Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 03:34:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438301.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_SRR8438301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438301_1.fastq.gz SRR8438301_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 03:34:51 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438301.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,417,839,826
Mapped reads	1,412,113,161 / 99.6%
Unmapped reads	5,726,665 / 0.4%
Mapped paired reads	1,412,113,161 / 99.6%
Mapped reads, first in pair	706,548,696 / 49.83%
Mapped reads, second in pair	705,564,465 / 49.76%
Mapped reads, both in pair	1,409,299,908 / 99.4%
Mapped reads, singletons	2,813,253 / 0.2%
Secondary alignments	0
Supplementary alignments	24,718,770 / 1.74%
Read min/max/mean length	30 / 149 / 113.55
Duplicated reads (estimated)	784,053,474 / 55.3%
Duplication rate	50.39%
Clipped reads	277,449,860 / 19.57%

2.2. ACGT Content

Number/percentage of A's	46,880,140,715 / 30.38%
Number/percentage of C's	30,543,250,937 / 19.79%
Number/percentage of T's	45,716,900,203 / 29.62%
Number/percentage of G's	31,197,187,801 / 20.21%
Number/percentage of N's	432,085 / 0%

GC Percentage	40%

2.3. Coverage

Mean	49.8672
Standard Deviation	565.4532

2.4. Mapping Quality

Mean Mapping Quality	52.68

2.5. Insert size

Mean	180,023.86
Standard Deviation	4,304,229.56
P25/Median/P75	75 / 120 / 195

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	512,875,408
Insertions	22,497,679
Mapped reads with at least one insertion	1.58%
Deletions	15,484,065
Mapped reads with at least one deletion	1.09%
Homopolymer indels	48.09%

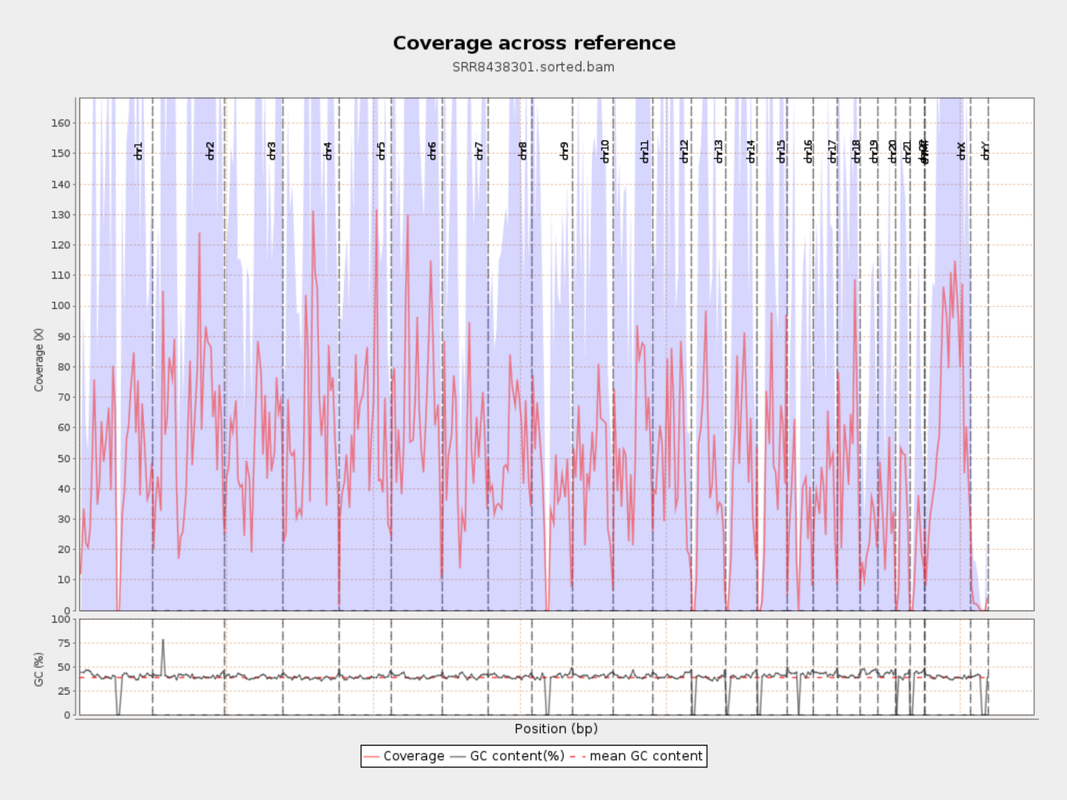
2.7. Chromosome stats

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

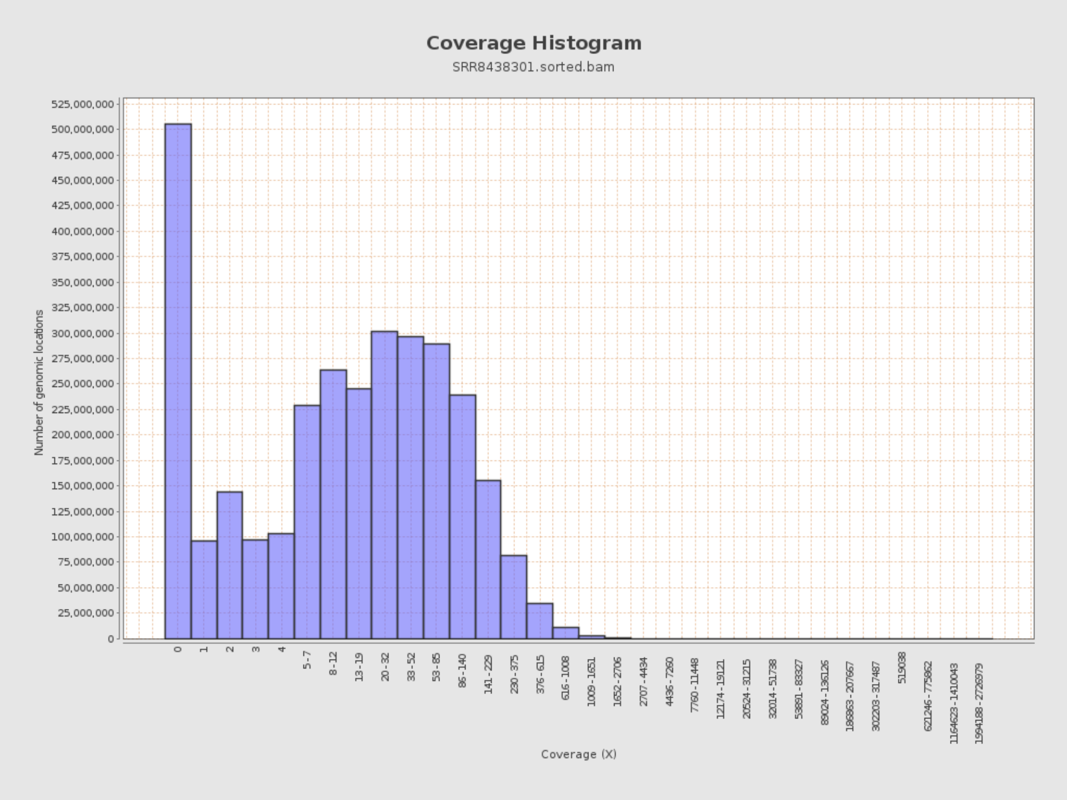
		bases	coverage	deviation
chr1	249250621	11681569307	46.8668	92.8689
chr2	243199373	15093778136	62.0634	1,990.9252
chr3	198022430	10706512673	54.0672	91.72
chr4	191154276	11972392758	62.6321	103.3967
chr5	180915260	10078276793	55.7072	98.0829
chr6	171115067	11865327074	69.3412	117.8802
chr7	159138663	8383876774	52.6828	95.4153
chr8	146364022	7530176688	51.4483	88.699
chr9	141213431	5322076003	37.6882	79.637
chr10	135534747	6563186432	48.4244	86.129
chr11	135006516	7561590581	56.0091	103.928
chr12	133851895	6710995927	50.1375	105.8092
chr13	115169878	4808962826	41.7554	85.9392
chr14	107349540	4943916104	46.0544	94.3983
chr15	102531392	4480558306	43.6994	96.878
chr16	90354753	2548146933	28.2016	64.7332
chr17	81195210	3124474144	38.481	77.3657
chr18	78077248	4489239384	57.4974	92.3548
chr19	59128983	1331217224	22.5138	52.6308
chr20	63025520	2042283379	32.4041	64.9461
chr21	48129895	1514013918	31.4568	74.744
chr22	51304566	831533586	16.2078	47.741
chrMT	16571	448326	27.0549	20.8919
chrX	155270560	10666421335	68.6957	131.5383

chrY	59373566	122702100	2.0666	13.5321

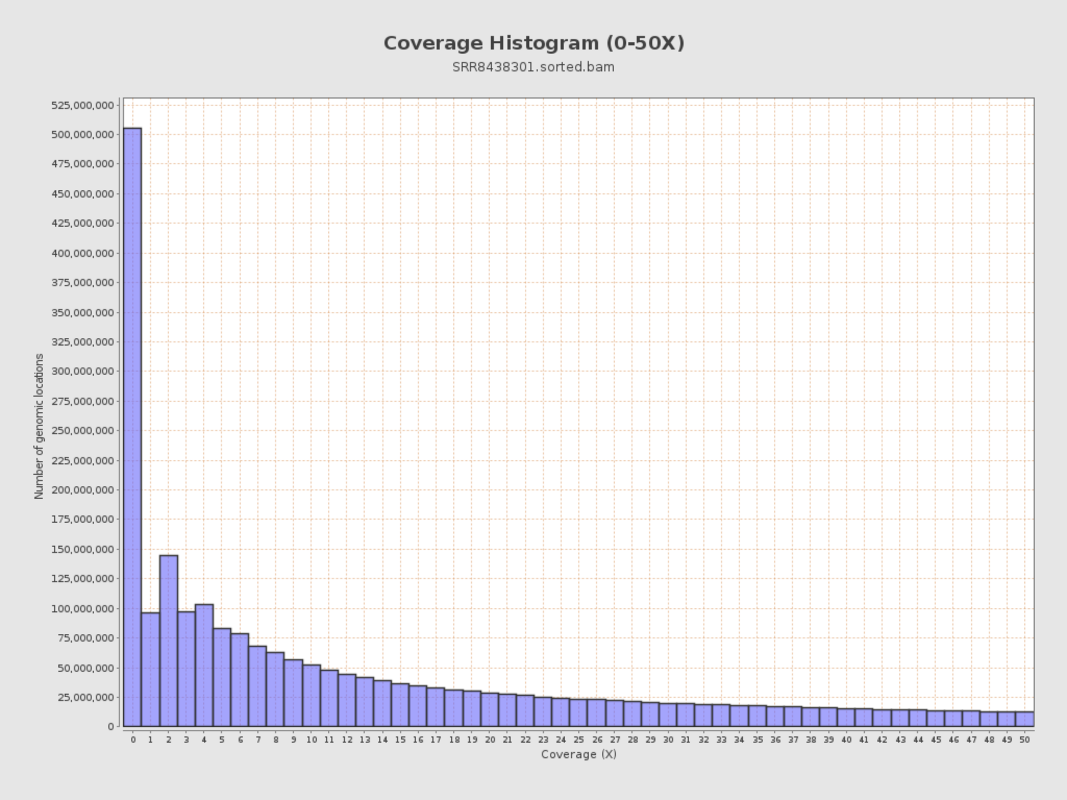
3. Results : Coverage across reference



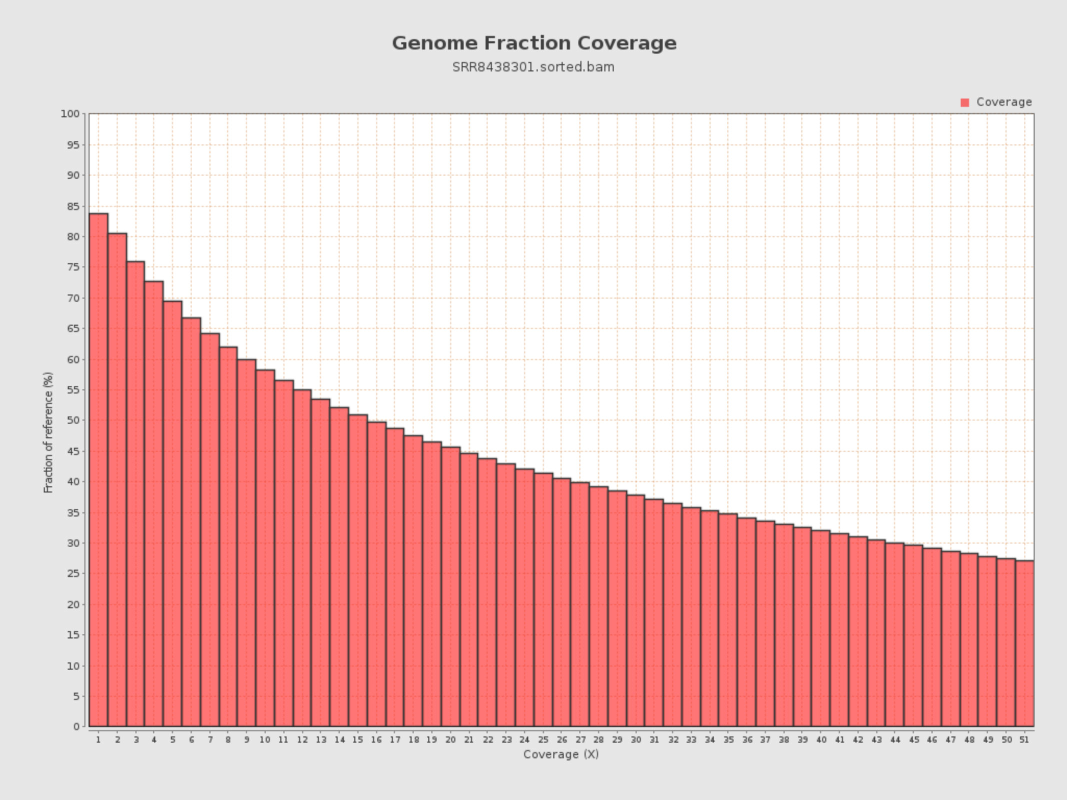
4. Results : Coverage Histogram



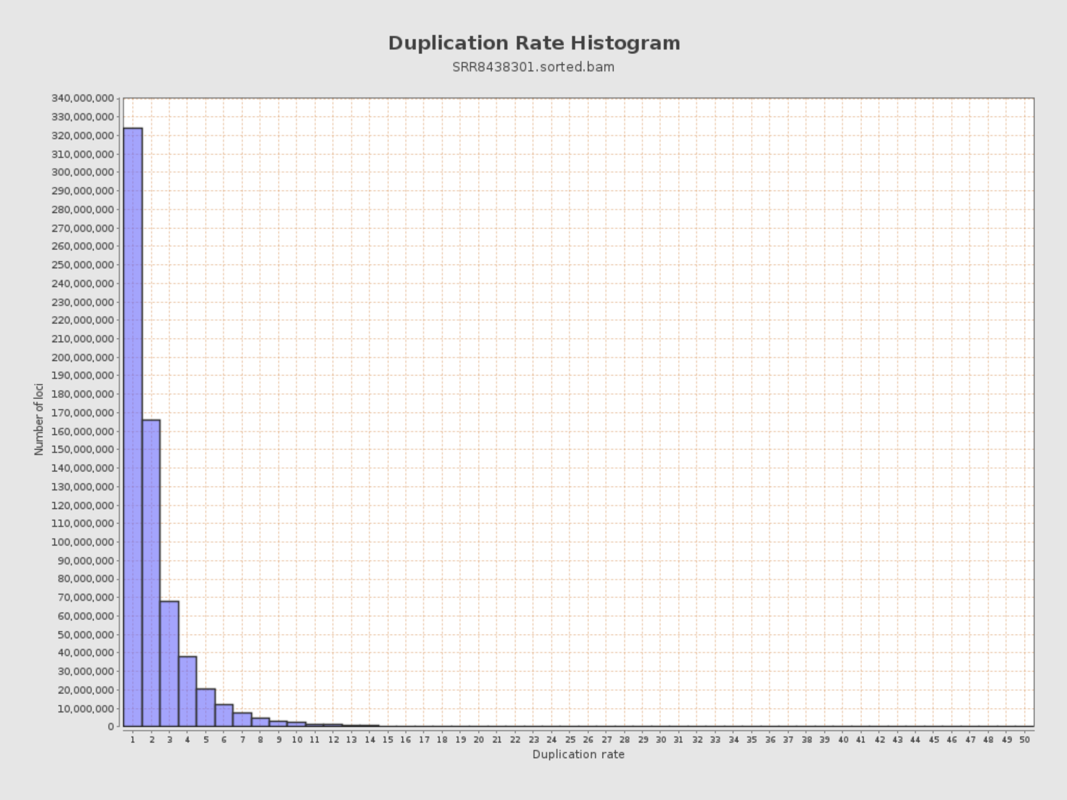
5. Results : Coverage Histogram (0-50X)



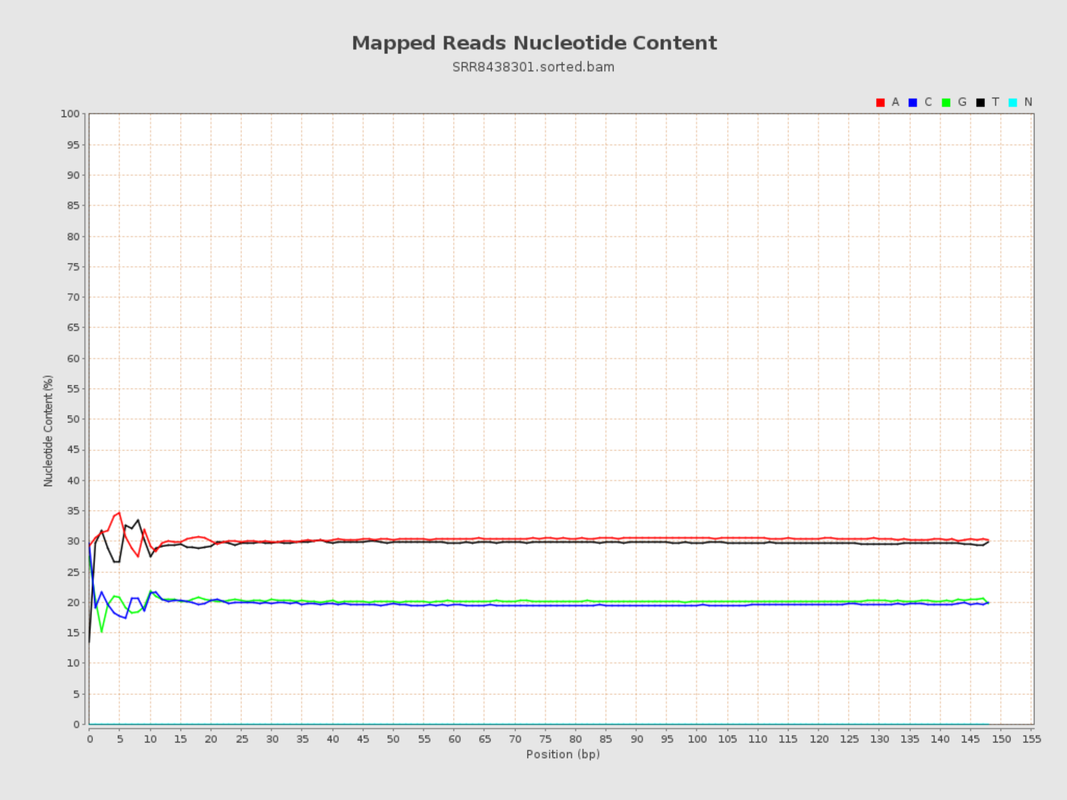
6. Results : Genome Fraction Coverage



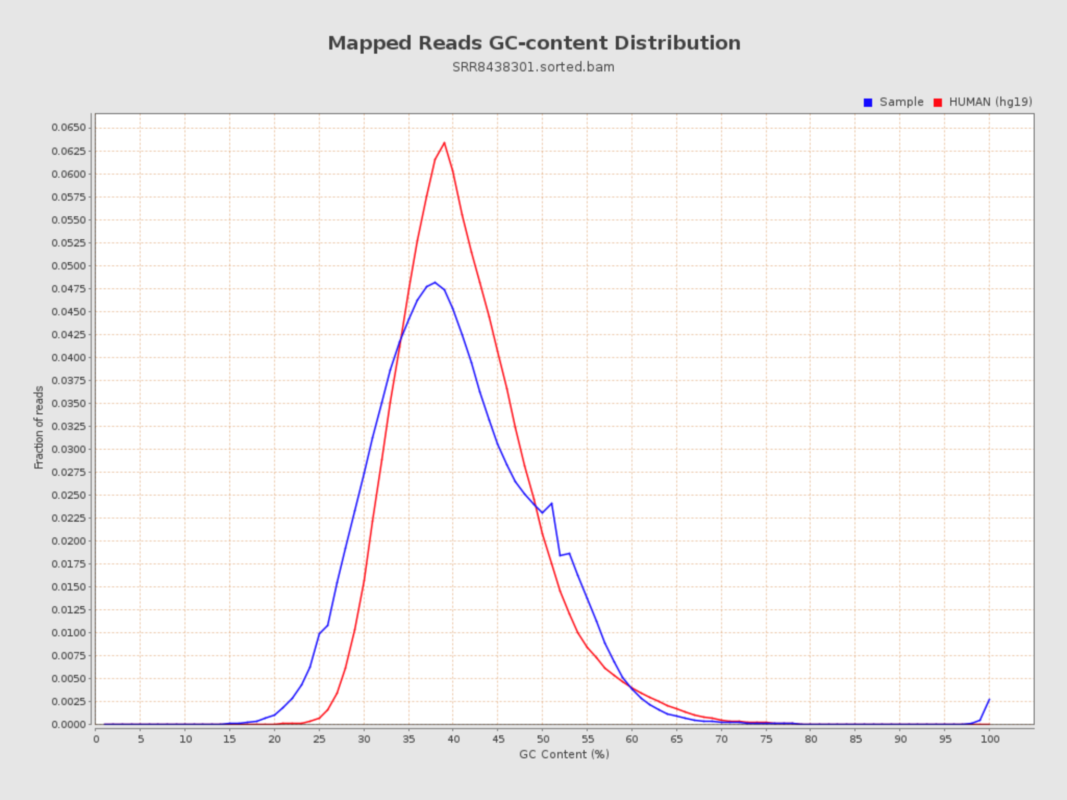
7. Results : Duplication Rate Histogram



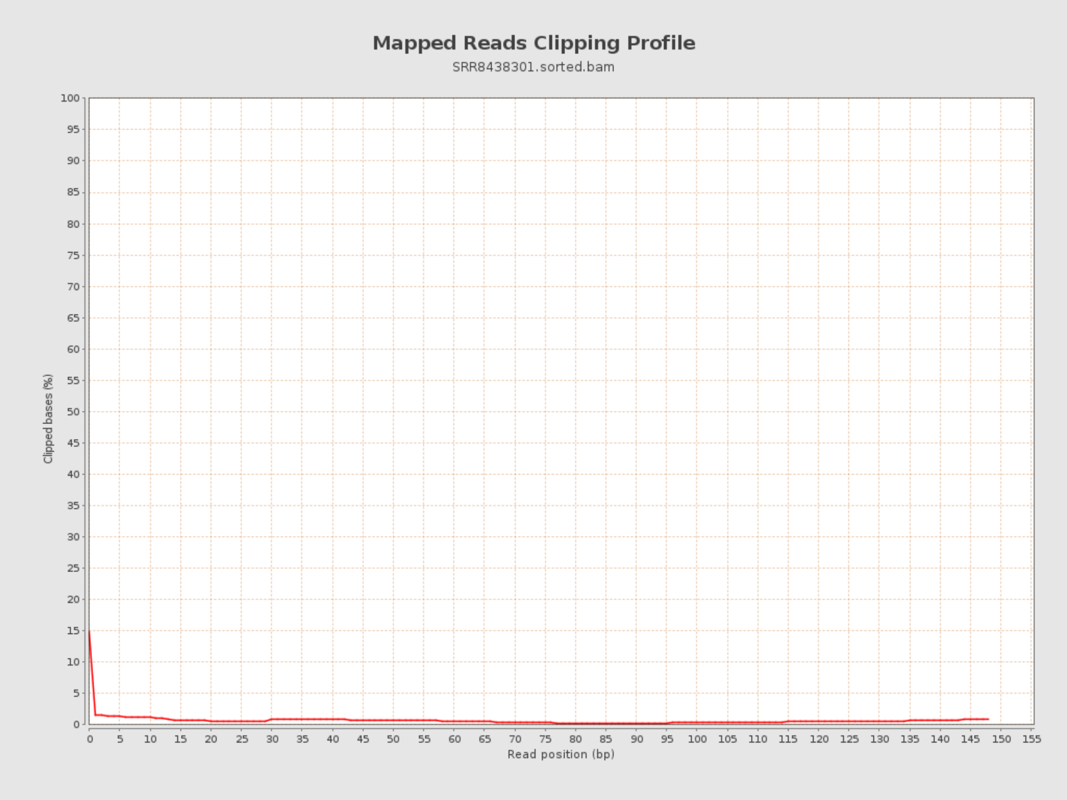
8. Results : Mapped Reads Nucleotide Content



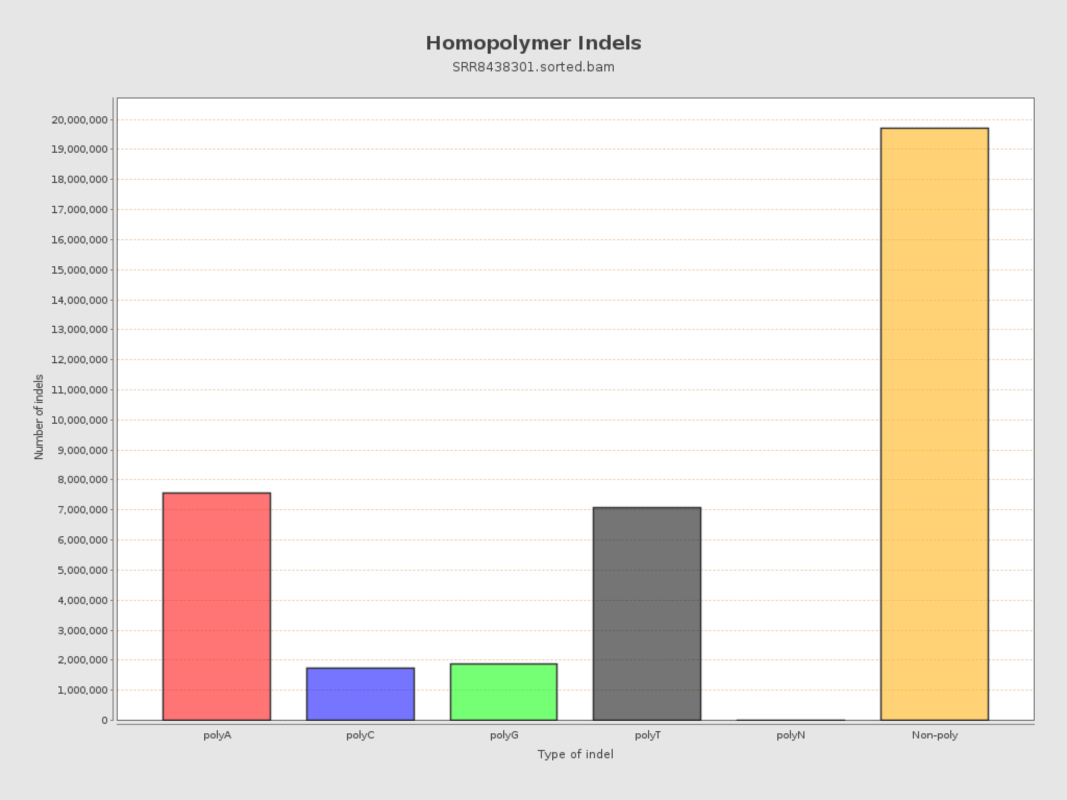
9. Results : Mapped Reads GC-content Distribution



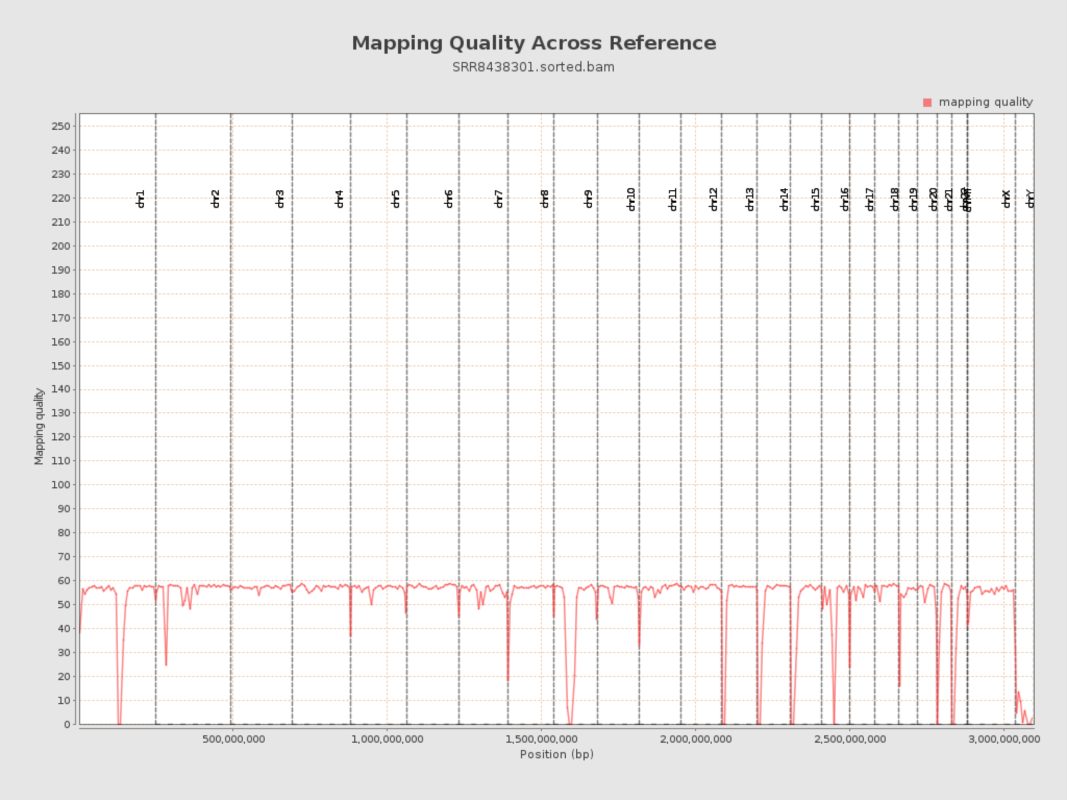
10. Results : Mapped Reads Clipping Profile



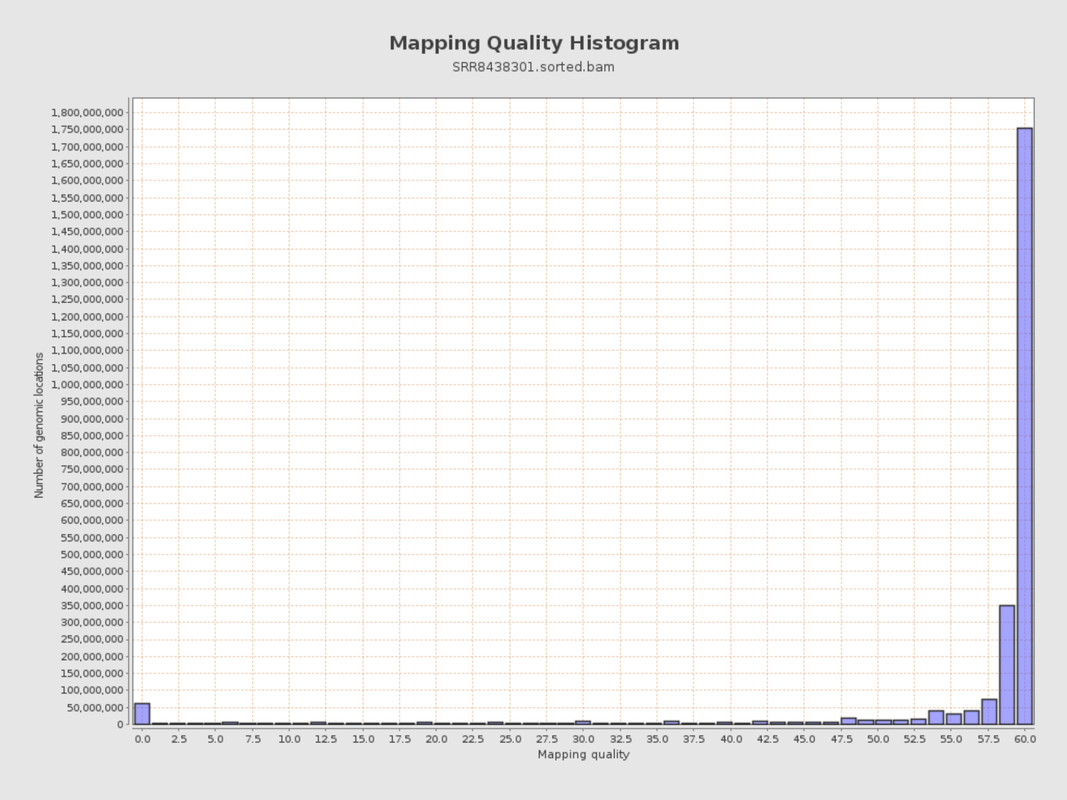
11. Results : Homopolymer Indels



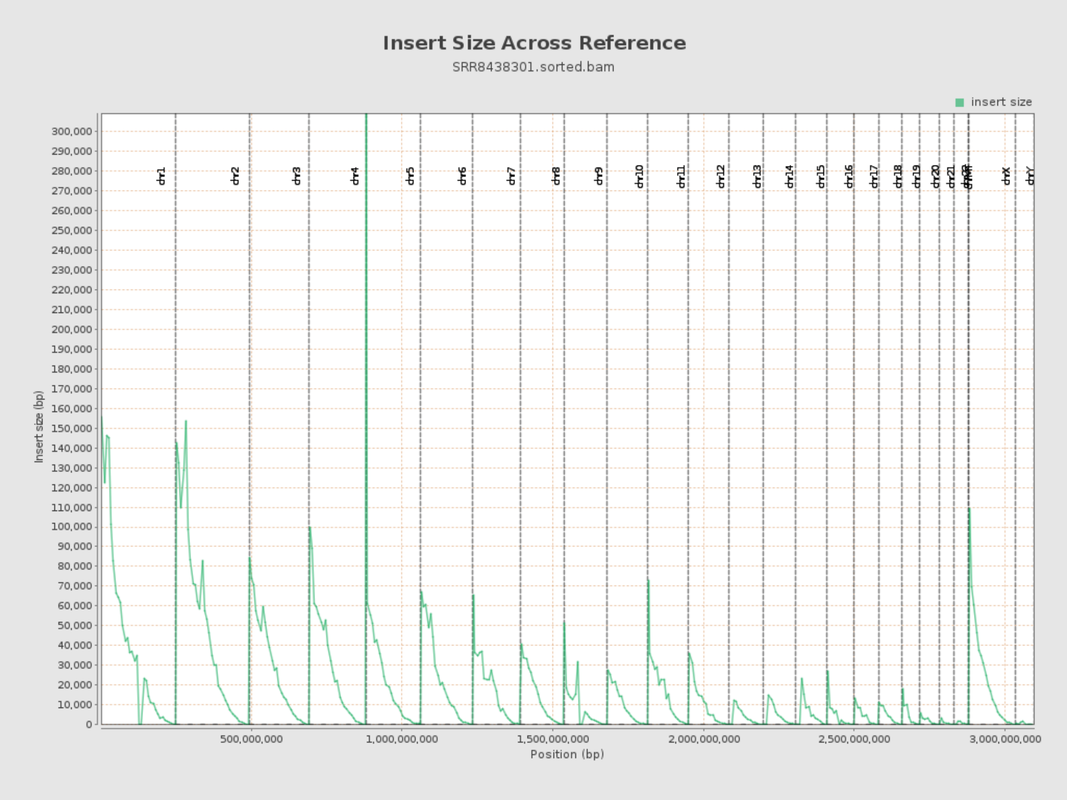
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram