

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/27 22:33:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438287.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_SRR8438287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438287_1.fastq.gz SRR8438287_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 27 22:33:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438287.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	641,799,970
Mapped reads	639,680,223 / 99.67%
Unmapped reads	2,119,747 / 0.33%
Mapped paired reads	639,680,223 / 99.67%
Mapped reads, first in pair	320,051,743 / 49.87%
Mapped reads, second in pair	319,628,480 / 49.8%
Mapped reads, both in pair	638,144,158 / 99.43%
Mapped reads, singletons	1,536,065 / 0.24%
Secondary alignments	0
Supplementary alignments	10,946,375 / 1.71%
Read min/max/mean length	28 / 151 / 145.82
Duplicated reads (estimated)	275,116,471 / 42.87%
Duplication rate	40.63%
Clipped reads	114,875,123 / 17.9%

2.2. ACGT Content

Number/percentage of A's	28,004,404,746 / 30.29%
Number/percentage of C's	18,429,285,440 / 19.94%
Number/percentage of T's	26,660,608,658 / 28.84%
Number/percentage of G's	19,350,331,906 / 20.93%
Number/percentage of N's	691,489 / 0%

GC Percentage	40.87%
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2.3. Coverage

Mean	29.8712
Standard Deviation	75.4997

2.4. Mapping Quality

Mean Mapping Quality	55.02
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2.5. Insert size

Mean	42,647.35
Standard Deviation	2,011,314.54
P25/Median/P75	198 / 259 / 359

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	472,355,783
Insertions	11,876,525
Mapped reads with at least one insertion	1.83%
Deletions	10,610,696
Mapped reads with at least one deletion	1.63%
Homopolymer indels	48.55%

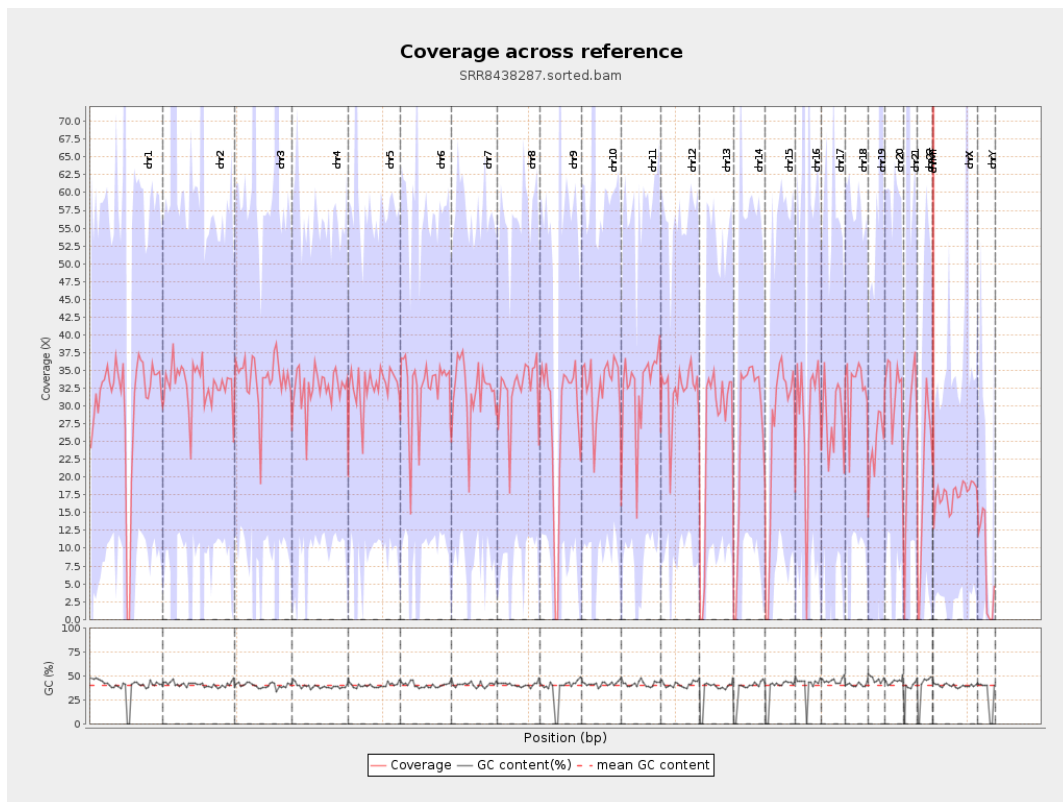
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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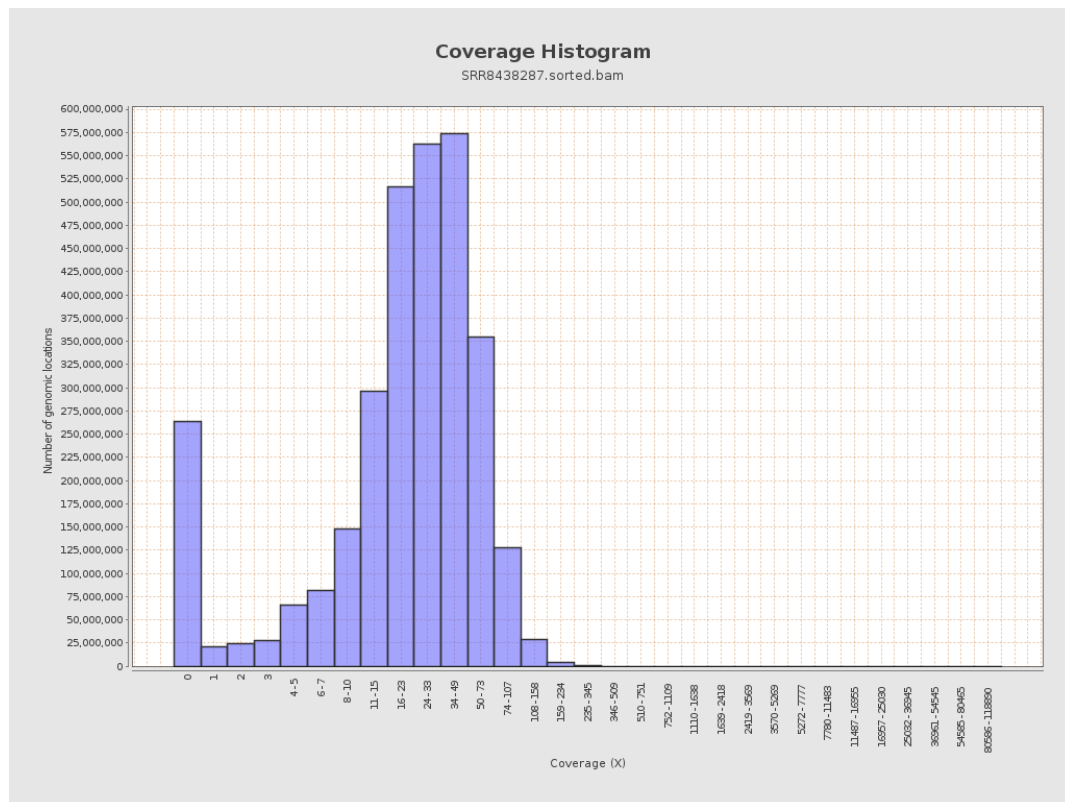
		bases	coverage	deviation
chr1	249250621	7597724332	30.4823	28.9912
chr2	243199373	8031816740	33.0256	112.3546
chr3	198022430	6685349150	33.7606	130.7482
chr4	191154276	6239930135	32.6434	23.7362
chr5	180915260	5915207686	32.696	25.9361
chr6	171115067	5603417133	32.7465	25.332
chr7	159138663	5106331162	32.0873	25.1167
chr8	146364022	4712024258	32.1939	24.2439
chr9	141213431	3957282520	28.0234	30.7298
chr10	135534747	4481017440	33.0618	37.3414
chr11	135006516	4427529040	32.7949	24.9024
chr12	133851895	4320836923	32.2807	23.6866
chr13	115169878	3043391285	26.4252	23.1992
chr14	107349540	2966702141	27.6359	27.5409
chr15	102531392	2721188398	26.5401	26.5051
chr16	90354753	2553221544	28.2577	40.155
chr17	81195210	2312879897	28.4854	30.1406
chr18	78077248	2556854908	32.7478	25.8521
chr19	59128983	1466871555	24.808	151.467
chr20	63025520	2023625825	32.108	27.0077
chr21	48129895	1217507247	25.2963	61.5297
chr22	51304566	1020914971	19.8991	25.7288
chrMT	16571	332220374	20,048.2997	7,829.2354
chrX	155270560	2728567763	17.573	25.5636

chrY	59373566	449653581	7.5733	23.1782
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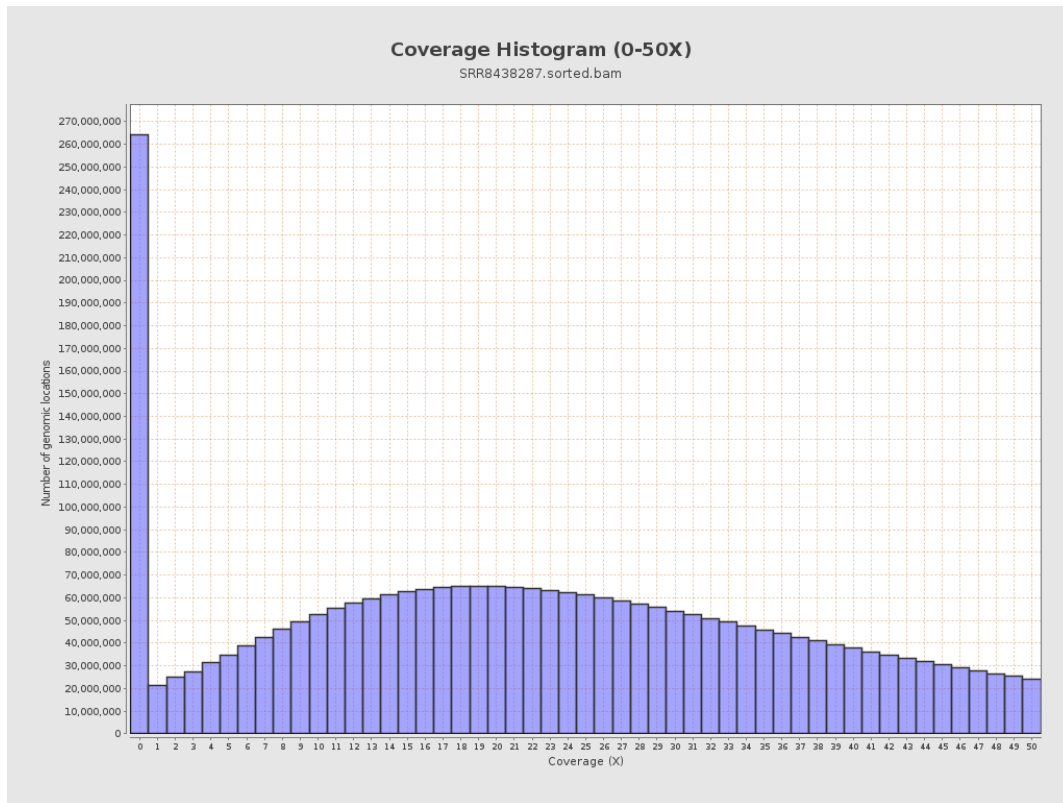
3. Results : Coverage across reference



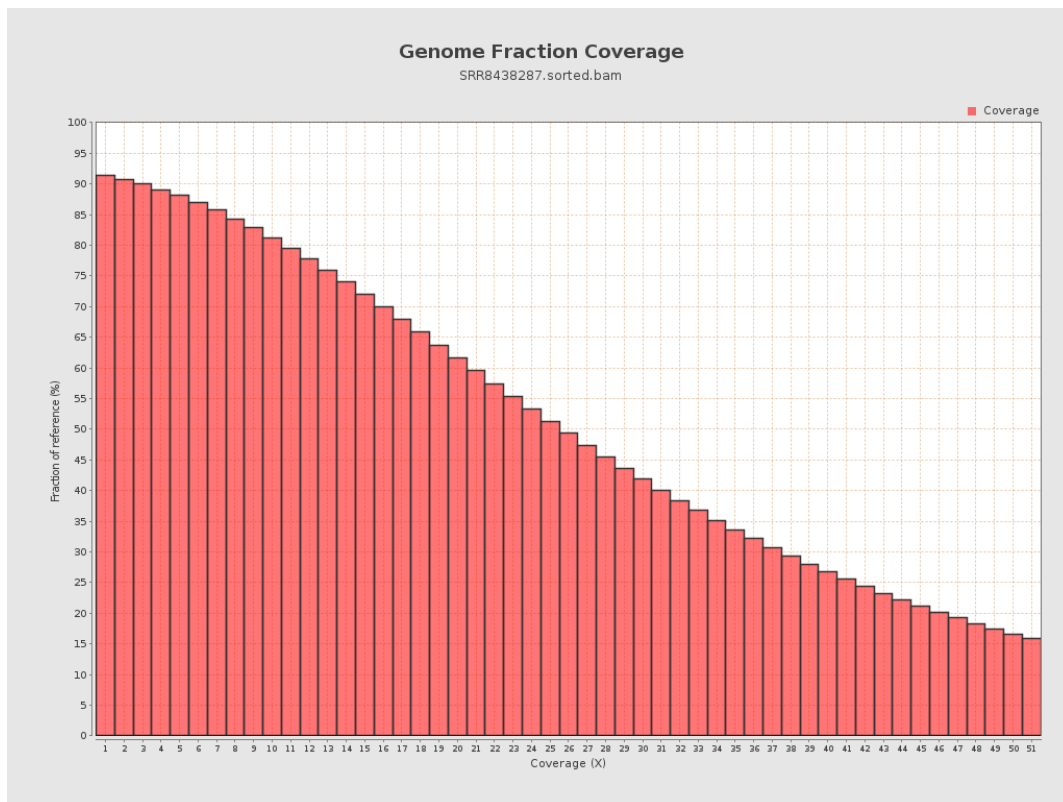
4. Results : Coverage Histogram



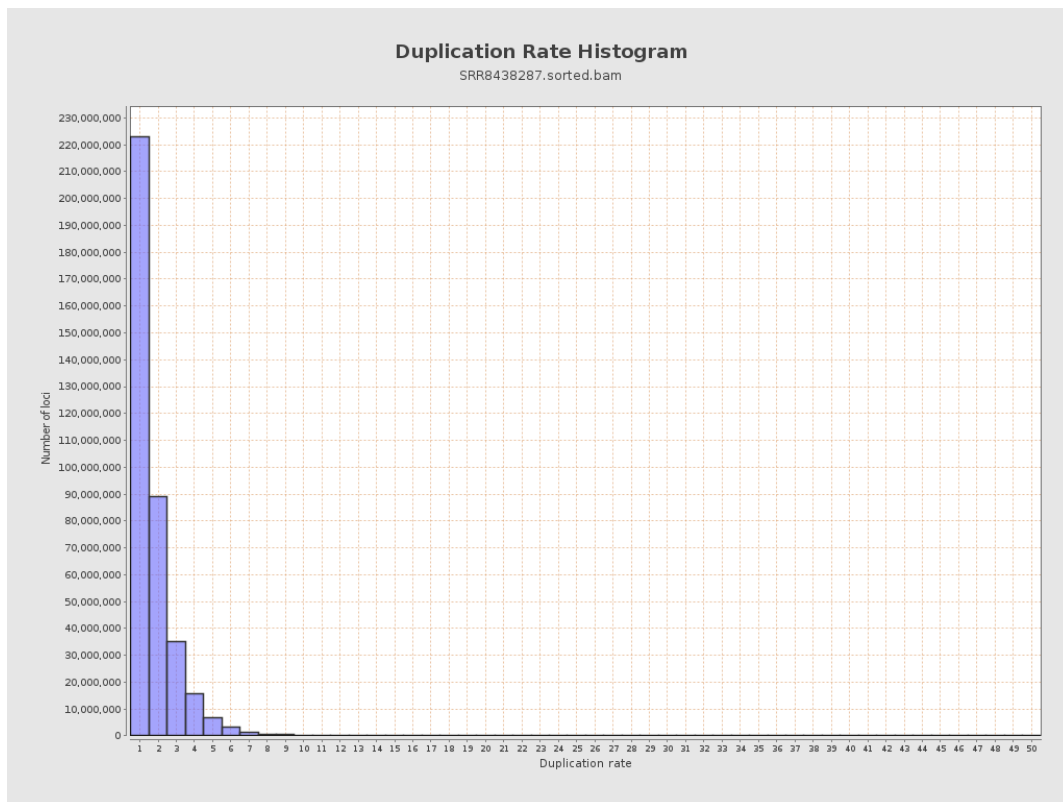
5. Results : Coverage Histogram (0-50X)



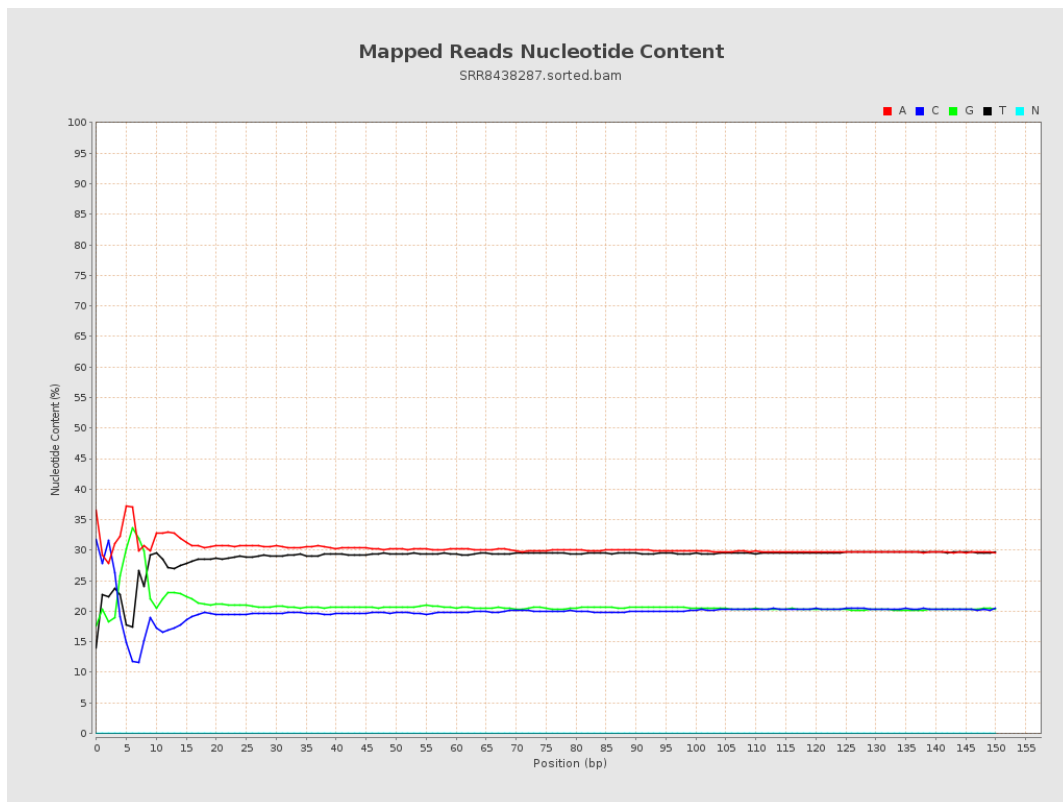
6. Results : Genome Fraction Coverage



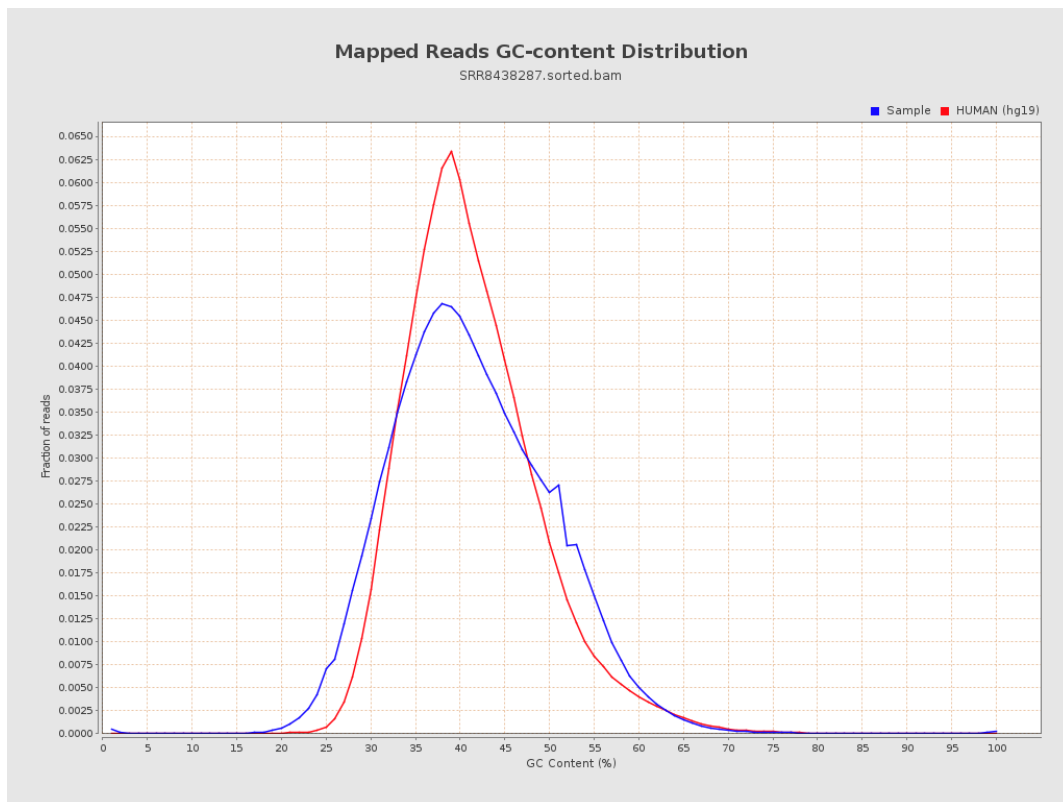
7. Results : Duplication Rate Histogram



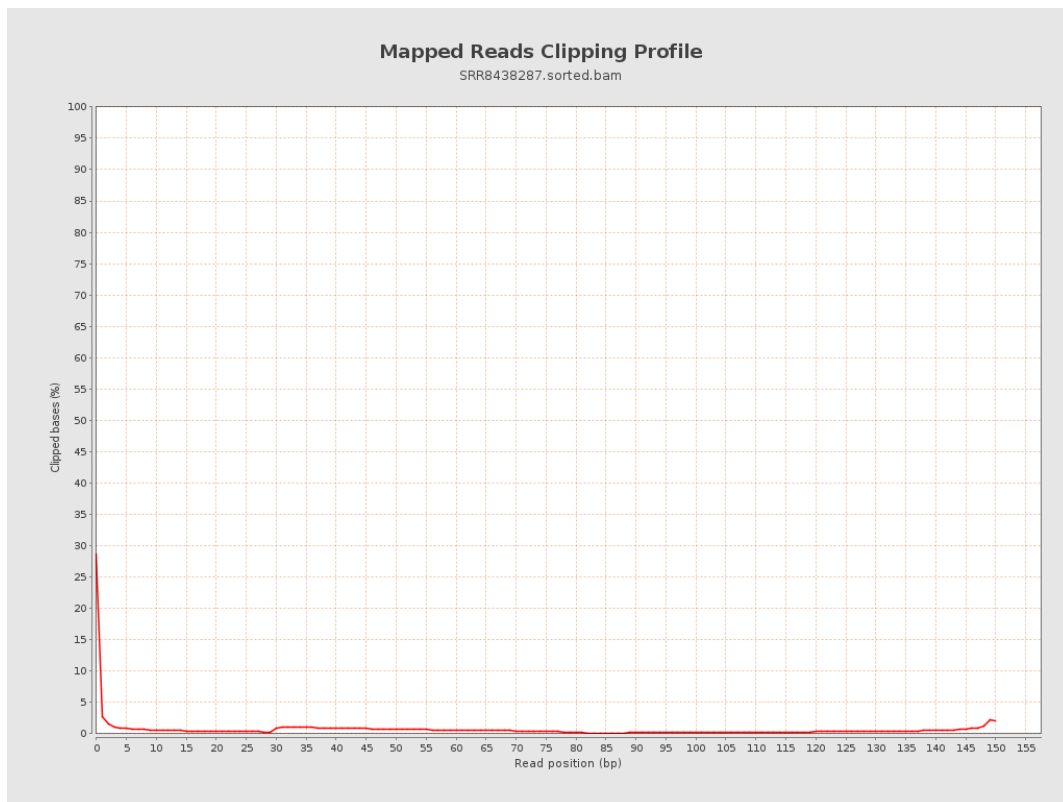
8. Results : Mapped Reads Nucleotide Content



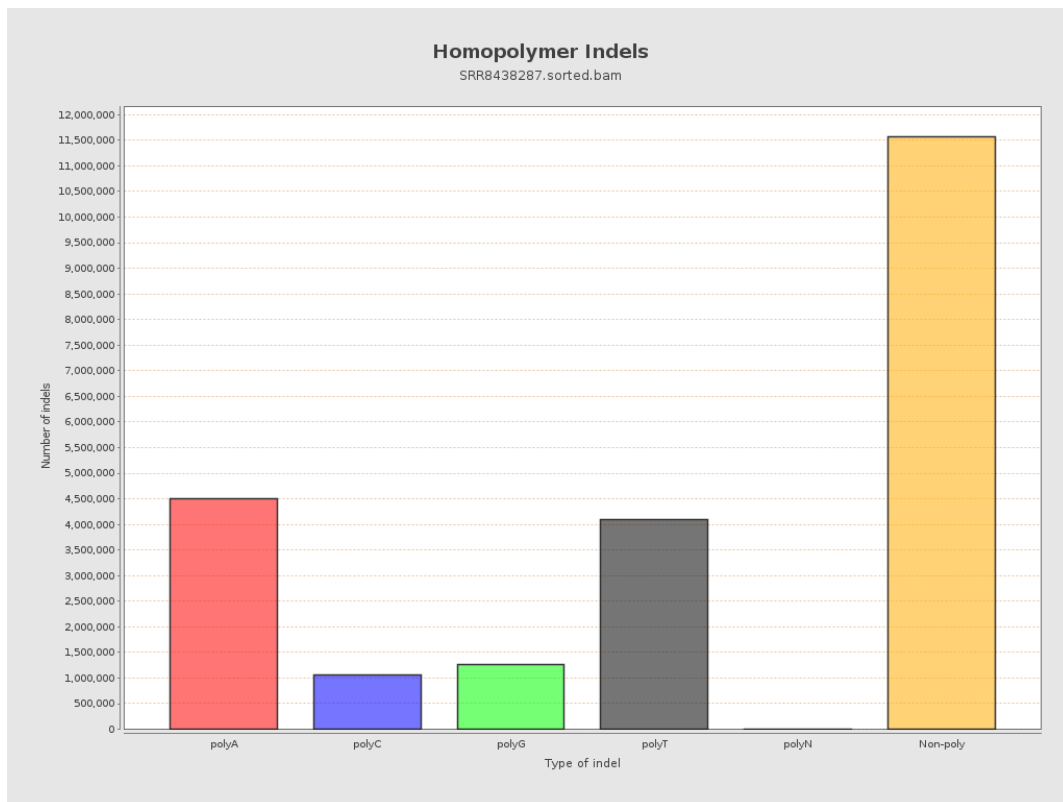
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



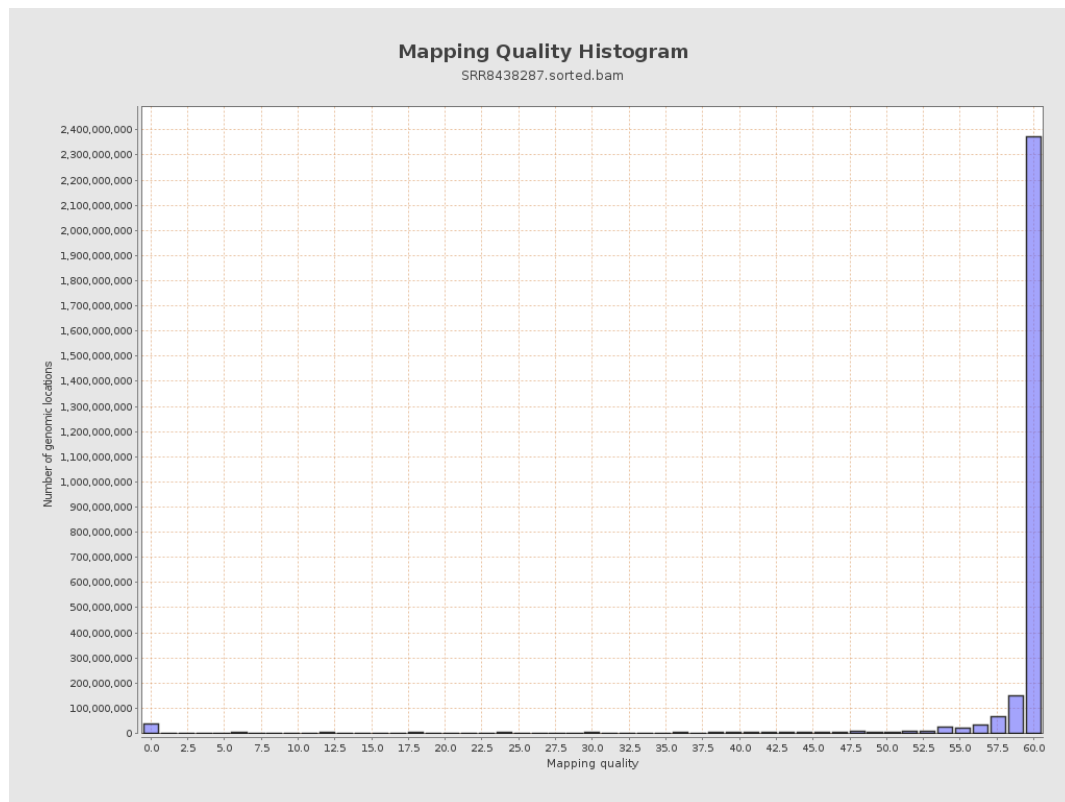
11. Results : Homopolymer Indels



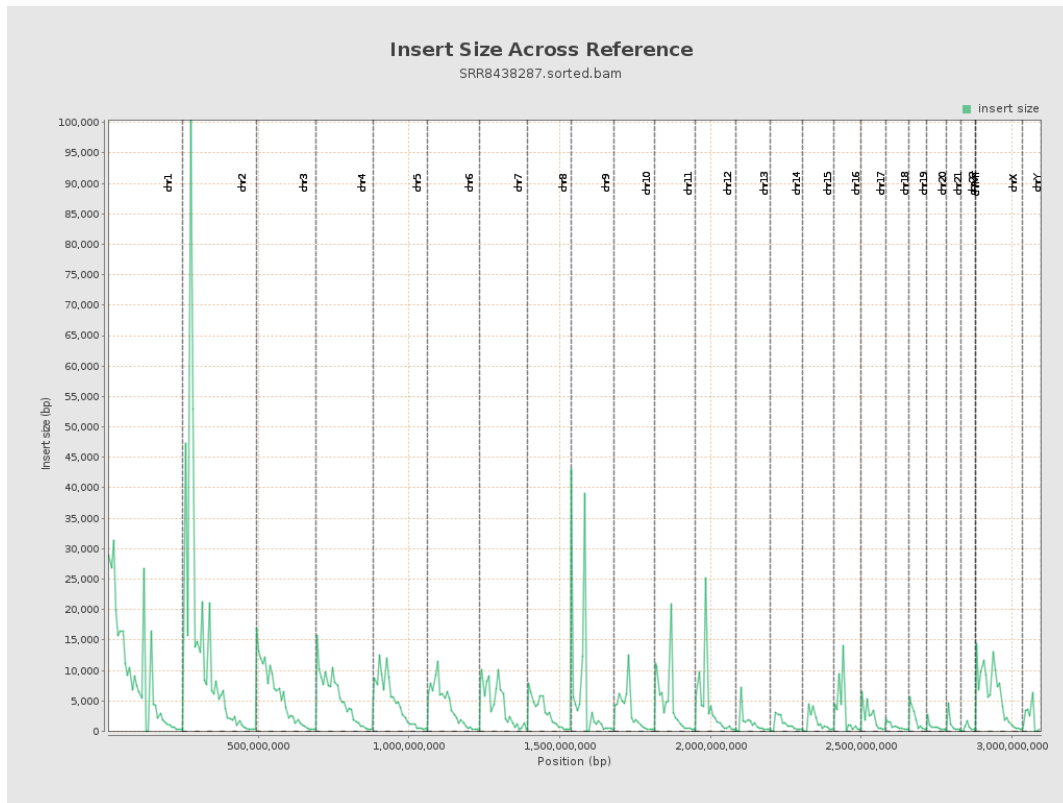
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

