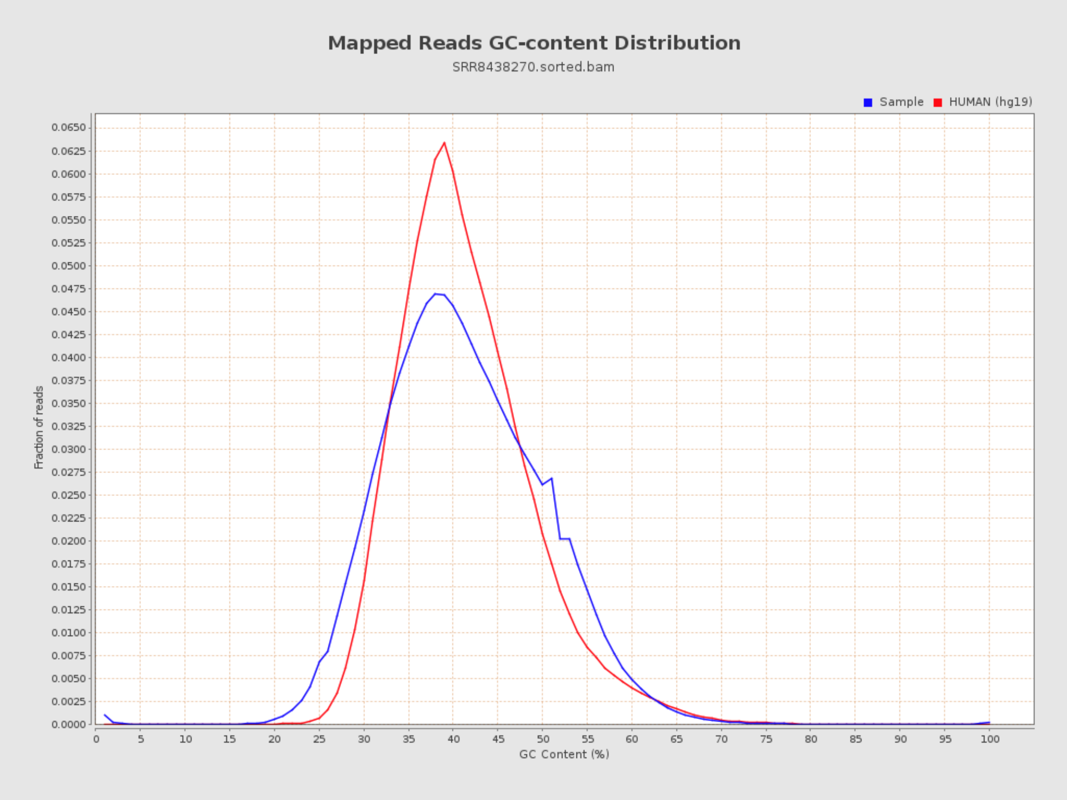
7. Results : Duplication Rate Histogram



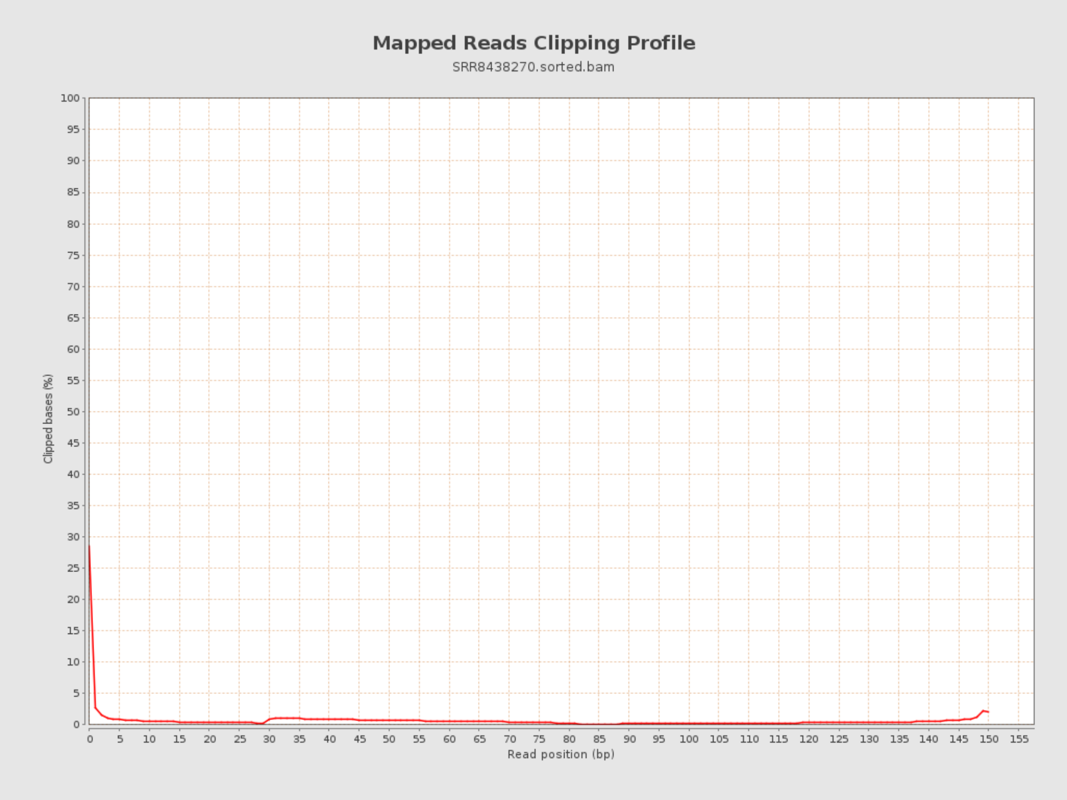
8. Results : Mapped Reads Nucleotide Content



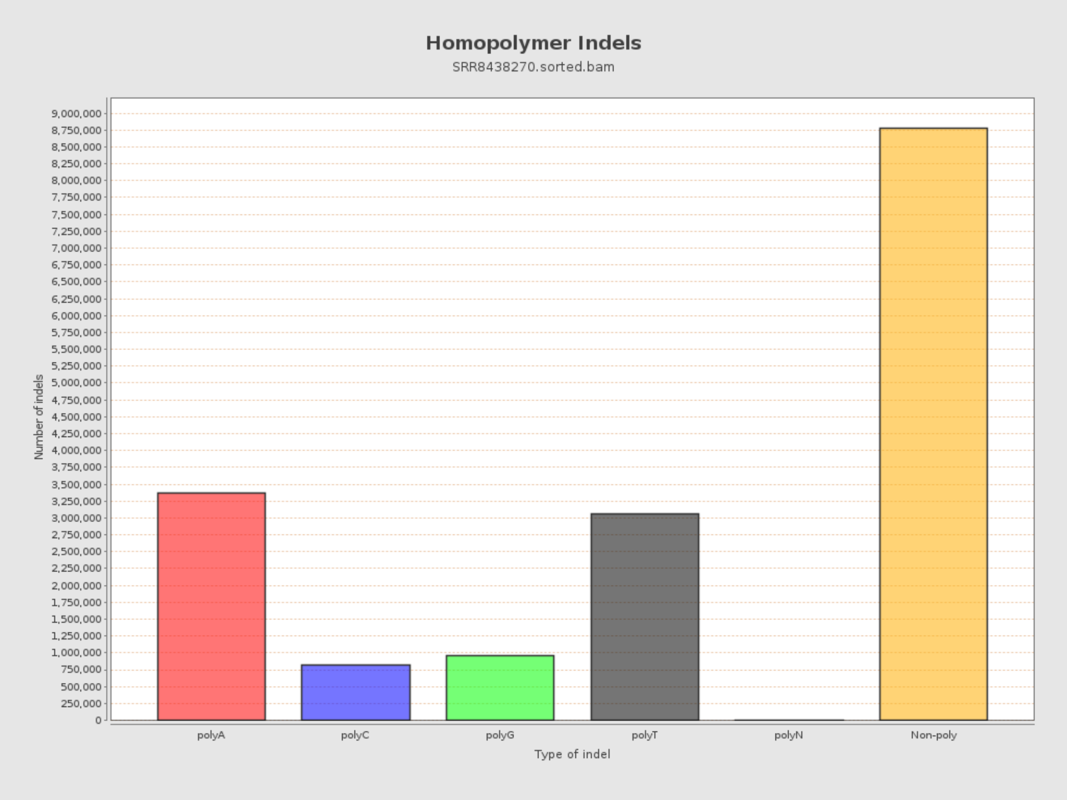
9. Results : Mapped Reads GC-content Distribution



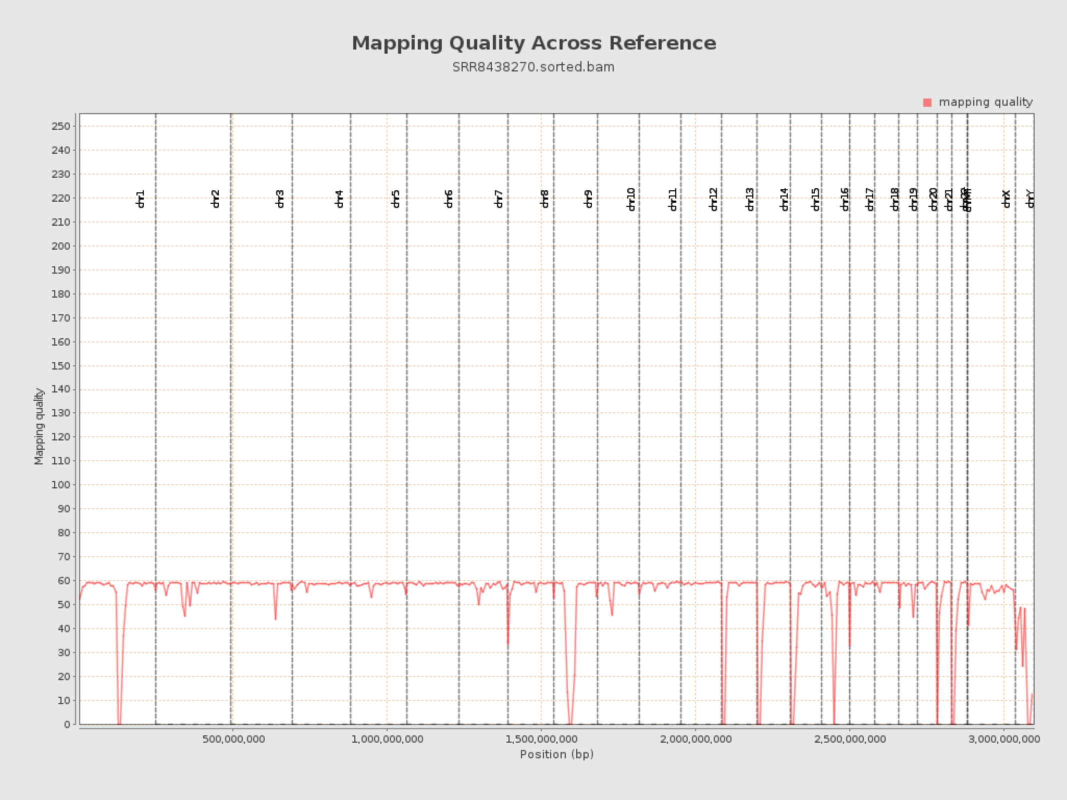
10. Results : Mapped Reads Clipping Profile



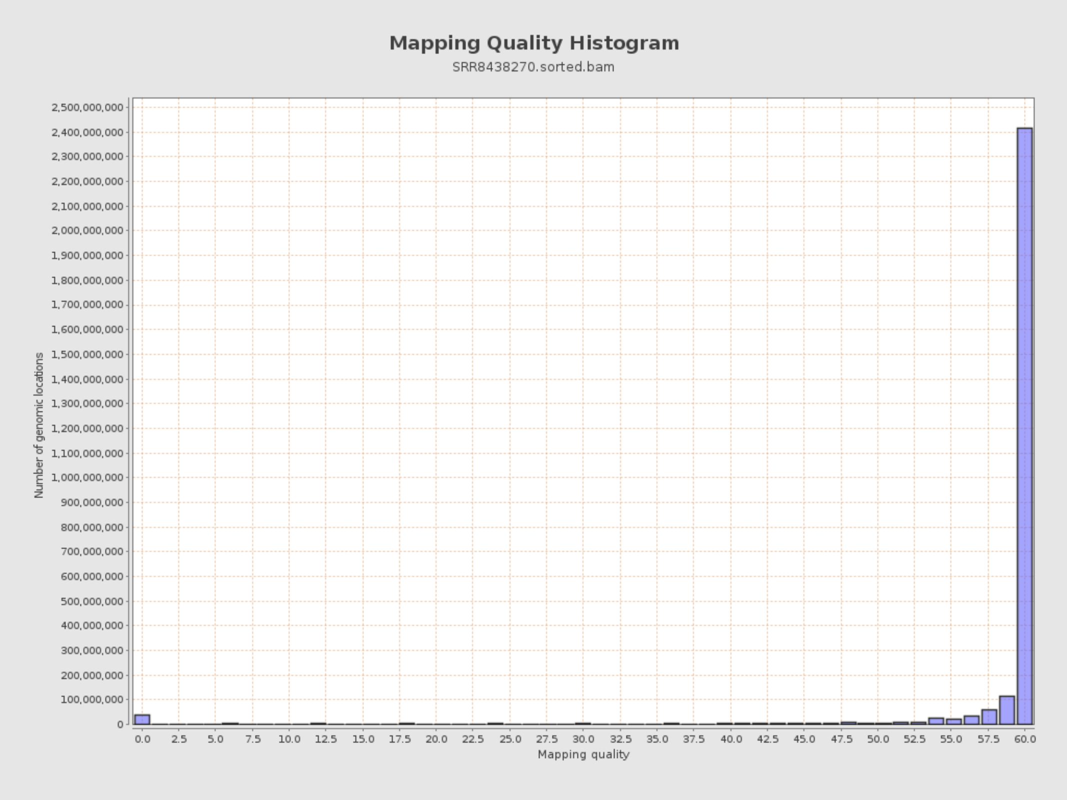
11. Results : Homopolymer Indels



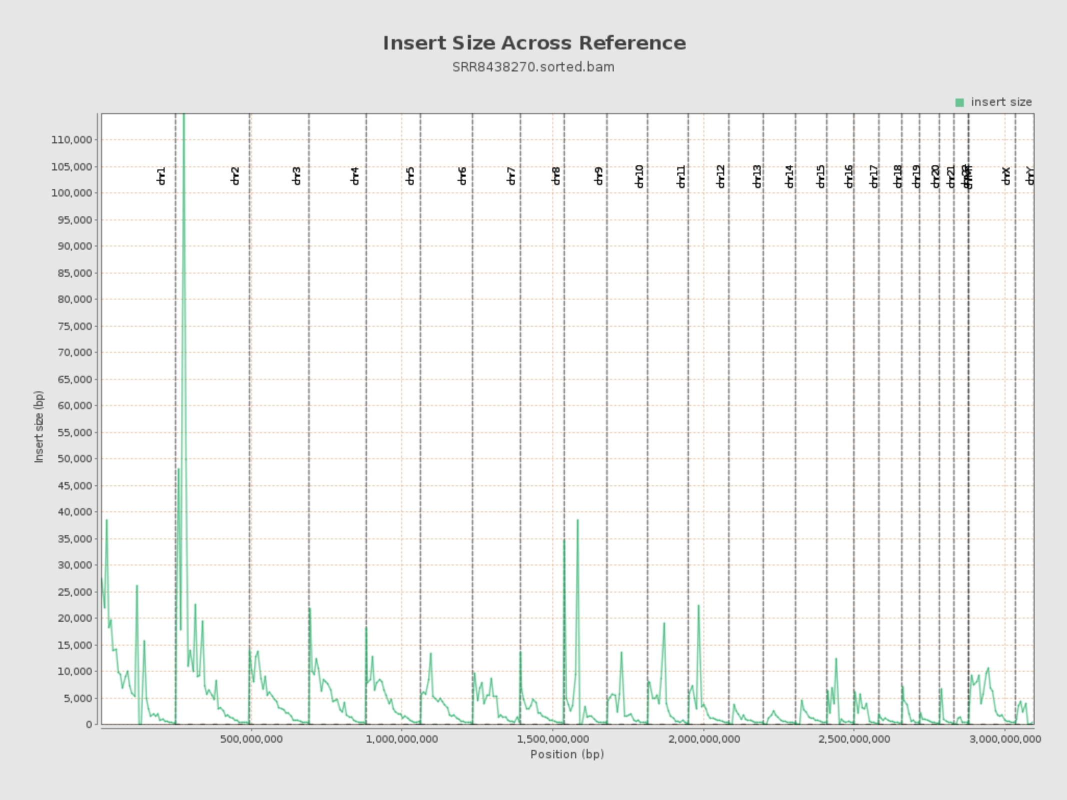
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram