Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/28 12:44:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438288.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_SRR8438288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438288_1.fastq.gz SRR8438288_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 28 12:44:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438288.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	693,577,926
Mapped reads	689,680,768 / 99.44%
Unmapped reads	3,897,158 / 0.56%
Mapped paired reads	689,680,768 / 99.44%
Mapped reads, first in pair	345,072,609 / 49.75%
Mapped reads, second in pair	344,608,159 / 49.69%
Mapped reads, both in pair	687,295,544 / 99.09%
Mapped reads, singletons	2,385,224 / 0.34%
Secondary alignments	0
Supplementary alignments	18,121,796 / 2.61%
Read min/max/mean length	30 / 149 / 143.06
Duplicated reads (estimated)	281,632,869 / 40.61%
Duplication rate	36%
Clipped reads	95,473,822 / 13.77%

2.2. ACGT Content

Number/percentage of A's	29,970,945,645 / 30.72%
Number/percentage of C's	18,495,675,959 / 18.96%
Number/percentage of T's	28,215,727,458 / 28.92%
Number/percentage of G's	20,879,687,272 / 21.4%
Number/percentage of N's	178,825 / 0%

GC Percentage	40.36%

2.3. Coverage

Mean	31.5255
Standard Deviation	133.1108

2.4. Mapping Quality

Mean Mapping Quality	54.22

2.5. Insert size

Mean	109,880.99
Standard Deviation	3,224,664.71
P25/Median/P75	407 / 480 / 596

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	543,072,472
Insertions	12,856,939
Mapped reads with at least one insertion	1.82%
Deletions	11,447,090
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47.91%

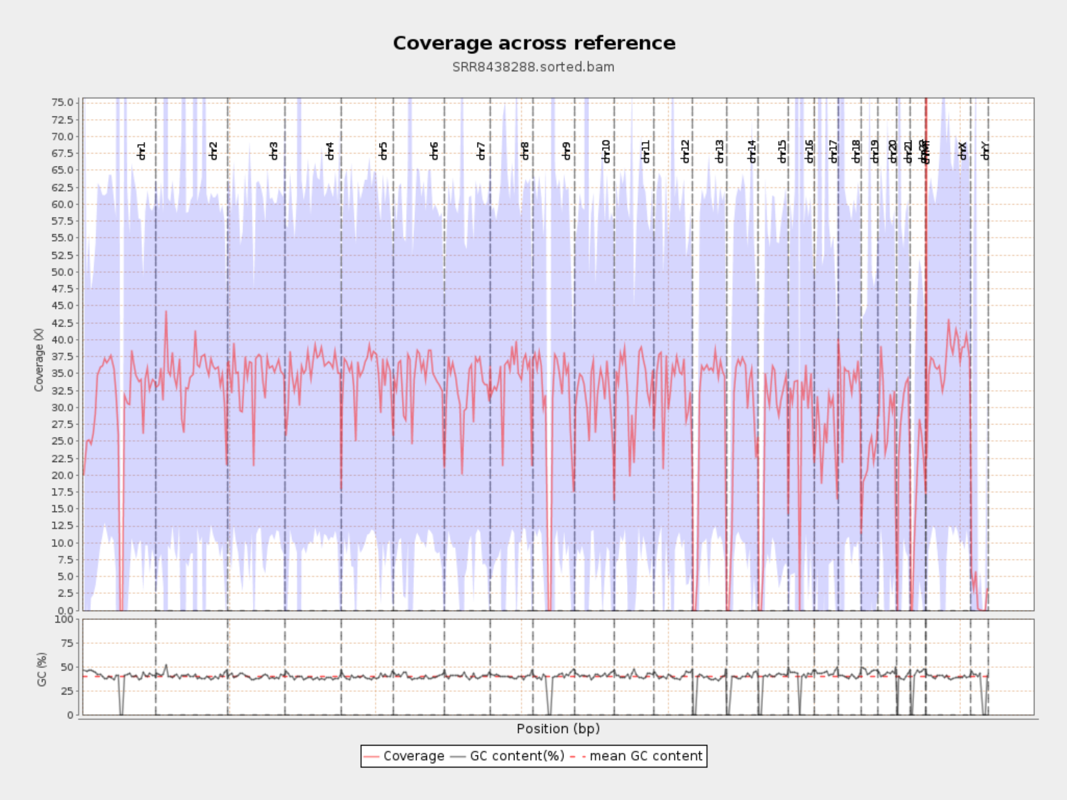
2.7. Chromosome stats

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

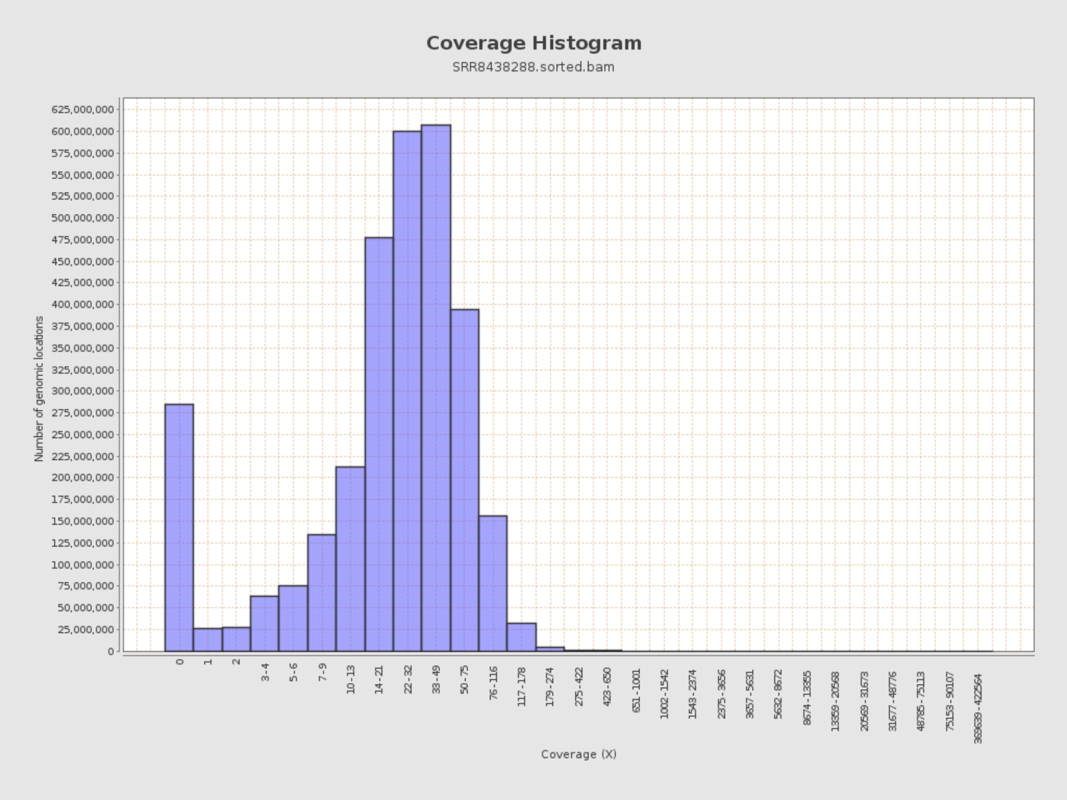
		bases	coverage	deviation
chr1	249250621	7532940806	30.2224	42.0097
chr2	243199373	8431203958	34.6679	320.1325
chr3	198022430	6884707406	34.7673	26.0514
chr4	191154276	6786929384	35.505	36.6727
chr5	180915260	6284780592	34.7388	26.4898
chr6	171115067	5878379128	34.3534	33.6881
chr7	159138663	5190438909	32.6158	29.6251
chr8	146364022	5029710054	34.3644	29.5425
chr9	141213431	4213147262	29.8353	53.3591
chr10	135534747	4352953235	32.1169	86.9006
chr11	135006516	4410736614	32.6705	29.1148
chr12	133851895	4429861670	33.0952	27.8209
chr13	115169878	3374651230	29.3015	26.7957
chr14	107349540	2957419403	27.5494	27.4265
chr15	102531392	2675154923	26.0911	26.2435
chr16	90354753	2570194945	28.4456	89.9411
chr17	81195210	2162433068	26.6325	45.9591
chr18	78077248	2638586085	33.7946	63.7505
chr19	59128983	1308782724	22.1344	30.0099
chr20	63025520	1870662882	29.681	30.5876
chr21	48129895	1267320336	26.3313	42.3208
chr22	51304566	870164705	16.9608	23.7349
chrMT	16571	604543576	36,482.0214	13,139.304
chrX	155270560	5740302903	36.9697	29.5595

chrY	59373566	127259462	2.1434	36.3646

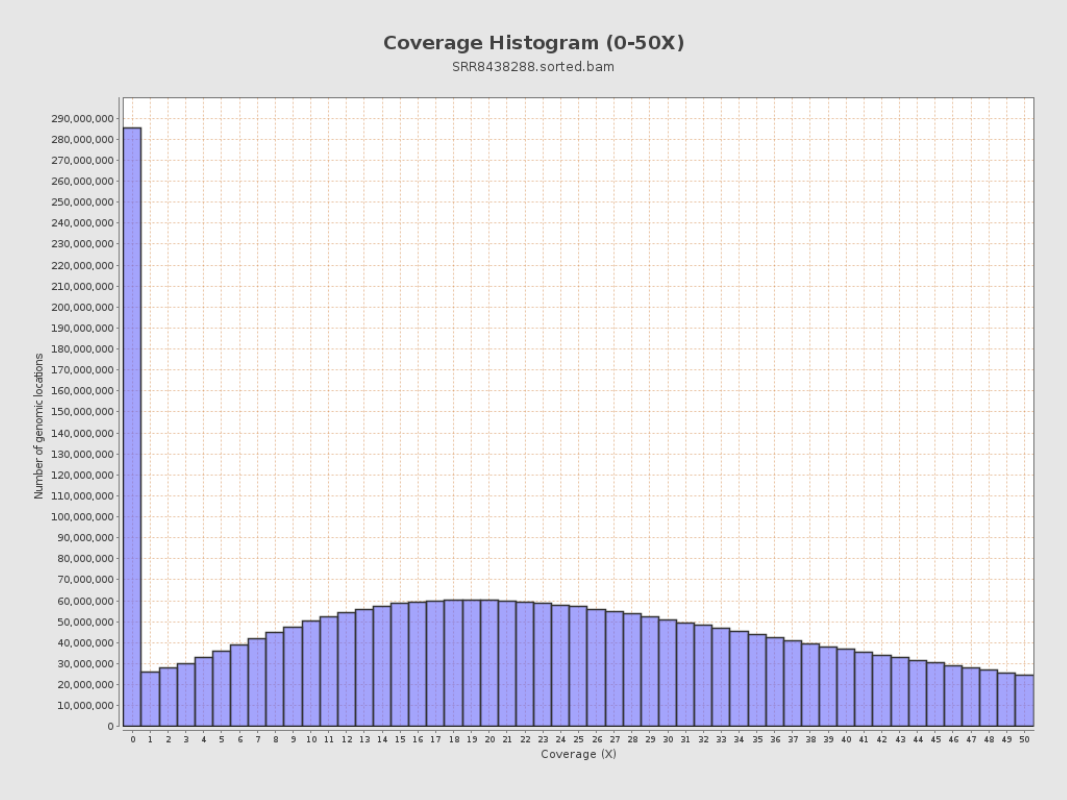
3. Results : Coverage across reference



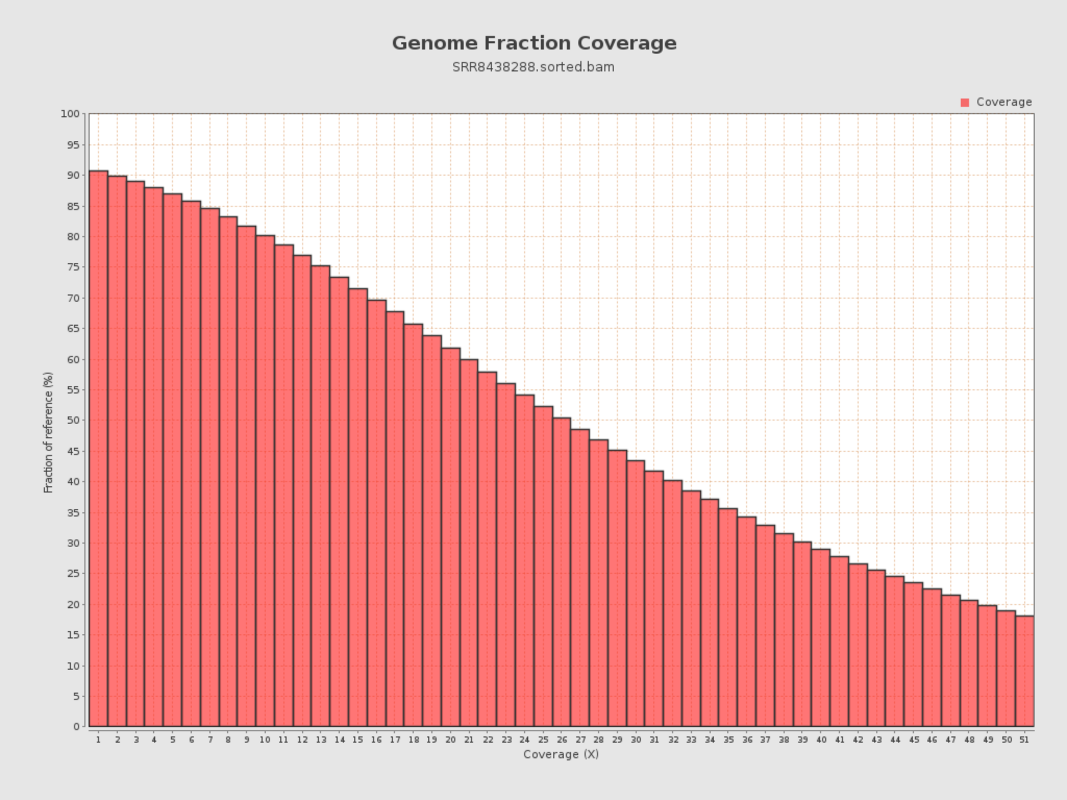
4. Results : Coverage Histogram



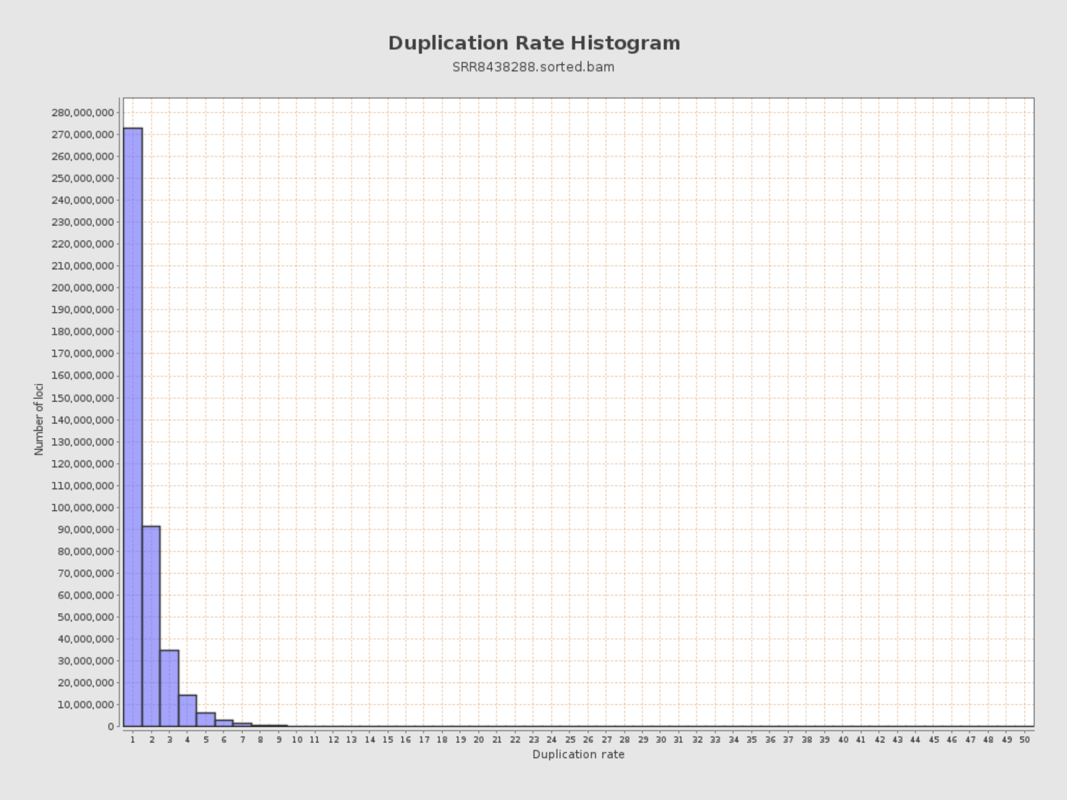
5. Results : Coverage Histogram (0-50X)



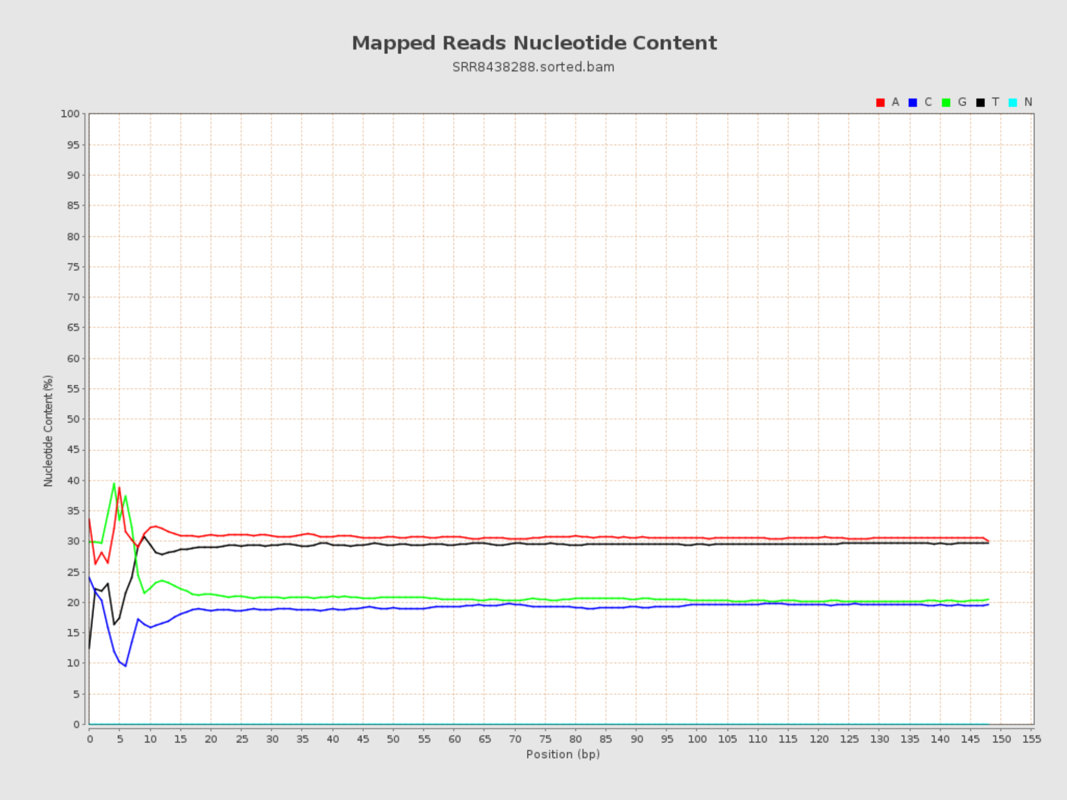
6. Results : Genome Fraction Coverage



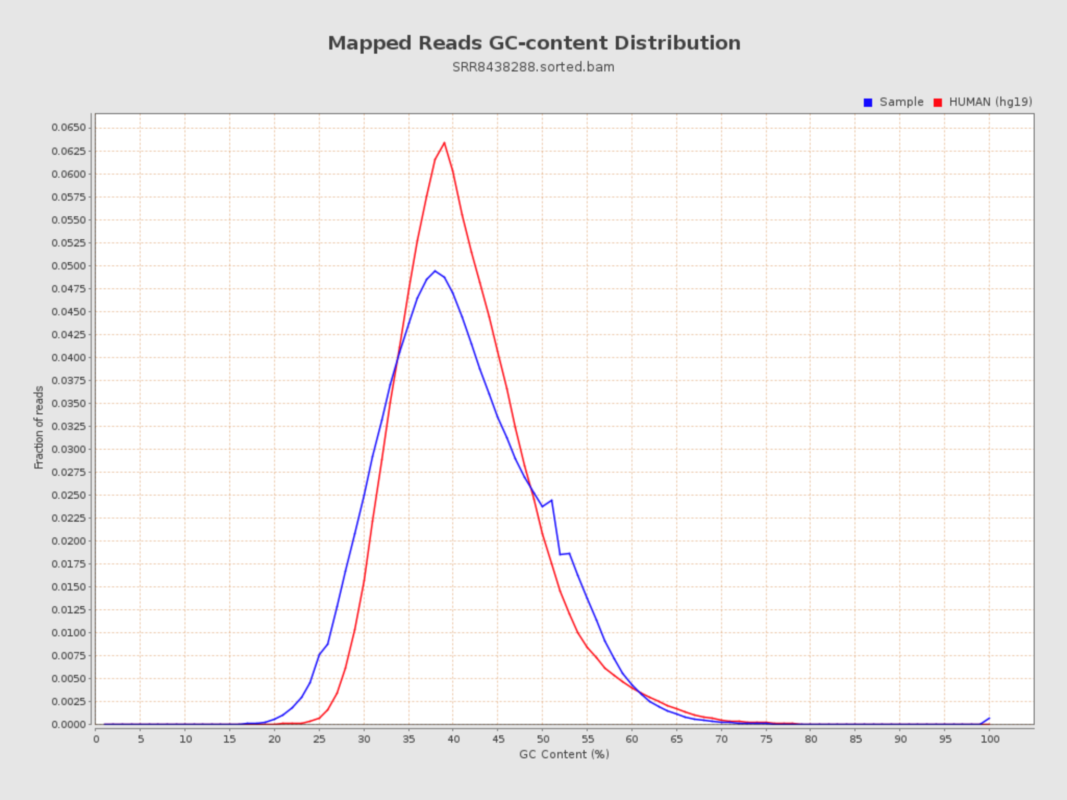
7. Results : Duplication Rate Histogram



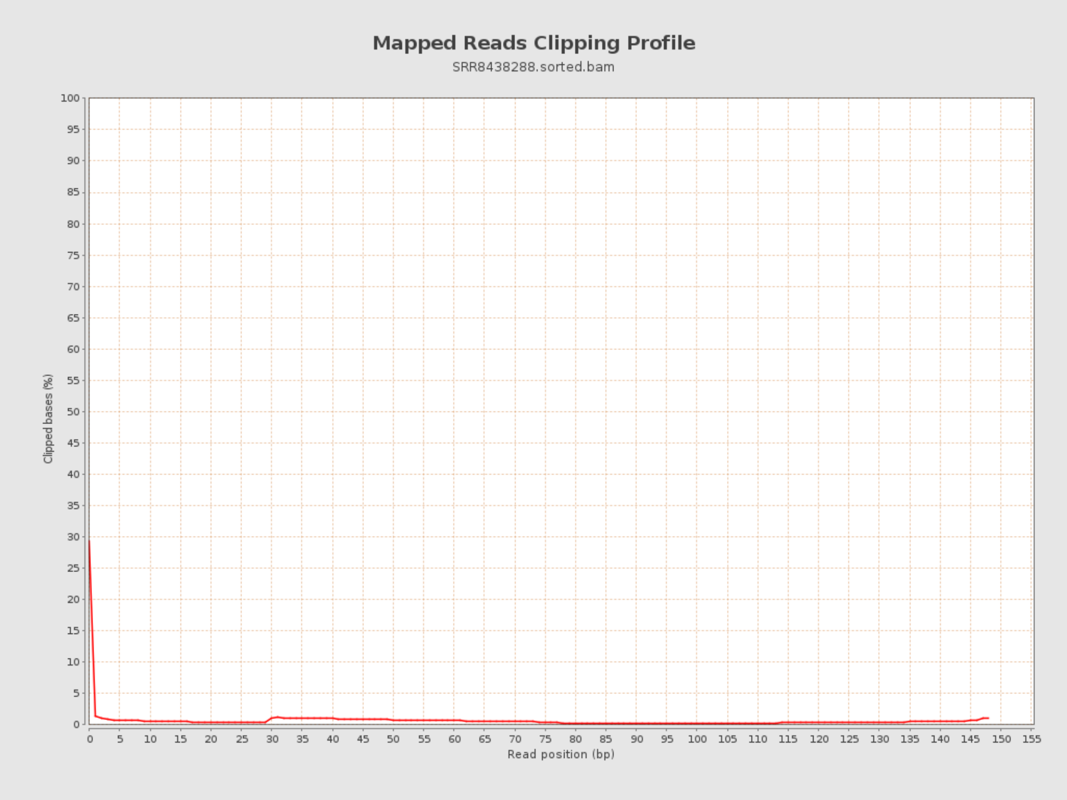
8. Results : Mapped Reads Nucleotide Content



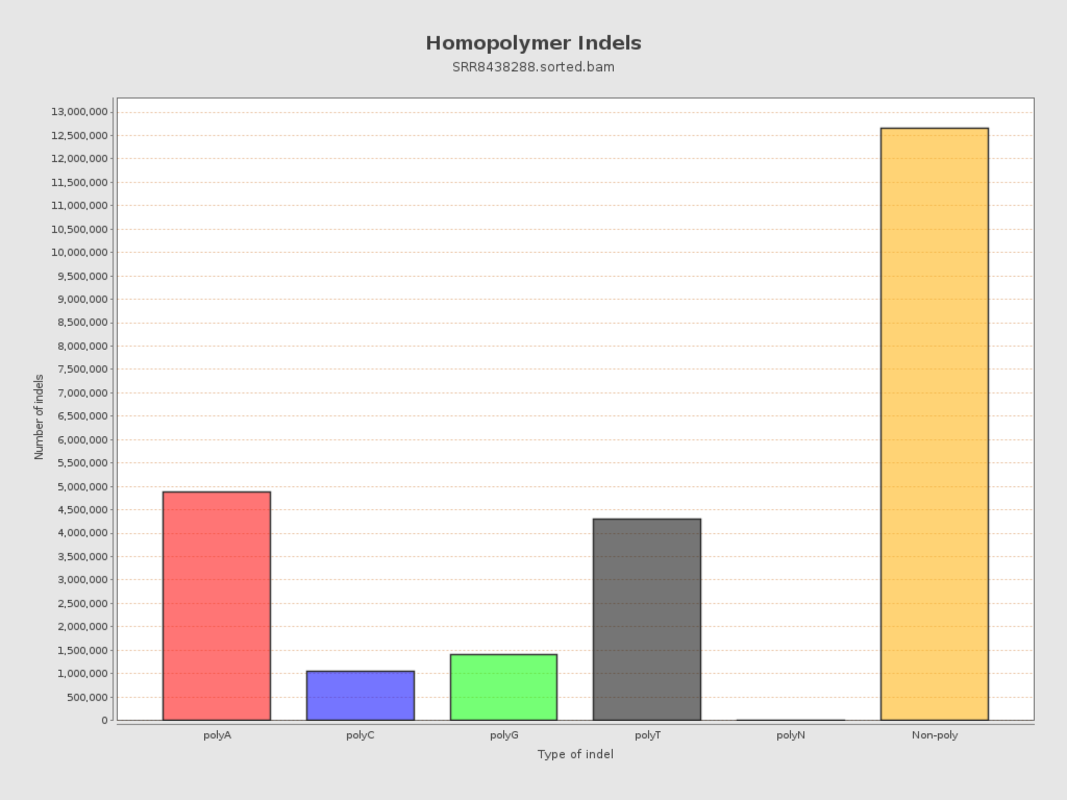
9. Results : Mapped Reads GC-content Distribution



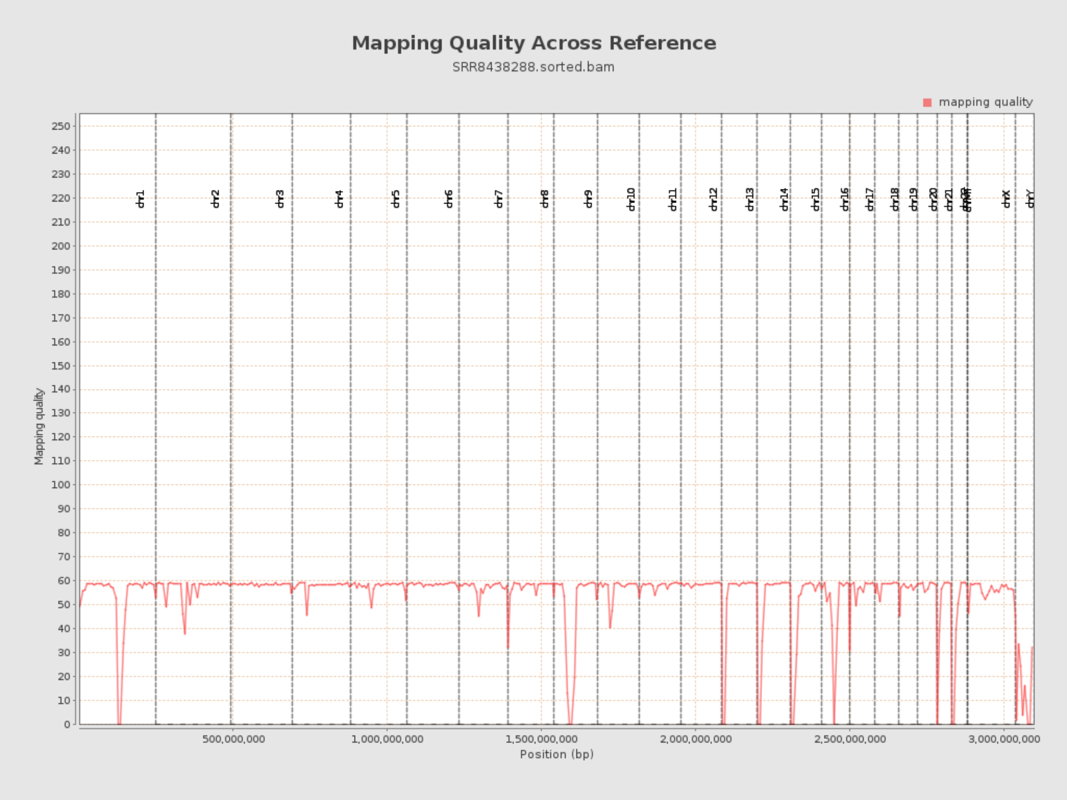
10. Results : Mapped Reads Clipping Profile



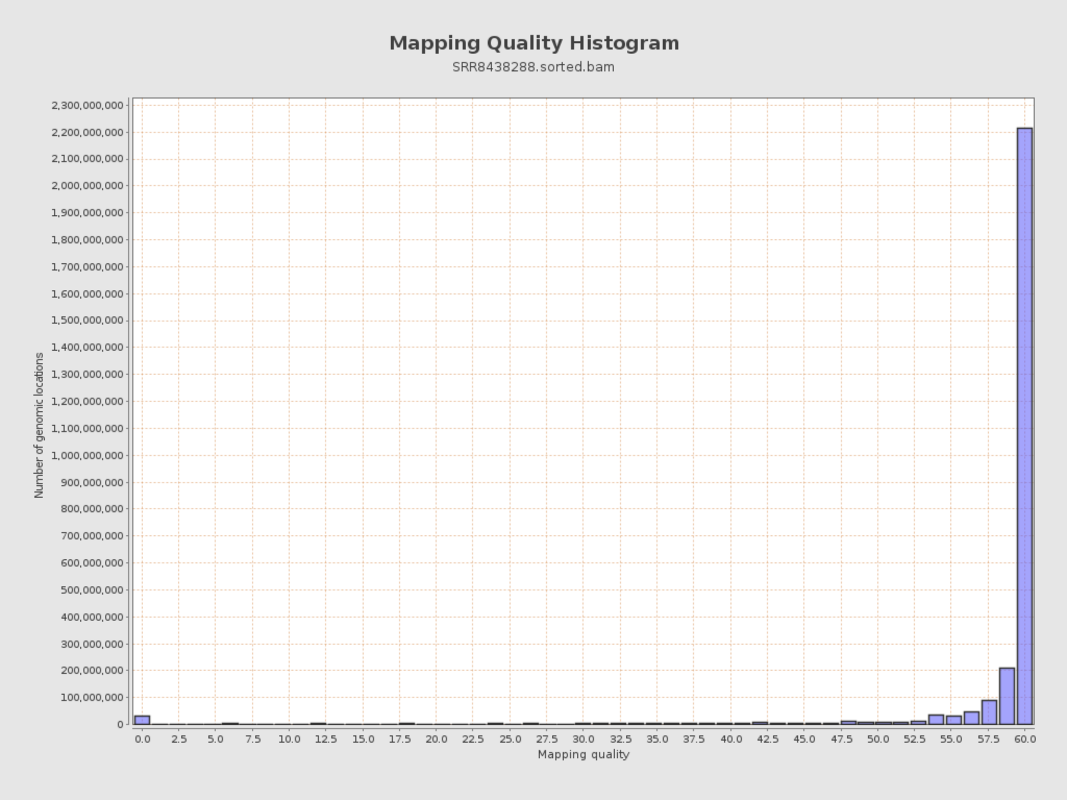
11. Results : Homopolymer Indels



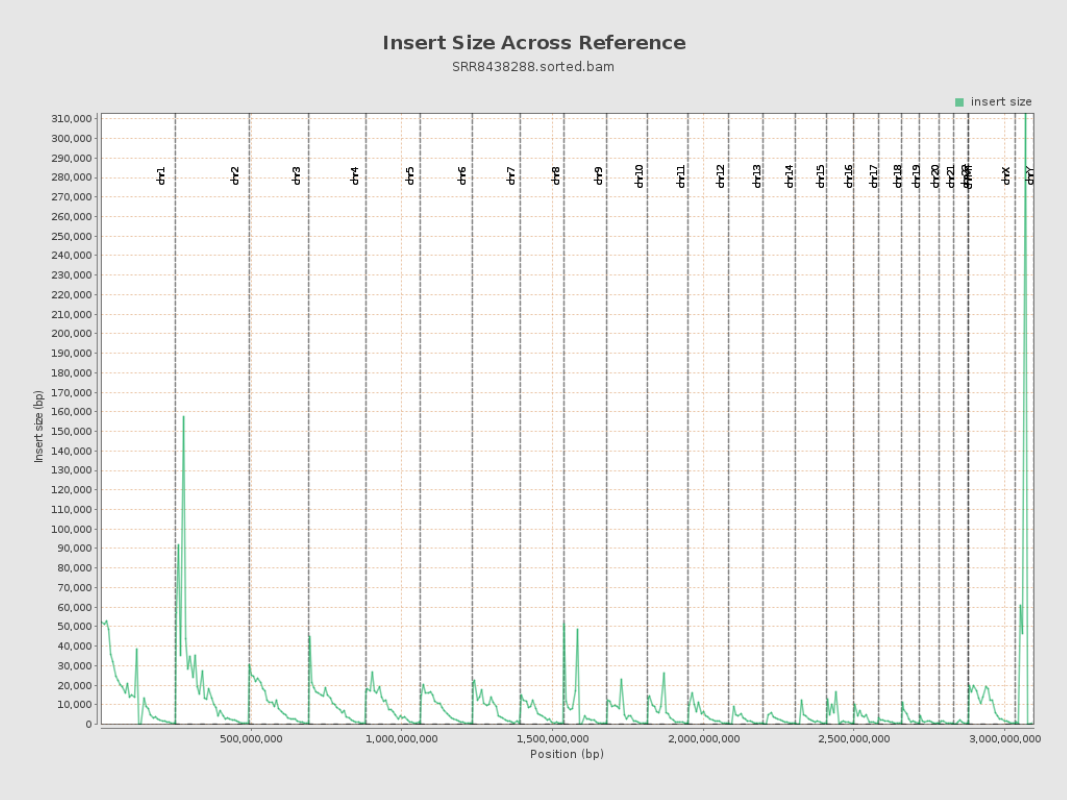
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram