Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/30 09:41:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438289.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_SRR8438289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438289_1.fastq.gz SRR8438289_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 30 09:41:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	772,820,886
Mapped reads	768,371,382 / 99.42%
Unmapped reads	4,449,504 / 0.58%
Mapped paired reads	768,371,382 / 99.42%
Mapped reads, first in pair	384,479,059 / 49.75%
Mapped reads, second in pair	383,892,323 / 49.67%
Mapped reads, both in pair	765,572,876 / 99.06%
Mapped reads, singletons	2,798,506 / 0.36%
Secondary alignments	0
Supplementary alignments	18,296,707 / 2.37%
Read min/max/mean length	30 / 149 / 142.54
Duplicated reads (estimated)	330,549,125 / 42.77%
Duplication rate	38%
Clipped reads	101,221,049 / 13.1%

2.2. ACGT Content

Number/percentage of A's	33,171,213,472 / 30.59%
Number/percentage of C's	20,686,457,970 / 19.08%
Number/percentage of T's	31,101,581,171 / 28.68%
Number/percentage of G's	23,467,724,770 / 21.64%
Number/percentage of N's	200,294 / 0%

GC Percentage	40.72%

2.3. Coverage

Mean	35.0364
Standard Deviation	108.6382

2.4. Mapping Quality

Mean Mapping Quality	54.31

2.5. Insert size

Mean	111,402.48
Standard Deviation	3,266,734.63
P25/Median/P75	408 / 488 / 612

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	613,468,235
Insertions	14,302,970
Mapped reads with at least one insertion	1.82%
Deletions	12,817,899
Mapped reads with at least one deletion	1.62%
Homopolymer indels	47.99%

2.7. Chromosome stats

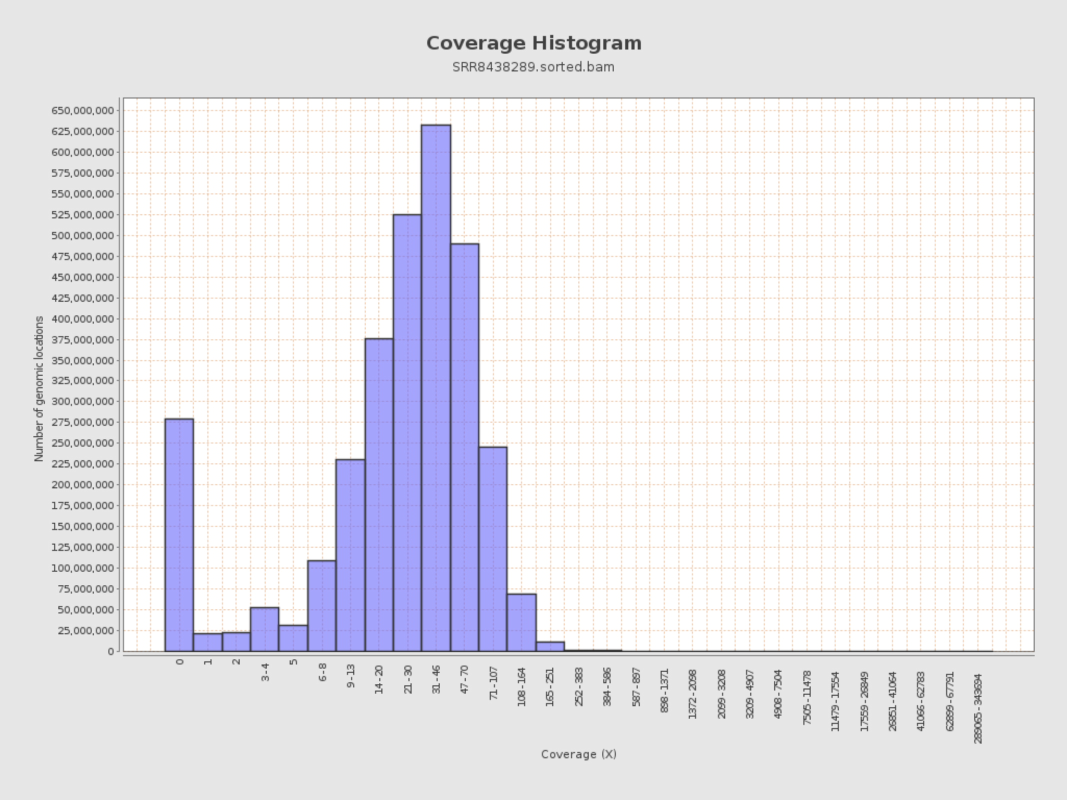
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	8817471353	35.3759	47.7623
chr2	243199373	9483964778	38.9967	260.525
chr3	198022430	7876795770	39.7773	29.4357
chr4	191154276	7000119462	36.6203	37.1791
chr5	180915260	6849535449	37.8605	28.8474
chr6	171115067	6526453024	38.1407	34.0834
chr7	159138663	5702360433	35.8327	29.8142
chr8	146364022	5515802607	37.6855	32.4173
chr9	141213431	4476321448	31.699	56.3187
chr10	135534747	5056704138	37.3093	78.9637
chr11	135006516	5249090637	38.8803	35.0152
chr12	133851895	5033783607	37.6071	30.7151
chr13	115169878	3278580587	28.4673	27.9232
chr14	107349540	3303138809	30.7699	30.571
chr15	102531392	3916060883	38.1938	37.6628
chr16	90354753	2834021367	31.3655	79.3846
chr17	81195210	2602352929	32.0506	51.1958
chr18	78077248	2793903103	35.7838	68.1478
chr19	59128983	1548592331	26.1901	34.3774
chr20	63025520	2234721837	35.4574	33.0945
chr21	48129895	1419461560	29.4923	45.8474
chr22	51304566	1112319060	21.6807	28.9721
chrMT	16571	464784355	28,048.0571	10,176.3696
chrX	155270560	5227402931	33.6664	27.4463

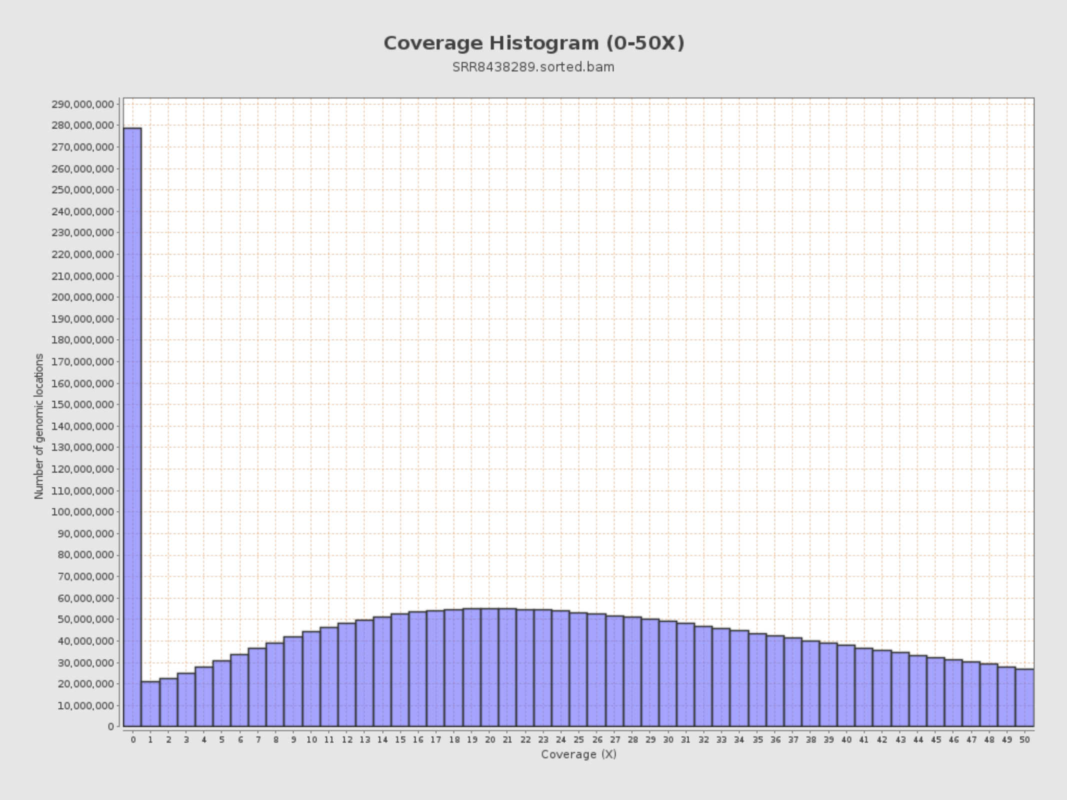
chrY	59373566	138267187	2.3288	39.1542

3. Results : Coverage across reference

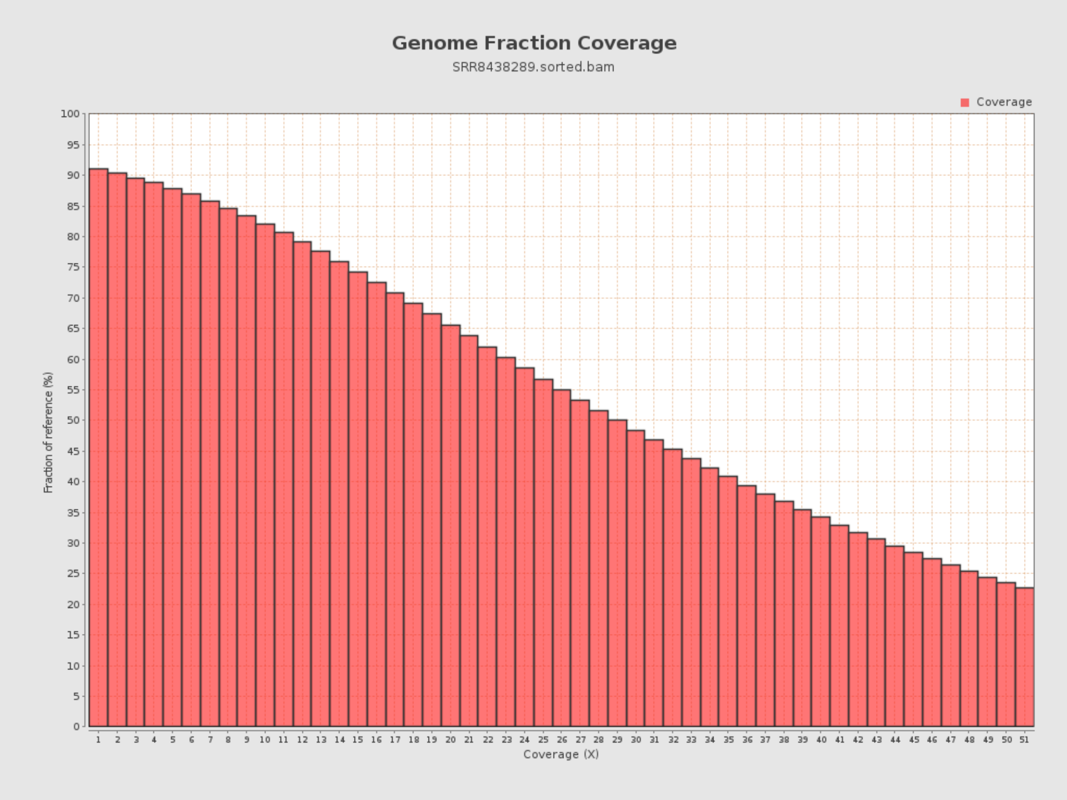
4. Results : Coverage Histogram



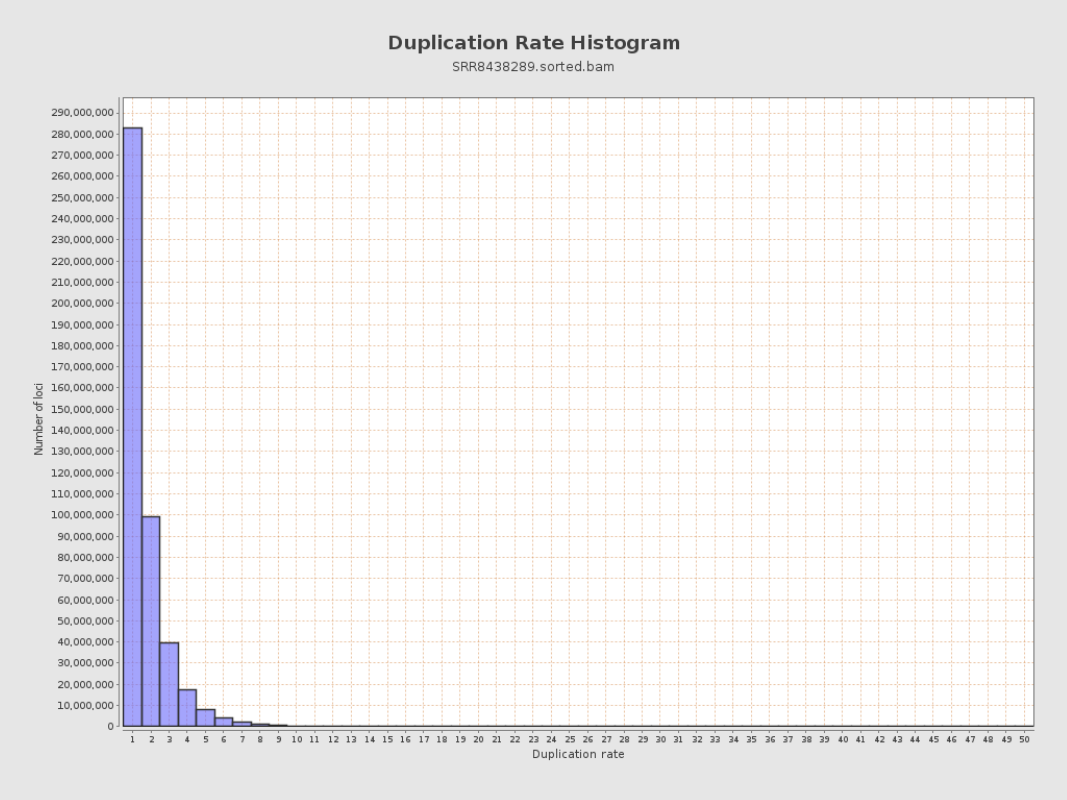
5. Results : Coverage Histogram (0-50X)



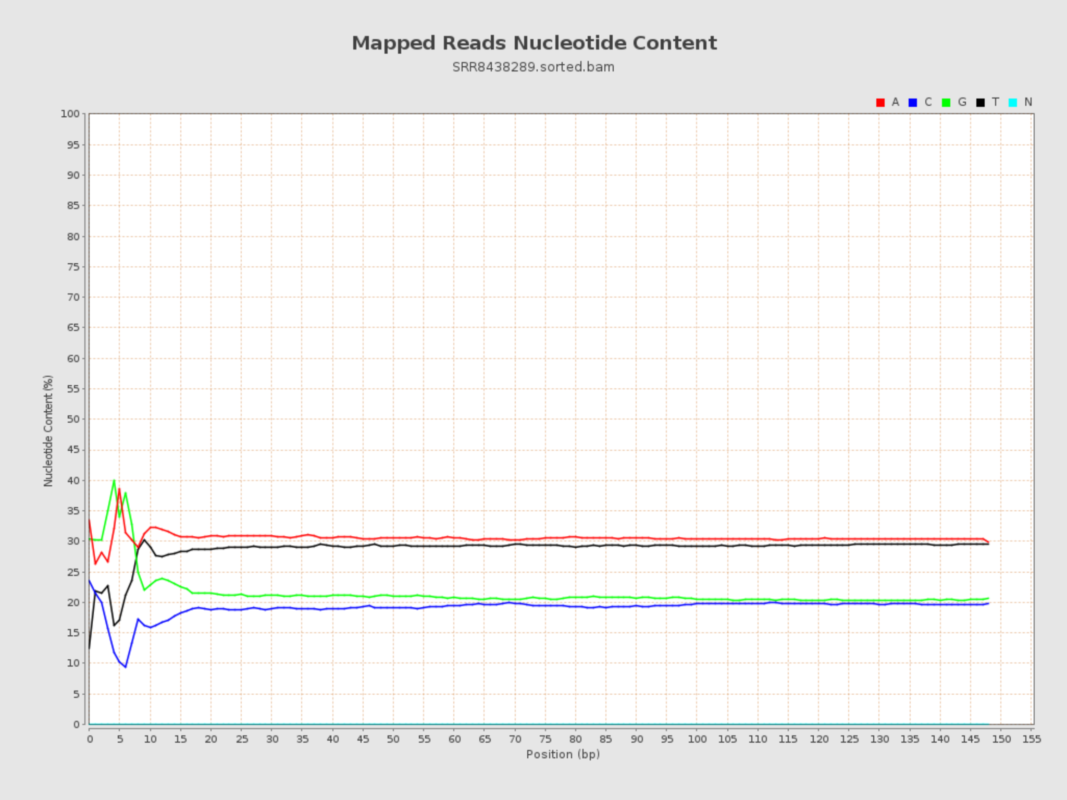
6. Results : Genome Fraction Coverage



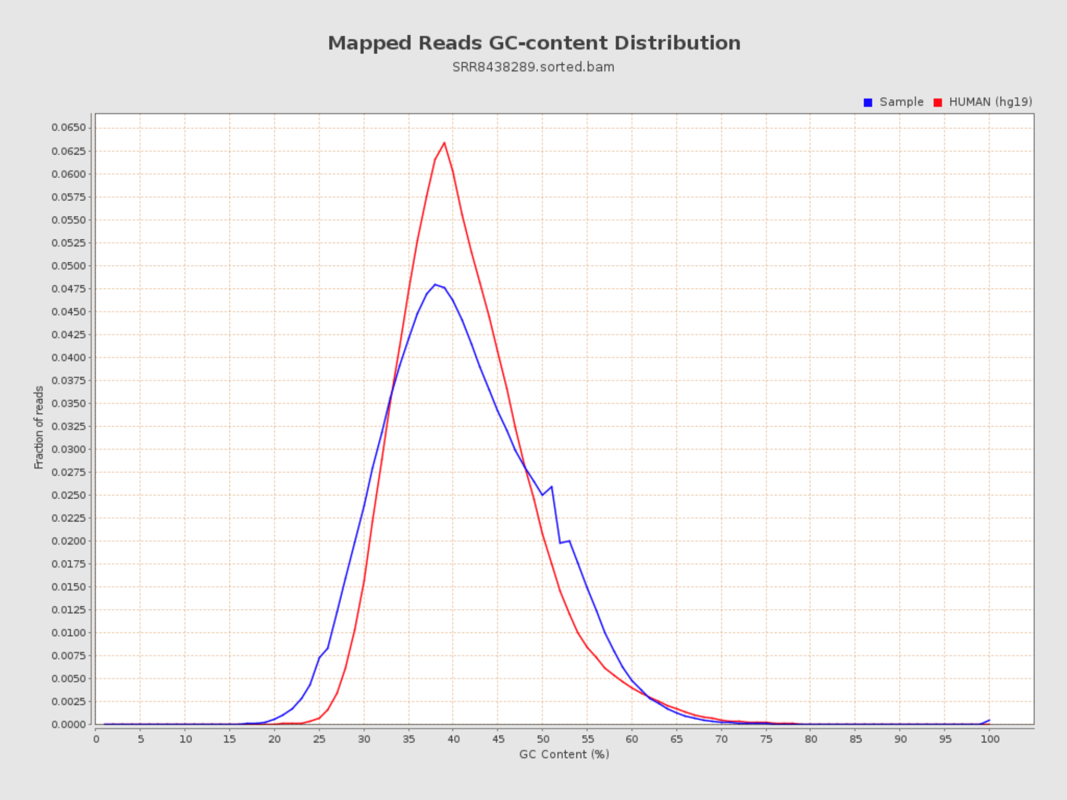
7. Results : Duplication Rate Histogram



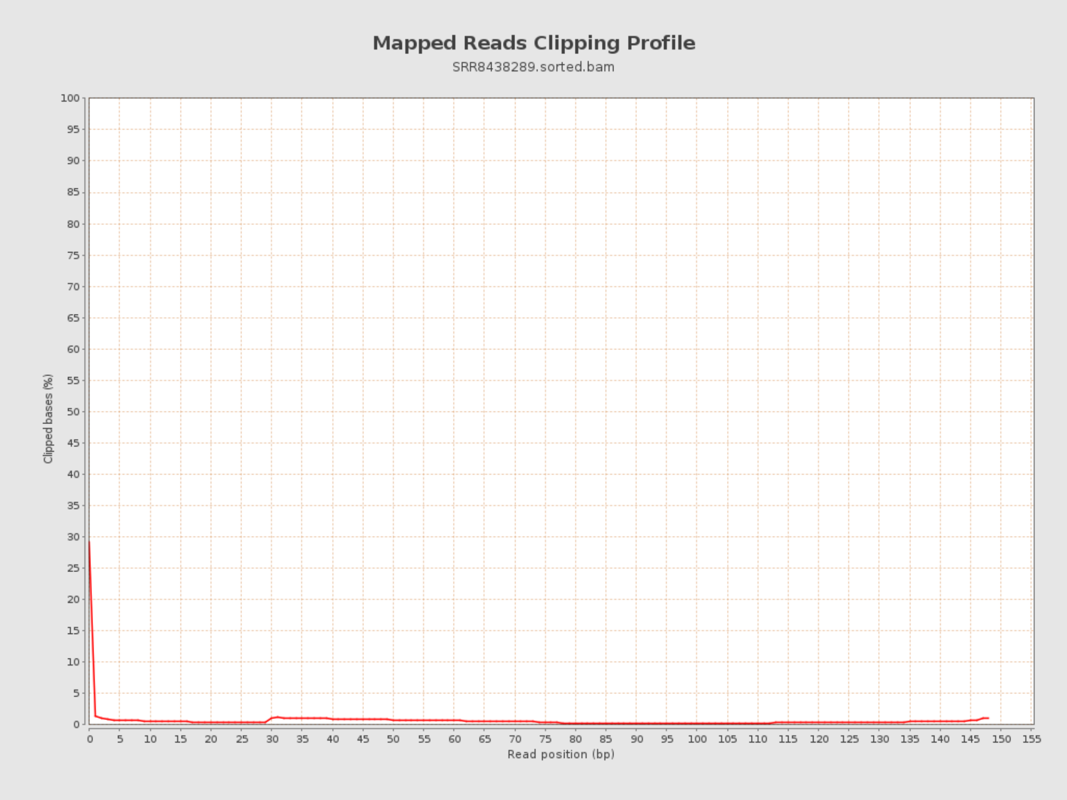
8. Results : Mapped Reads Nucleotide Content



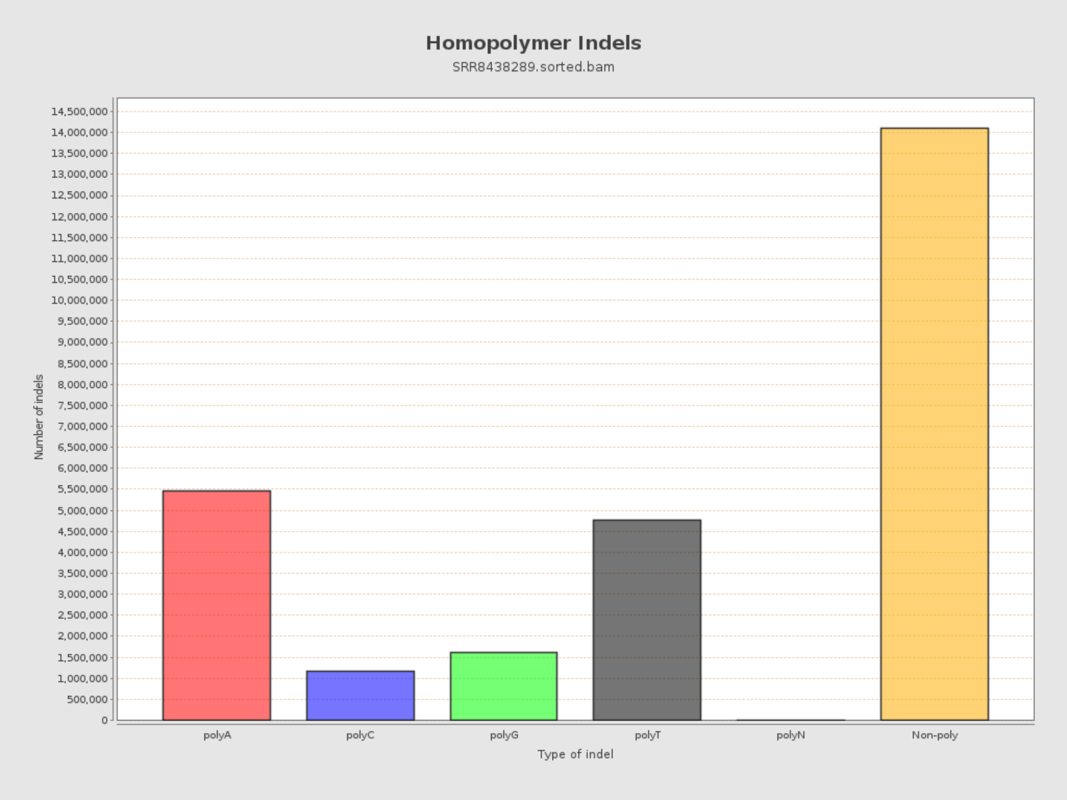
9. Results : Mapped Reads GC-content Distribution



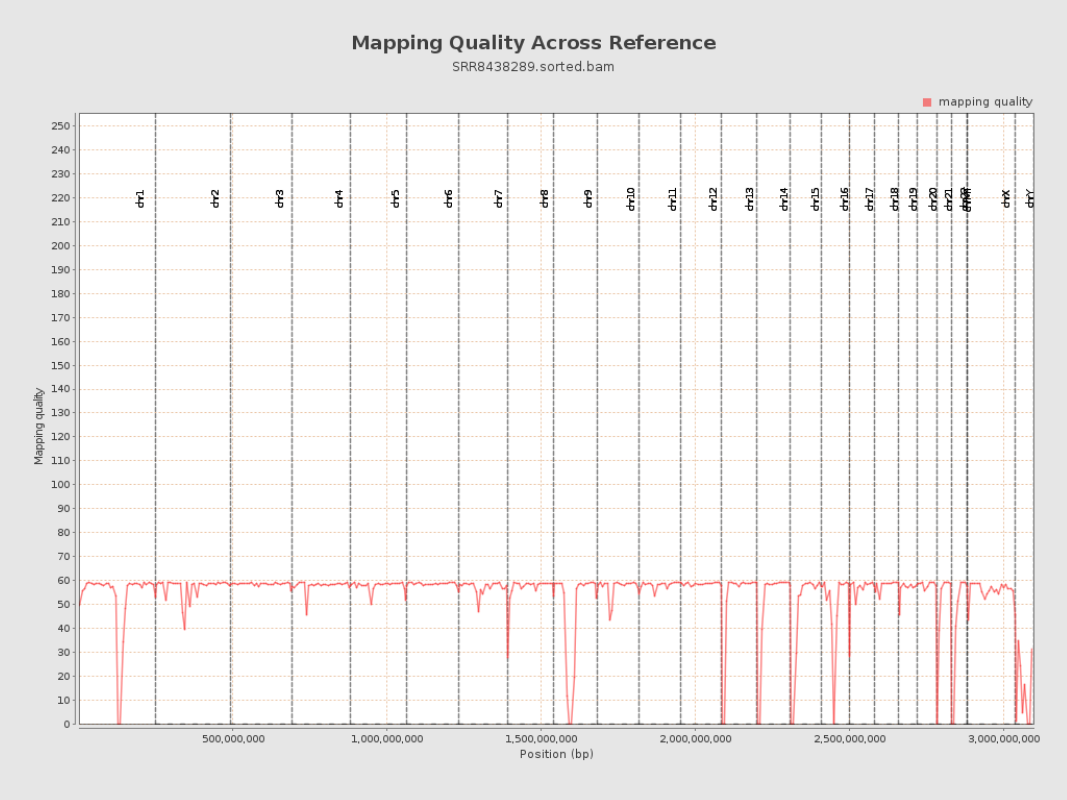
10. Results : Mapped Reads Clipping Profile



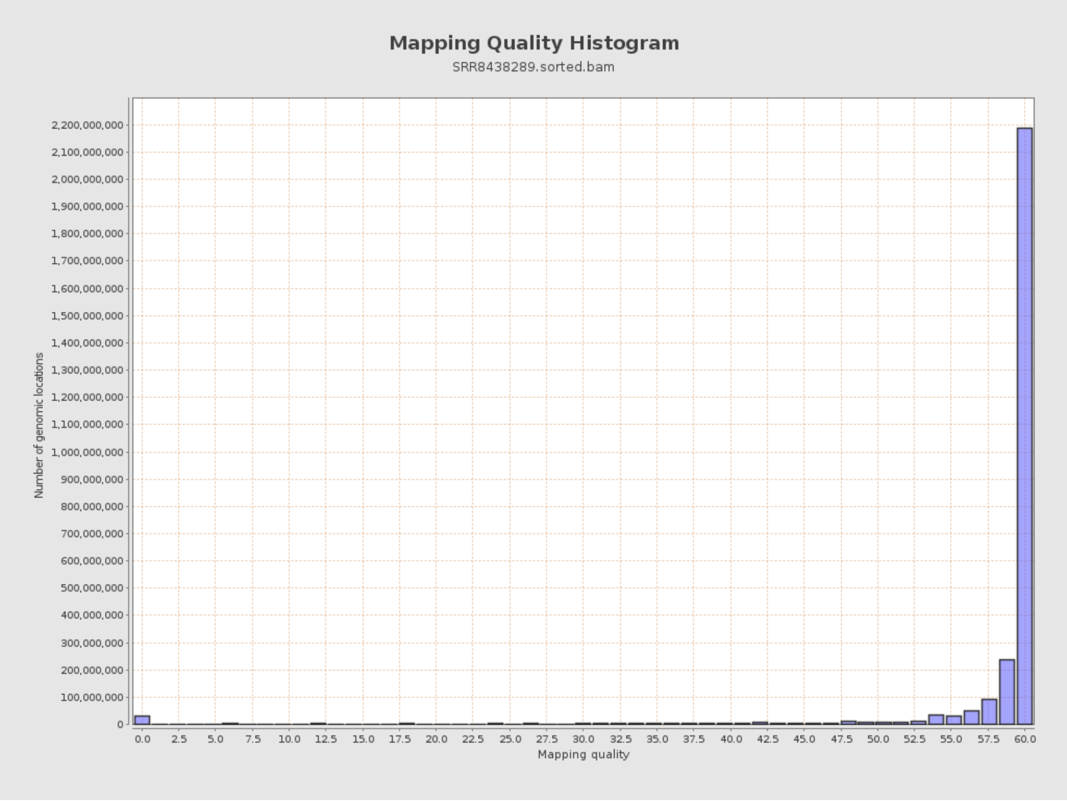
11. Results : Homopolymer Indels



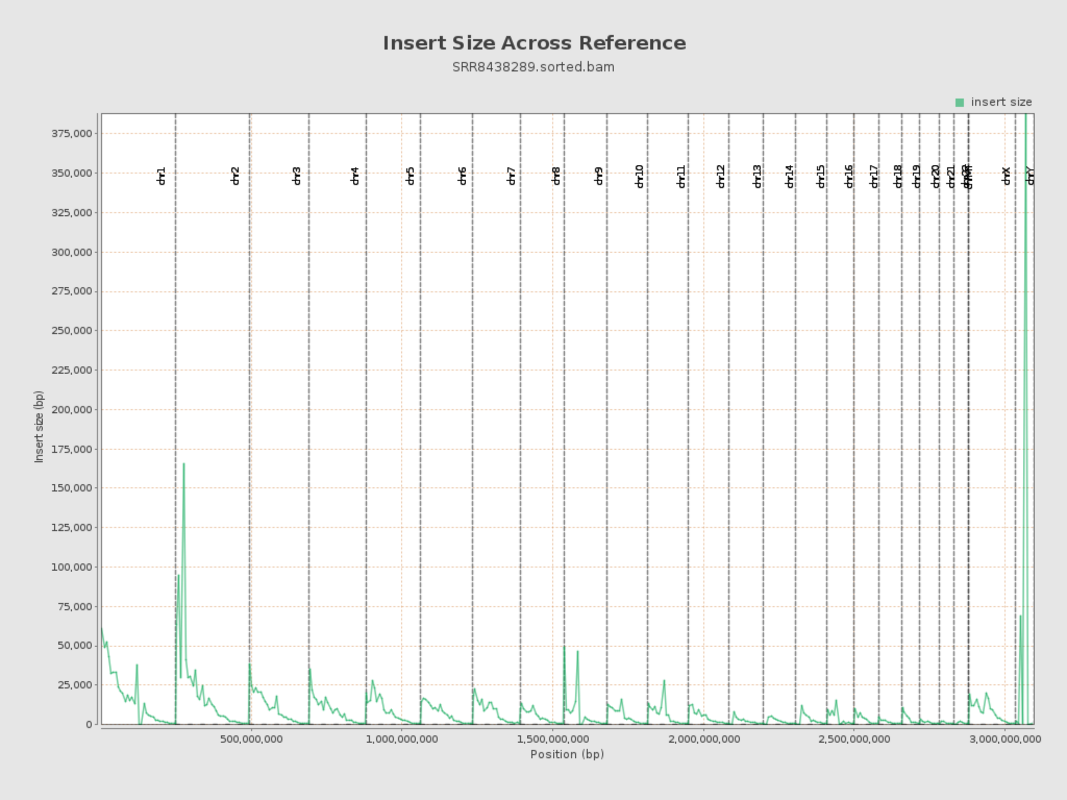
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram