

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 00:23:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438253.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_SRR8438253 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438253_1.fastq.gz SRR8438253_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 00:23:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,330,220,306
Mapped reads	1,325,160,856 / 99.62%
Unmapped reads	5,059,450 / 0.38%
Mapped paired reads	1,325,160,856 / 99.62%
Mapped reads, first in pair	662,897,664 / 49.83%
Mapped reads, second in pair	662,263,192 / 49.79%
Mapped reads, both in pair	1,322,809,830 / 99.44%
Mapped reads, singletons	2,351,026 / 0.18%
Secondary alignments	0
Supplementary alignments	17,074,614 / 1.28%
Read min/max/mean length	30 / 149 / 115.22
Duplicated reads (estimated)	840,936,444 / 63.22%
Duplication rate	54.99%
Clipped reads	247,140,395 / 18.58%

2.2. ACGT Content

Number/percentage of A's	45,079,732,827 / 30.58%
Number/percentage of C's	28,921,757,517 / 19.62%
Number/percentage of T's	44,064,573,318 / 29.89%
Number/percentage of G's	29,346,120,985 / 19.91%
Number/percentage of N's	406,455 / 0%

GC Percentage	39.53%
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2.3. Coverage

Mean	47.6296
Standard Deviation	511.8684

2.4. Mapping Quality

Mean Mapping Quality	52.41
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2.5. Insert size

Mean	86,274.64
Standard Deviation	2,908,220.33
P25/Median/P75	78 / 128 / 209

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	473,201,899
Insertions	21,925,262
Mapped reads with at least one insertion	1.64%
Deletions	14,864,600
Mapped reads with at least one deletion	1.11%
Homopolymer indels	48.28%

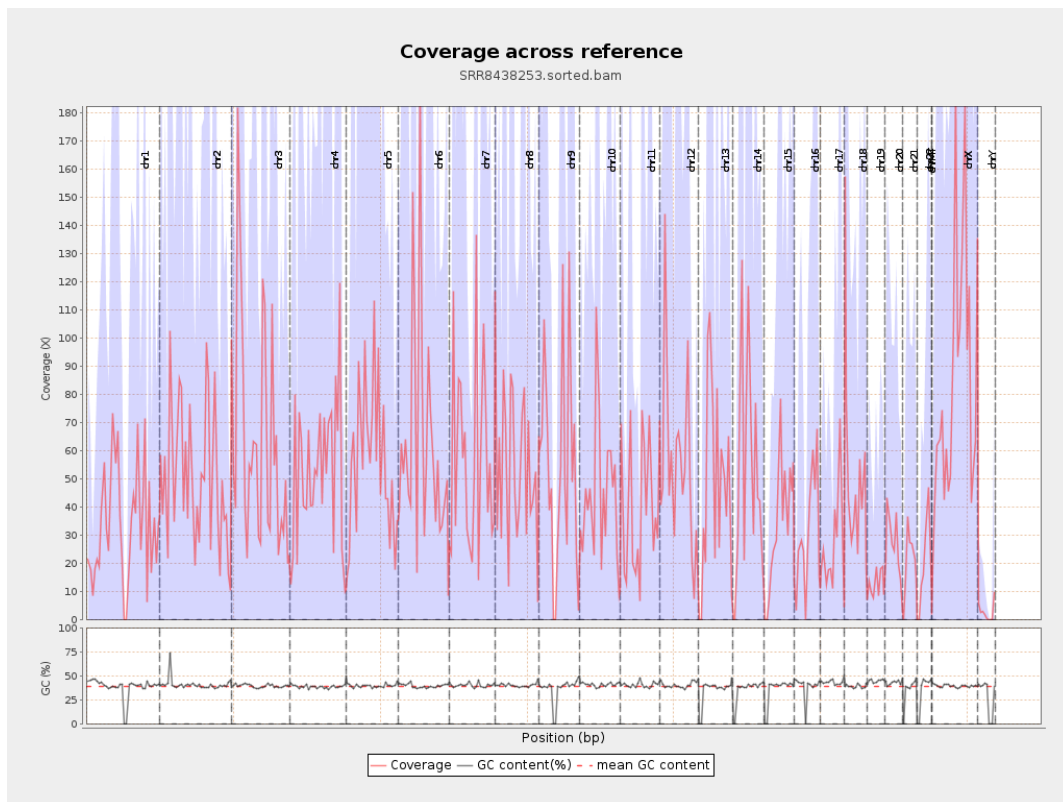
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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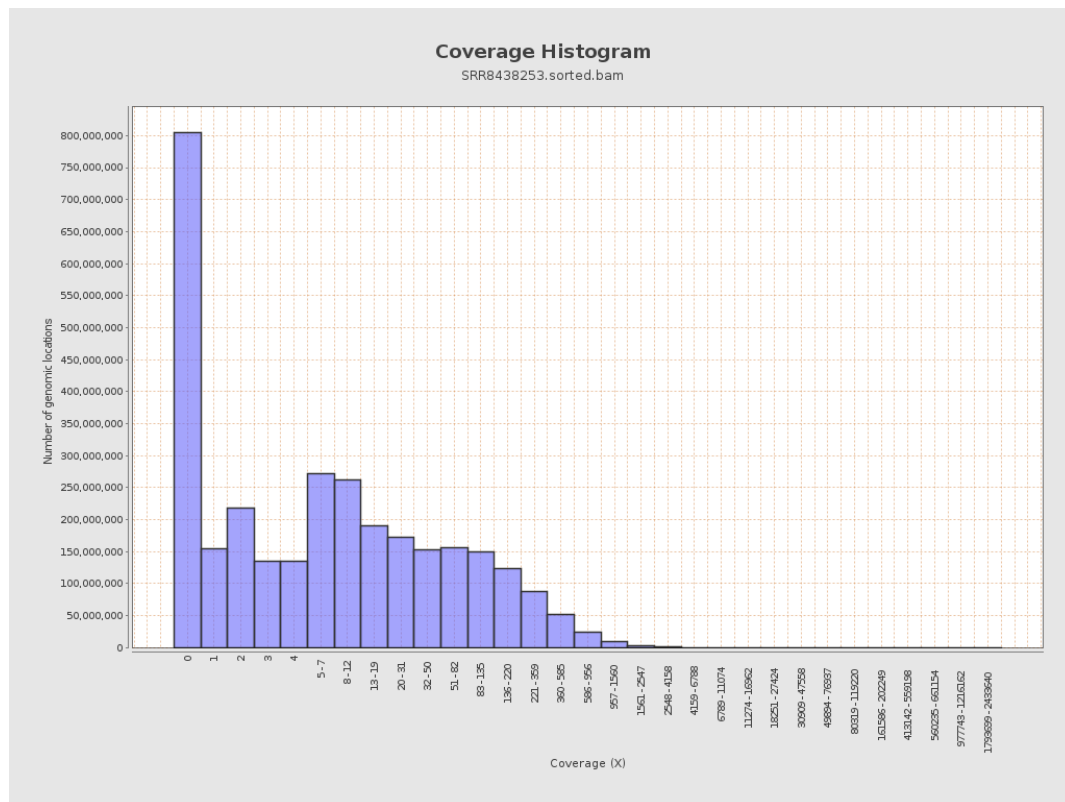
		bases	coverage	deviation
chr1	249250621	8307733518	33.3308	96.1261
chr2	243199373	12266586150	50.4384	1,766.5168
chr3	198022430	12320381011	62.2171	156.9792
chr4	191154276	10157020189	53.1352	133.0699
chr5	180915260	10182114000	56.2811	142.3239
chr6	171115067	10816584450	63.2123	164.2096
chr7	159138663	8964299808	56.3301	139.225
chr8	146364022	7566718420	51.6979	144.7266
chr9	141213431	7398459572	52.392	156.5745
chr10	135534747	5966949696	44.0252	117.7751
chr11	135006516	5258518657	38.9501	115.6428
chr12	133851895	7346329411	54.884	150.9391
chr13	115169878	5534117230	48.0518	132.2564
chr14	107349540	5633492938	52.478	144.6925
chr15	102531392	3477906474	33.9204	108.065
chr16	90354753	2678035898	29.6391	99.2919
chr17	81195210	2167268153	26.6921	81.7726
chr18	78077248	3783796431	48.4622	124.554
chr19	59128983	772322196	13.0617	53.5826
chr20	63025520	1678528343	26.6325	76.8013
chr21	48129895	1055139594	21.9227	77.8522
chr22	51304566	999607448	19.4838	81.0415
chrMT	16571	31167	1.8808	4.5341
chrX	155270560	12954875131	83.4342	210.7708

chrY	59373566	159993470	2.6947	26.576
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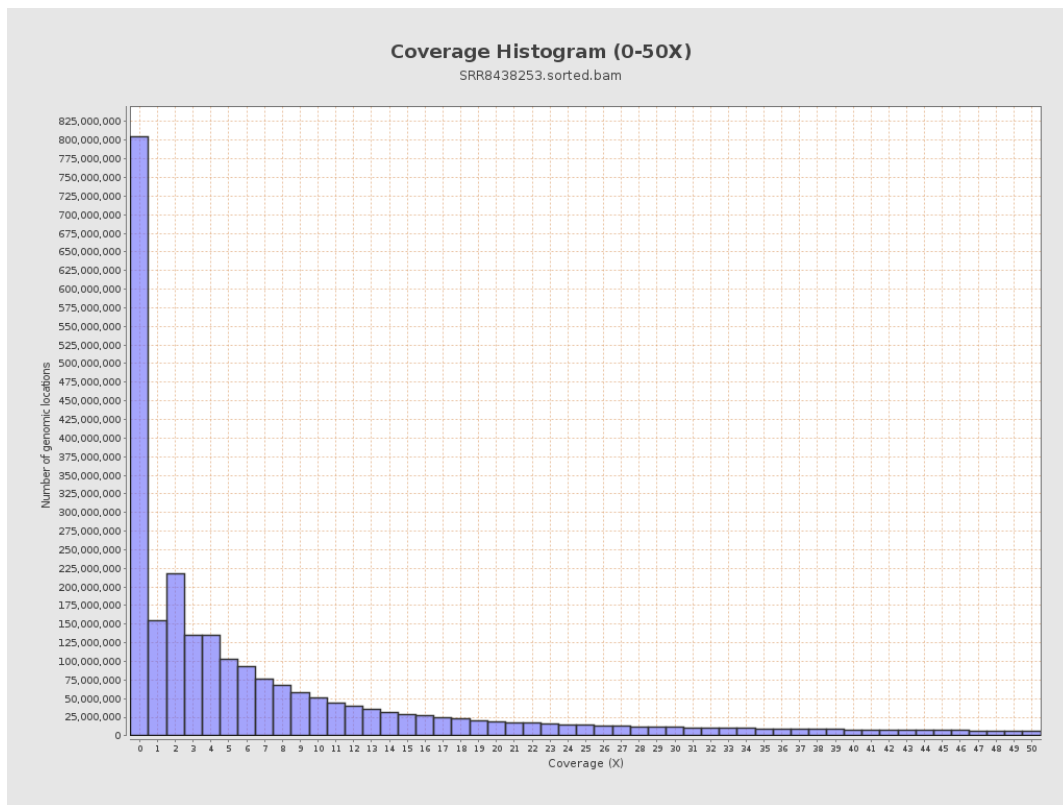
3. Results : Coverage across reference



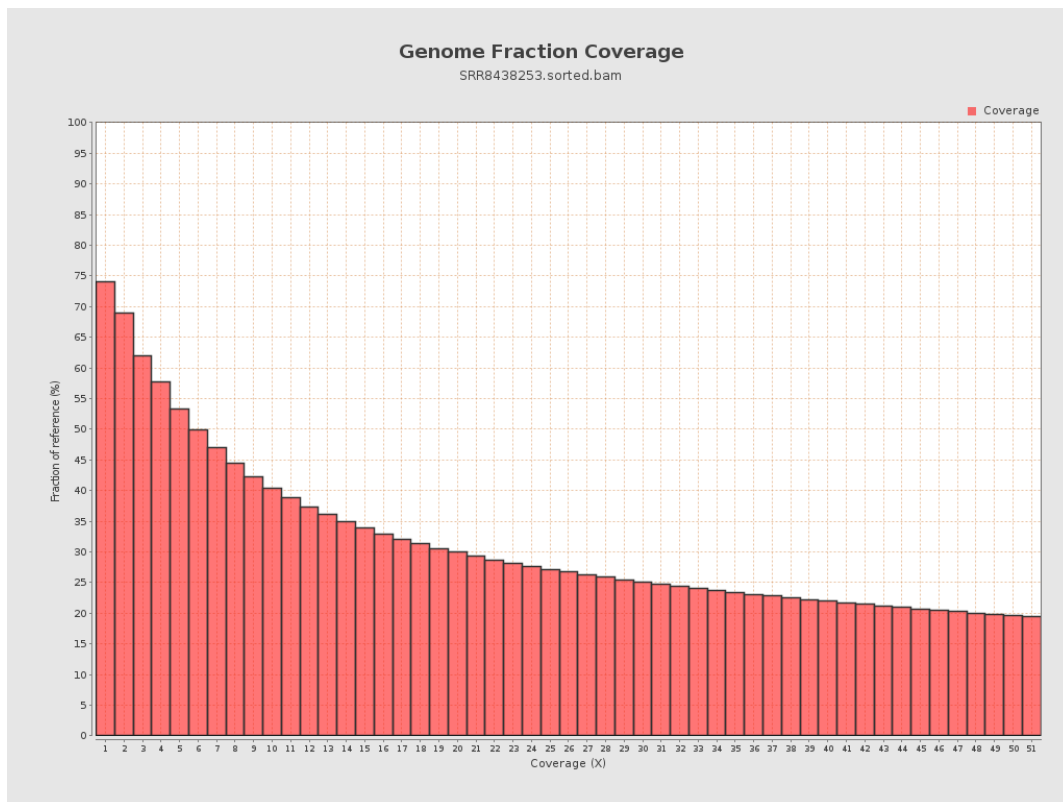
4. Results : Coverage Histogram



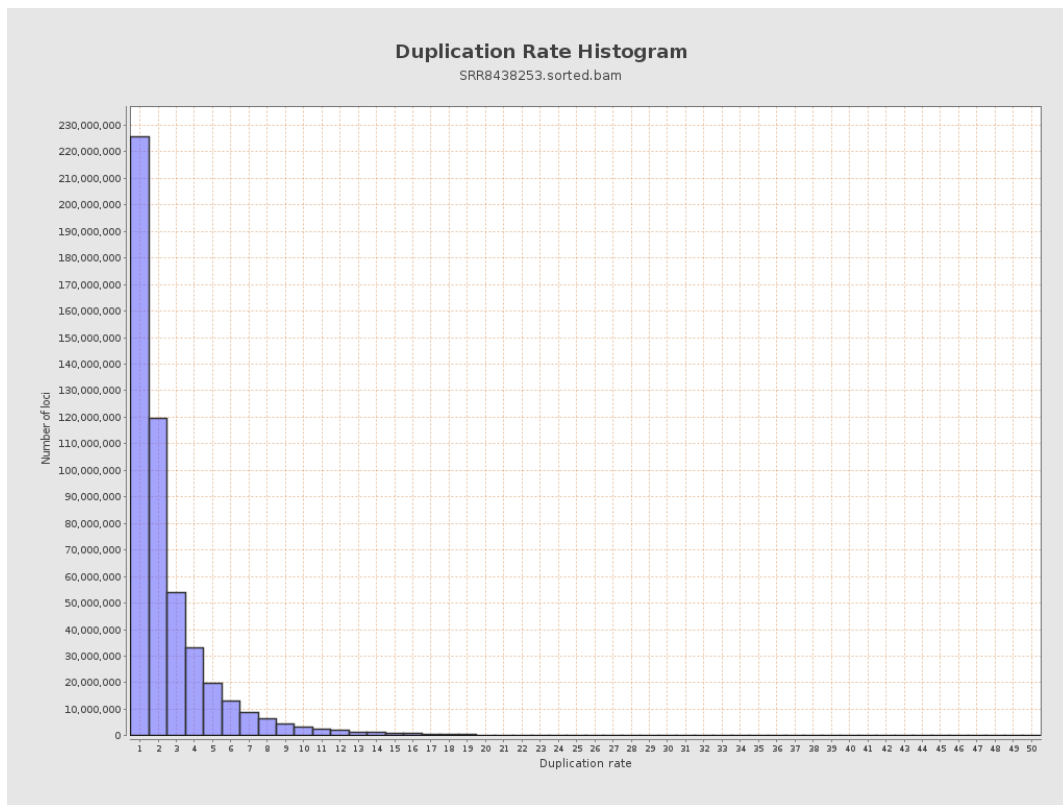
5. Results : Coverage Histogram (0-50X)



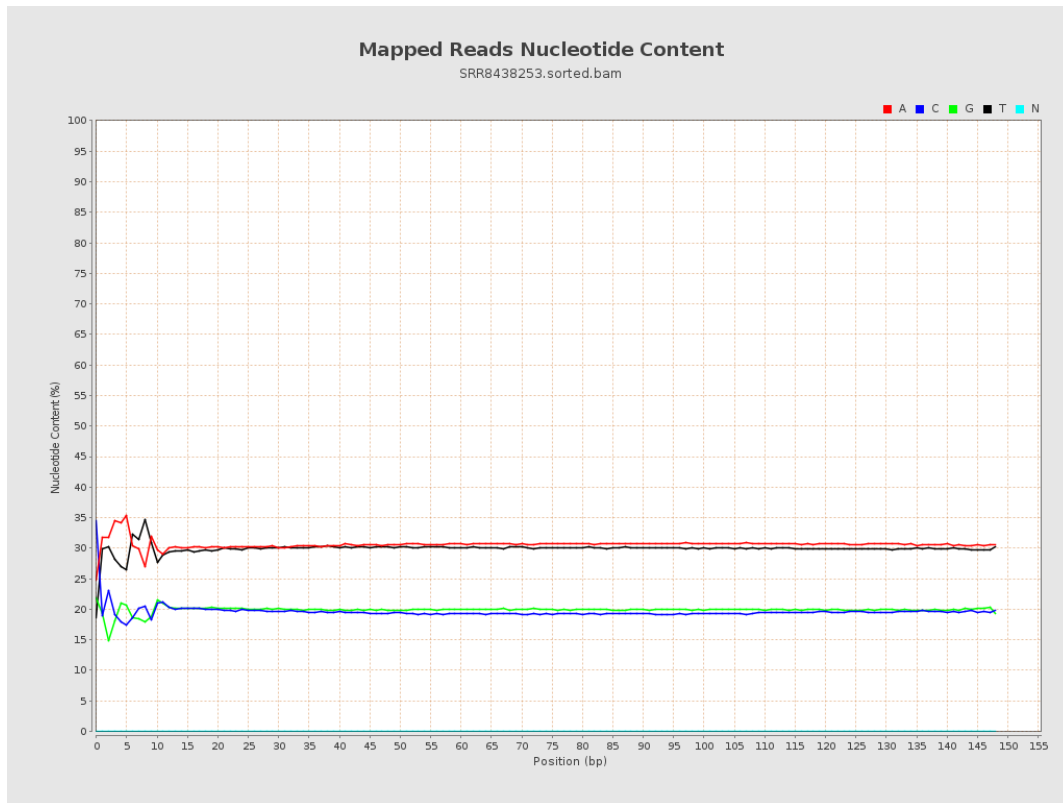
6. Results : Genome Fraction Coverage



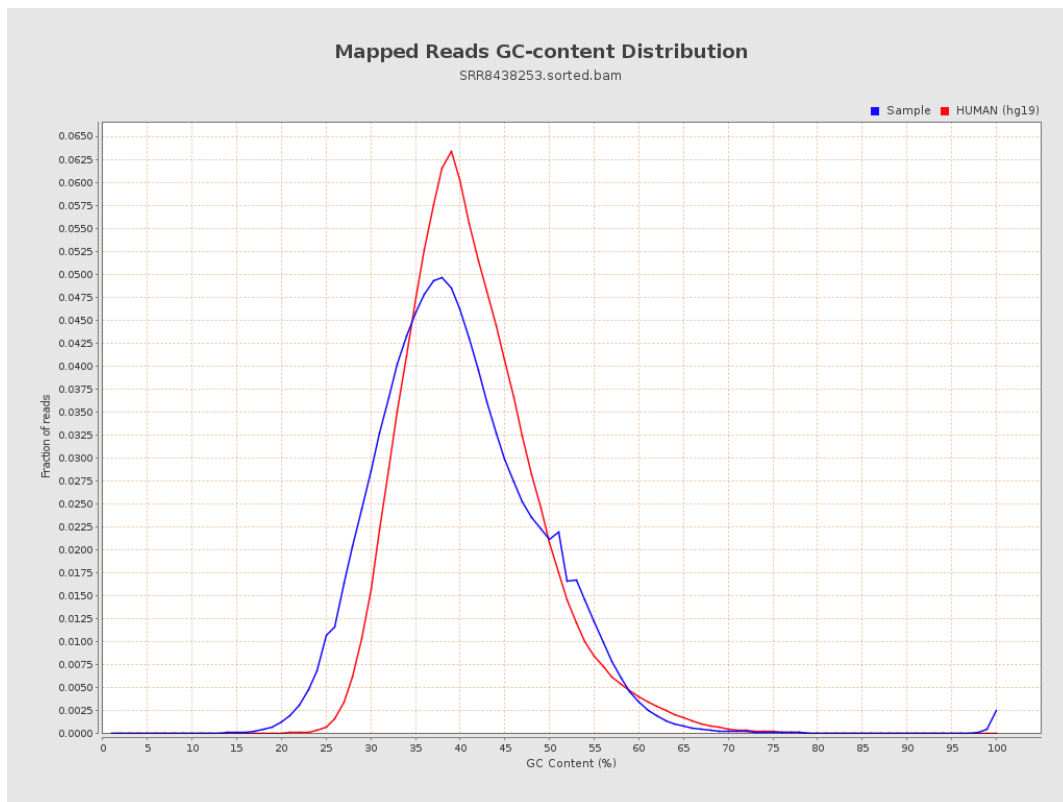
7. Results : Duplication Rate Histogram



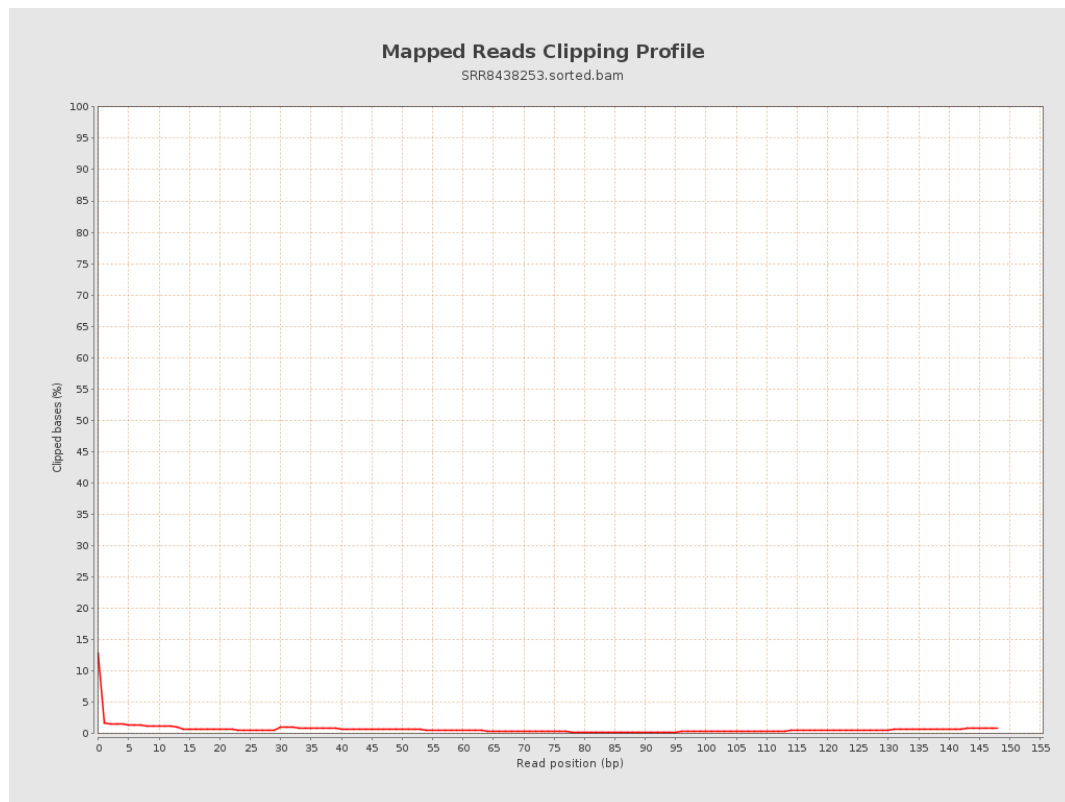
8. Results : Mapped Reads Nucleotide Content



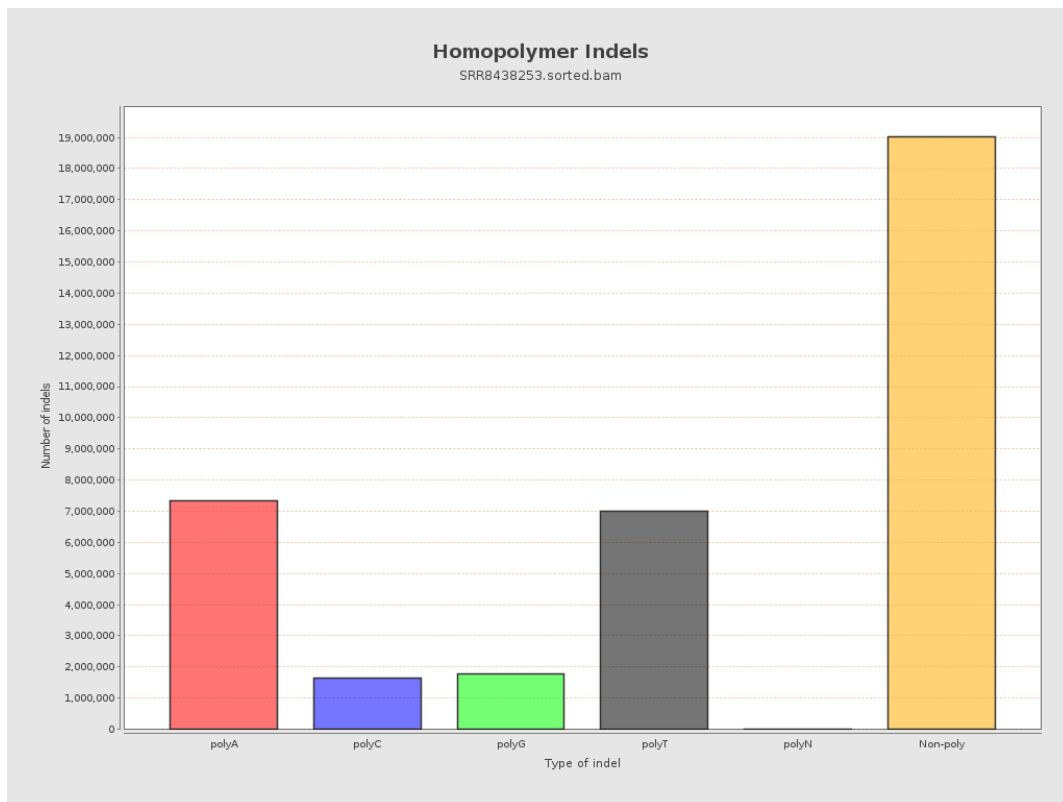
9. Results : Mapped Reads GC-content Distribution



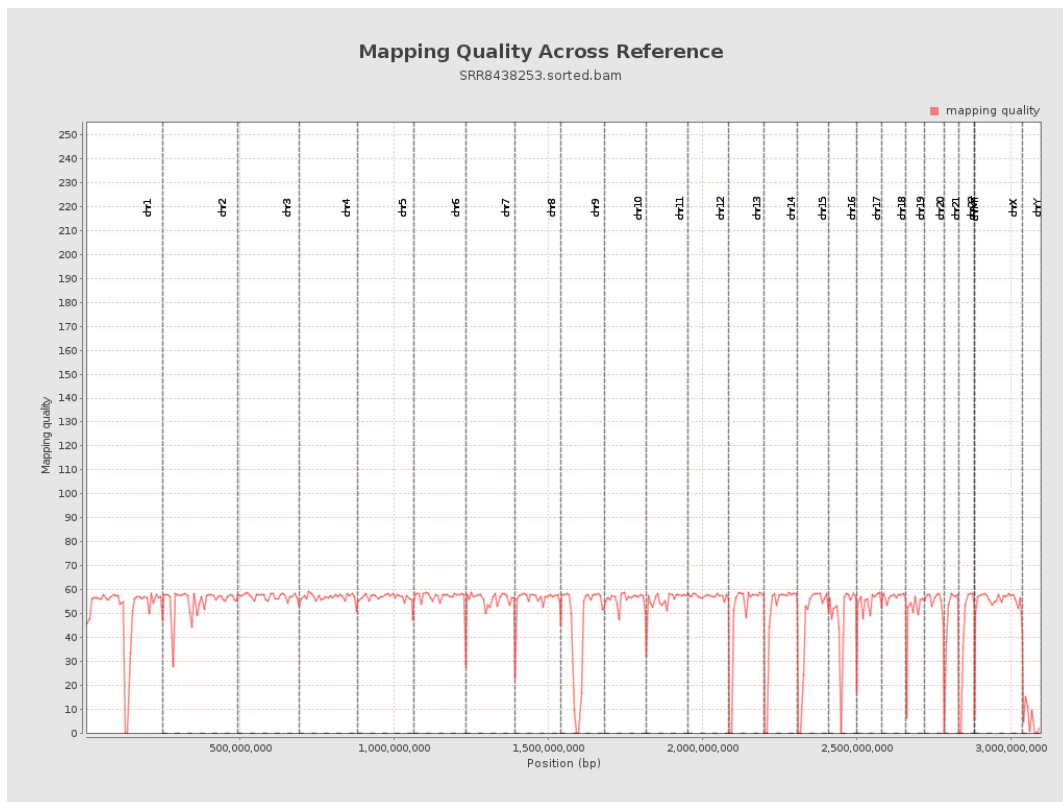
10. Results : Mapped Reads Clipping Profile



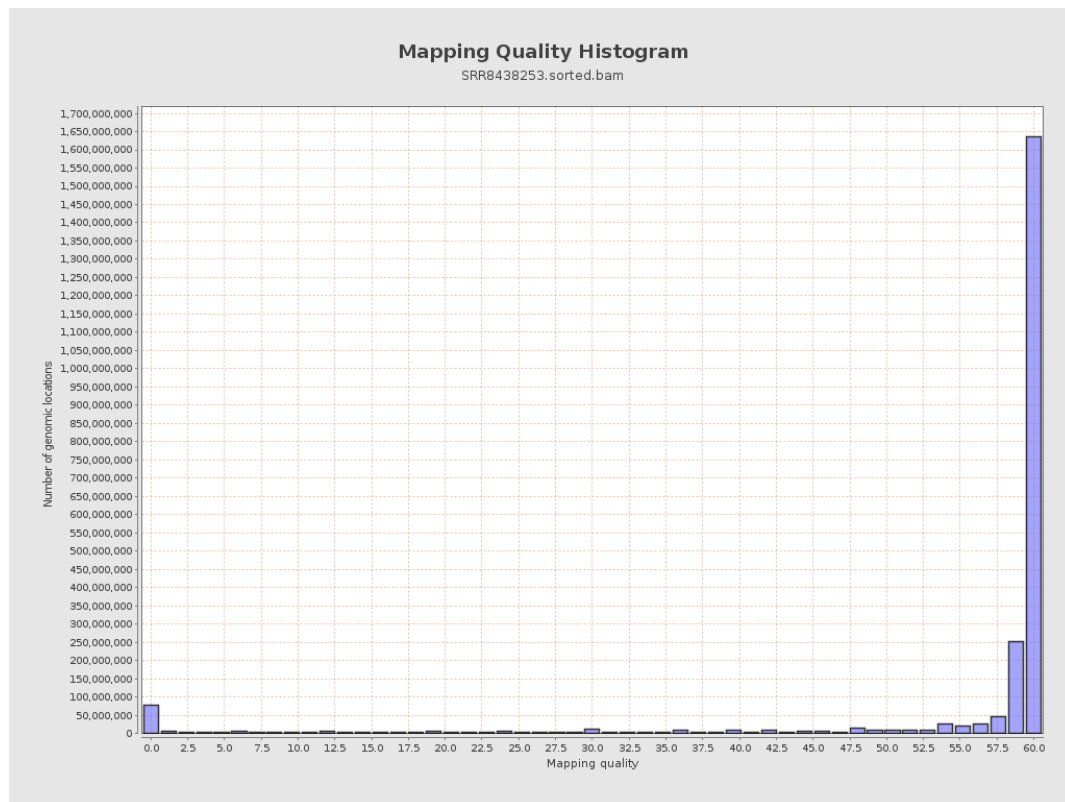
11. Results : Homopolymer Indels



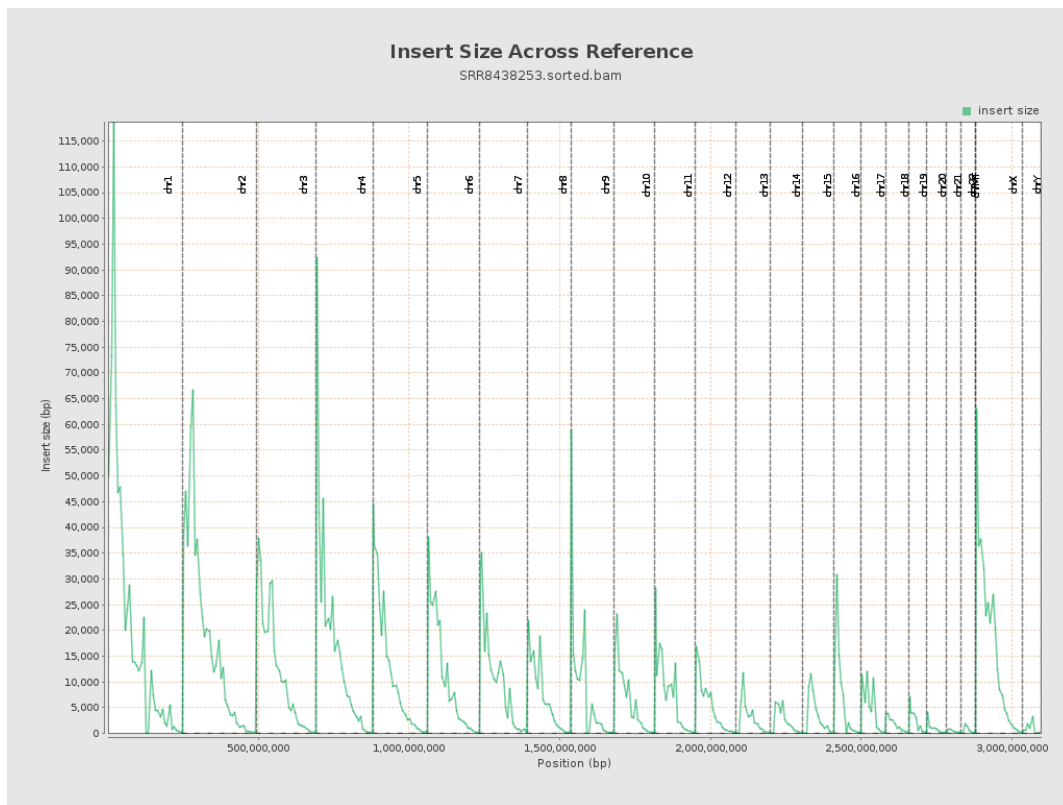
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

