

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 12:35:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617486.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_SRR617486 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617486_1.fastq.gz SRR617486_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 12:35:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617486.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,374,919 / 94.92%
Unmapped reads	1,625,081 / 5.08%
Mapped paired reads	30,374,919 / 94.92%
Mapped reads, first in pair	15,350,082 / 47.97%
Mapped reads, second in pair	15,024,837 / 46.95%
Mapped reads, both in pair	29,791,500 / 93.1%
Mapped reads, singletons	583,419 / 1.82%
Secondary alignments	0
Supplementary alignments	136,059 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	6,203,931 / 19.39%
Duplication rate	9.88%
Clipped reads	5,982,068 / 18.69%

2.2. ACGT Content

Number/percentage of A's	872,445,755 / 29.49%
Number/percentage of C's	598,245,127 / 20.22%
Number/percentage of T's	871,694,776 / 29.46%
Number/percentage of G's	612,654,593 / 20.71%
Number/percentage of N's	3,434,745 / 0.12%

GC Percentage	40.93%
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2.3. Coverage

Mean	0.9562
Standard Deviation	9.6611

2.4. Mapping Quality

Mean Mapping Quality	52.77
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2.5. Insert size

Mean	29,759.29
Standard Deviation	1,587,568.47
P25/Median/P75	173 / 219 / 289

2.6. Mismatches and indels

General error rate	1.26%
Mismatches	36,313,147
Insertions	439,028
Mapped reads with at least one insertion	1.42%
Deletions	1,027,385
Mapped reads with at least one deletion	3.31%
Homopolymer indels	47.42%

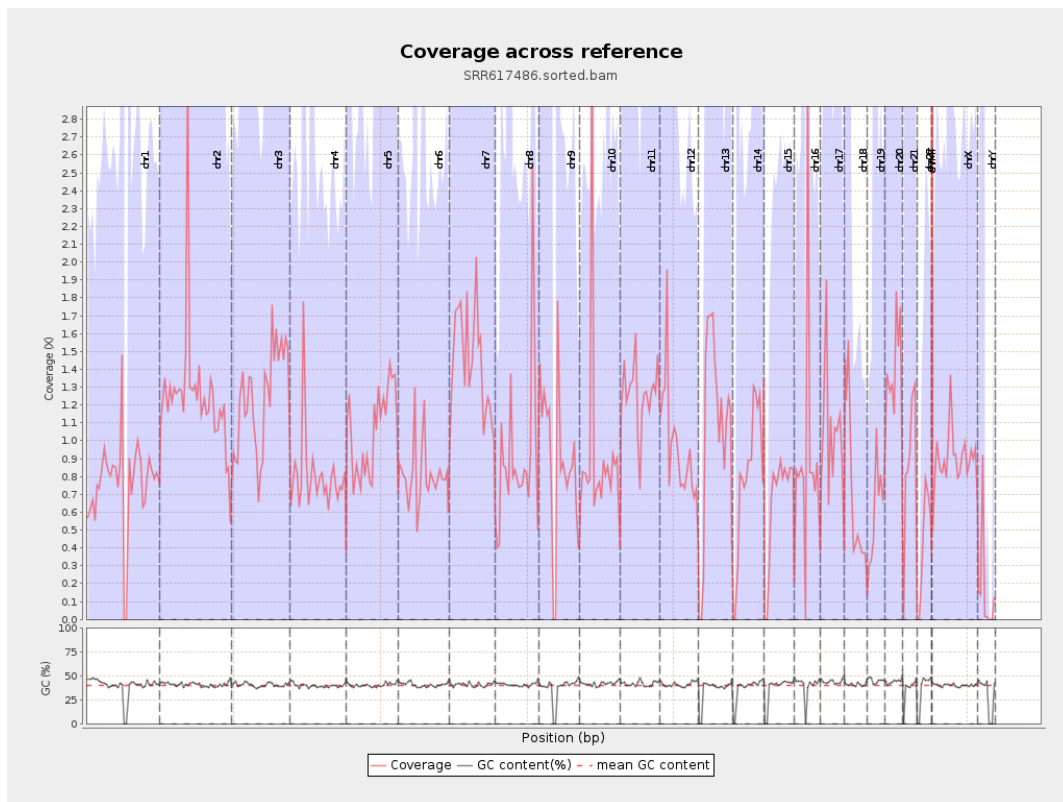
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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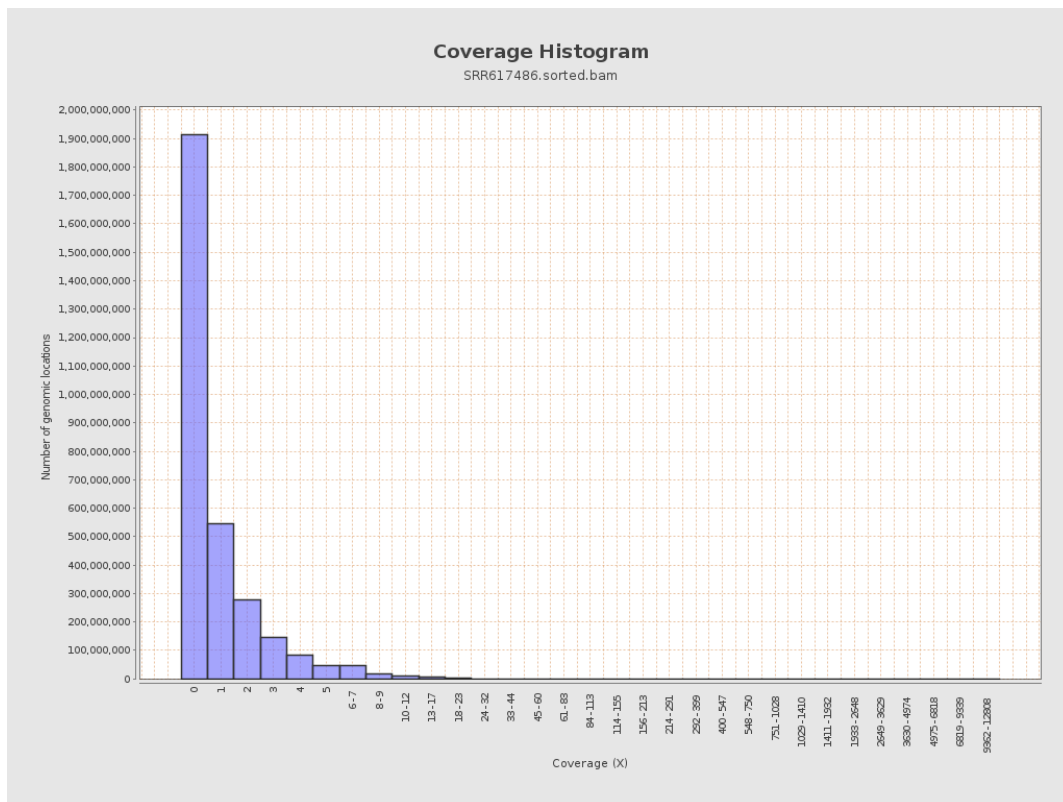
		bases	coverage	deviation
chr1	249250621	190295929	0.7635	9.4158
chr2	243199373	305987765	1.2582	11.3747
chr3	198022430	244769673	1.2361	2.2381
chr4	191154276	153159403	0.8012	6.0542
chr5	180915260	189668859	1.0484	2.0647
chr6	171115067	139487113	0.8152	5.3365
chr7	159138663	228313639	1.4347	13.0912
chr8	146364022	131120050	0.8958	3.8155
chr9	141213431	122374610	0.8666	18.1533
chr10	135534747	125408535	0.9253	18.7074
chr11	135006516	167038081	1.2373	12.583
chr12	133851895	129149075	0.9649	1.9632
chr13	115169878	125678251	1.0912	2.1107
chr14	107349540	86385802	0.8047	2.24
chr15	102531392	66956689	0.653	1.4415
chr16	90354753	79913050	0.8844	14.8848
chr17	81195210	82698881	1.0185	13.4947
chr18	78077248	52967381	0.6784	17.096
chr19	59128983	35335713	0.5976	5.7684
chr20	63025520	87408742	1.3869	2.794
chr21	48129895	42718866	0.8876	3.7924
chr22	51304566	22116648	0.4311	1.2501
chrMT	16571	2036418	122.8905	93.1012
chrX	155270560	139003954	0.8952	4.0887

chrY	59373566	10225589	0.1722	13.7155
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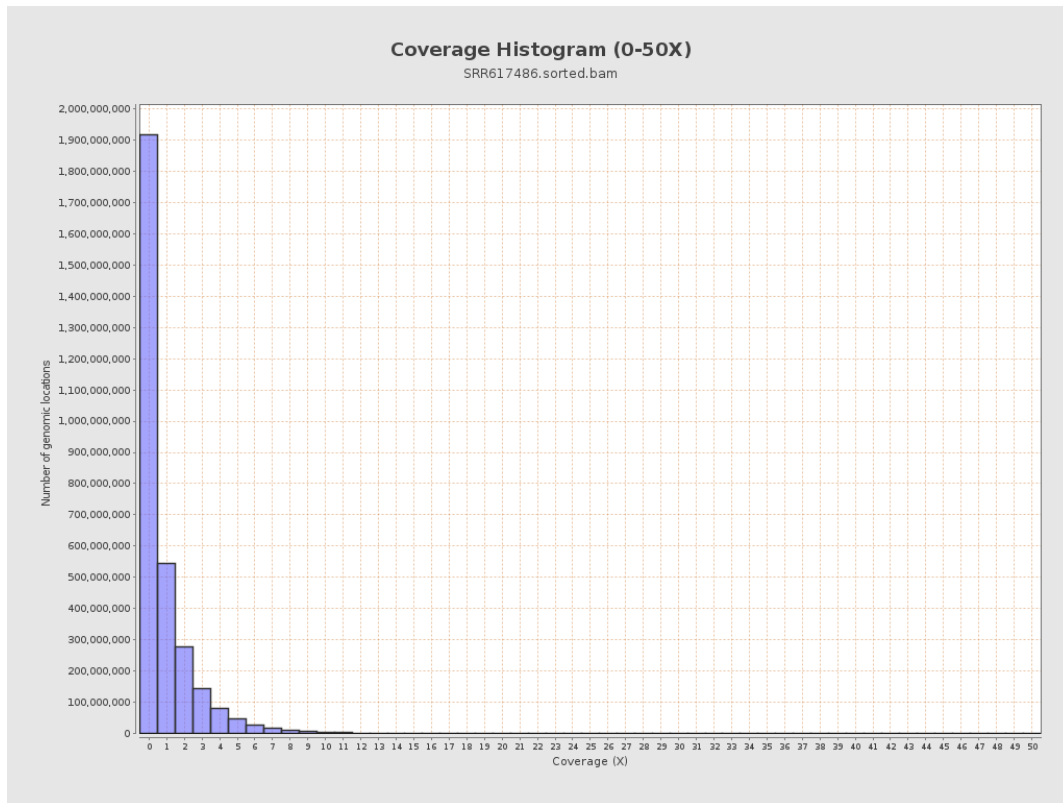
3. Results : Coverage across reference



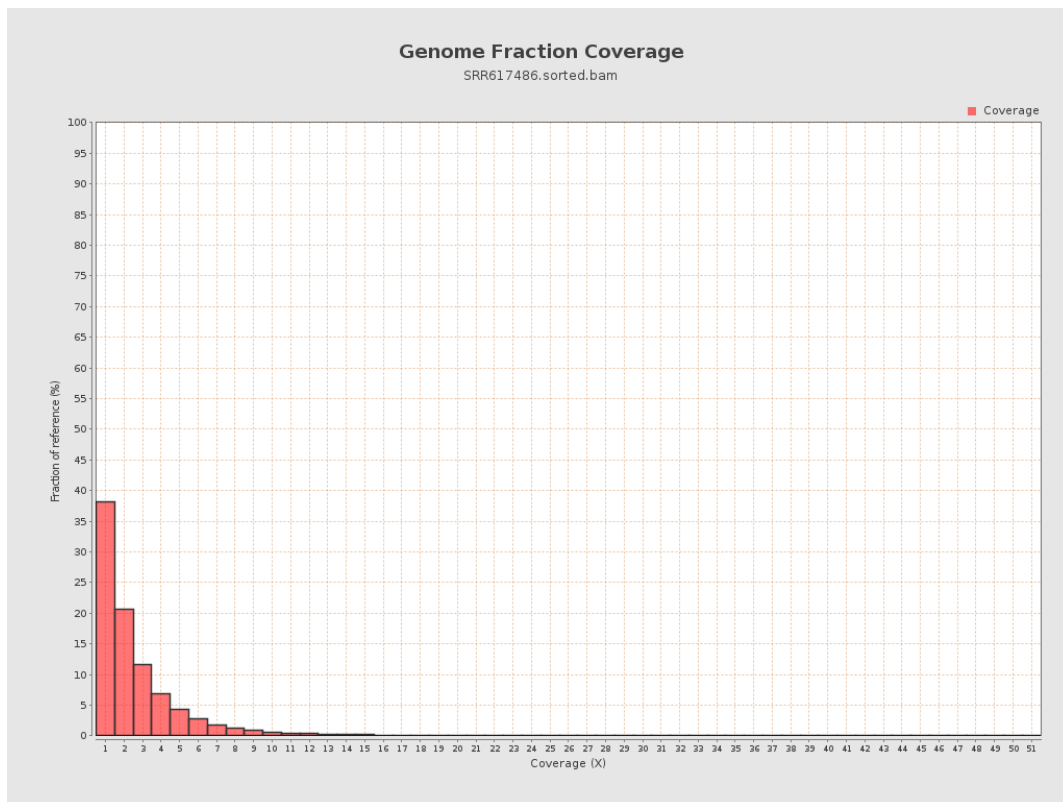
4. Results : Coverage Histogram



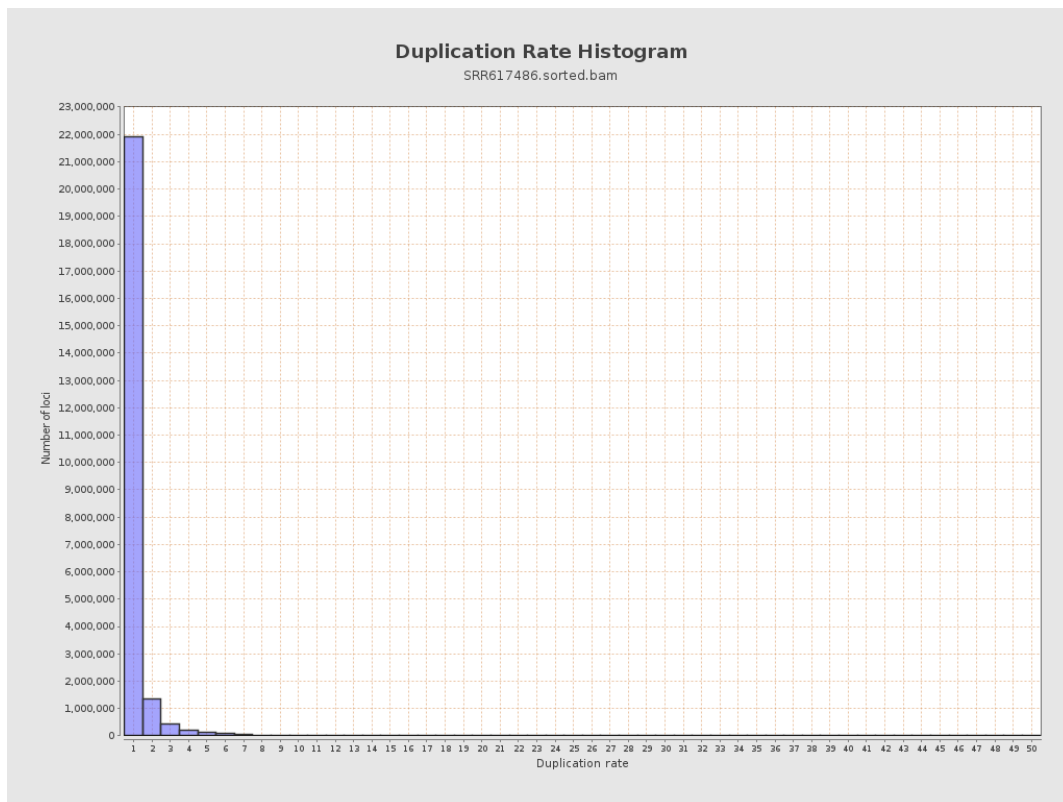
5. Results : Coverage Histogram (0-50X)



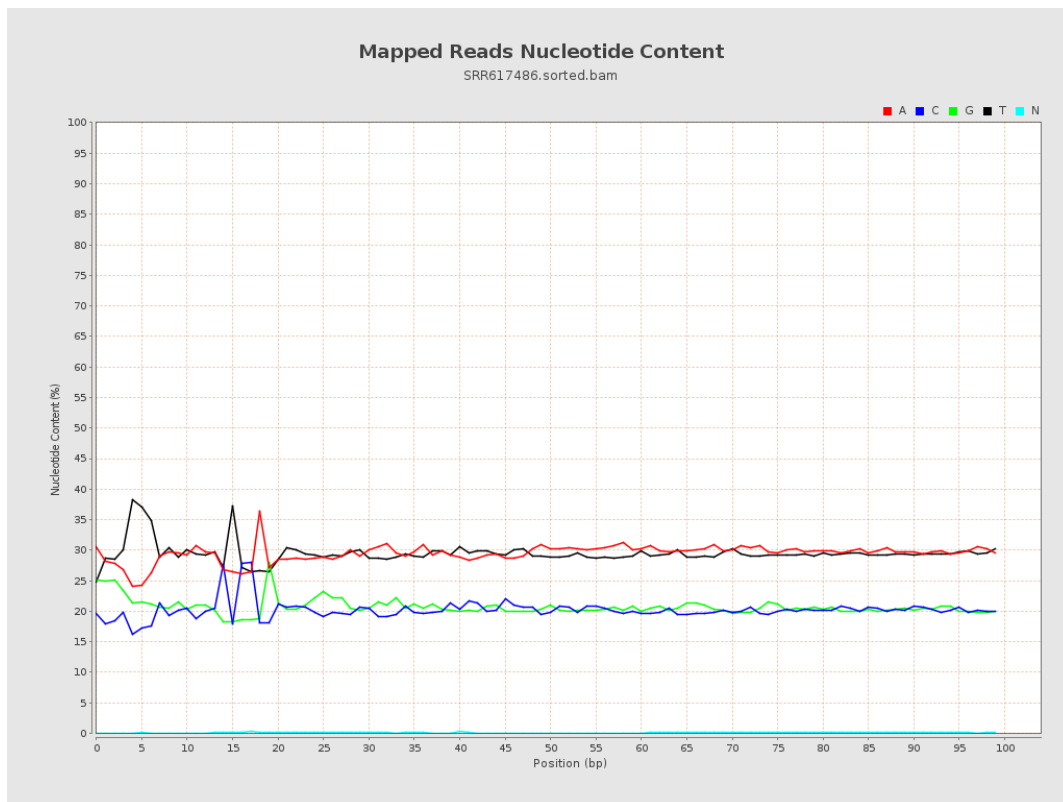
6. Results : Genome Fraction Coverage



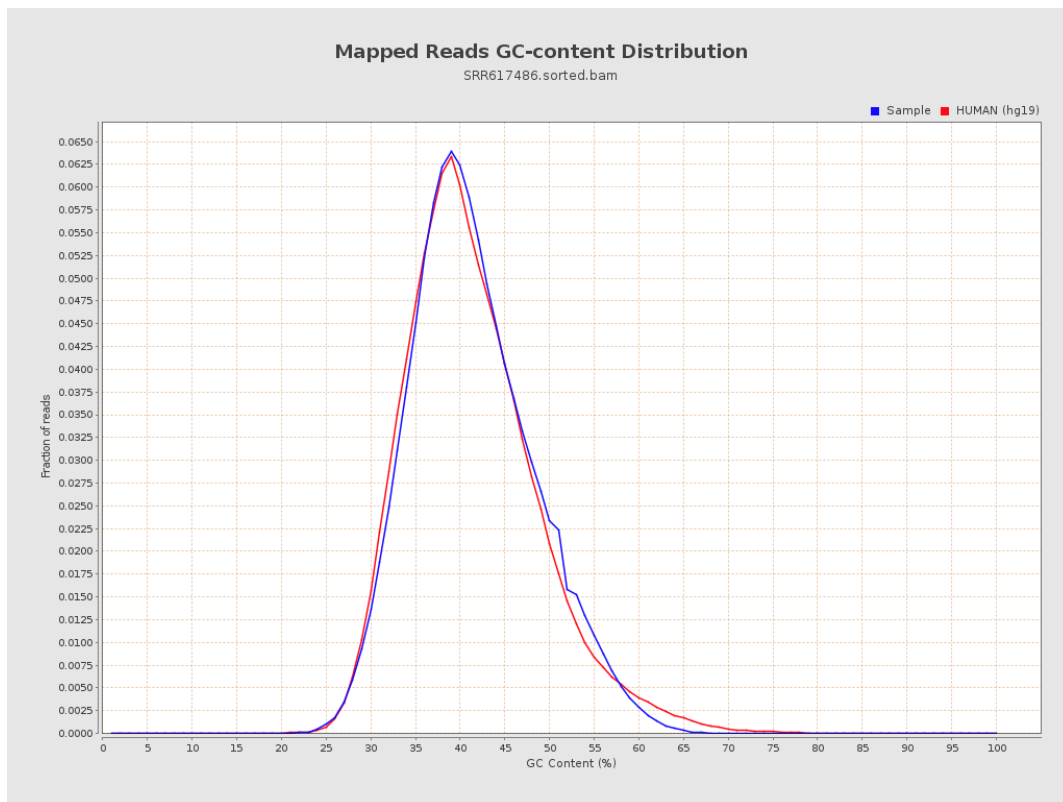
7. Results : Duplication Rate Histogram



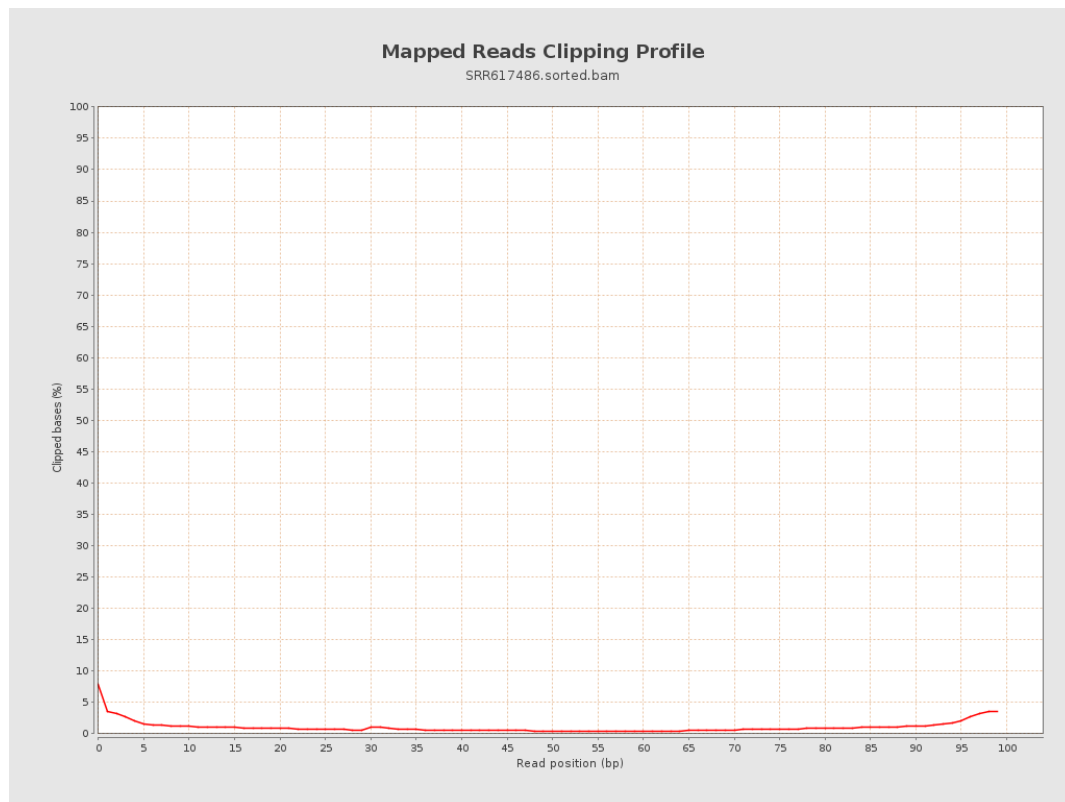
8. Results : Mapped Reads Nucleotide Content



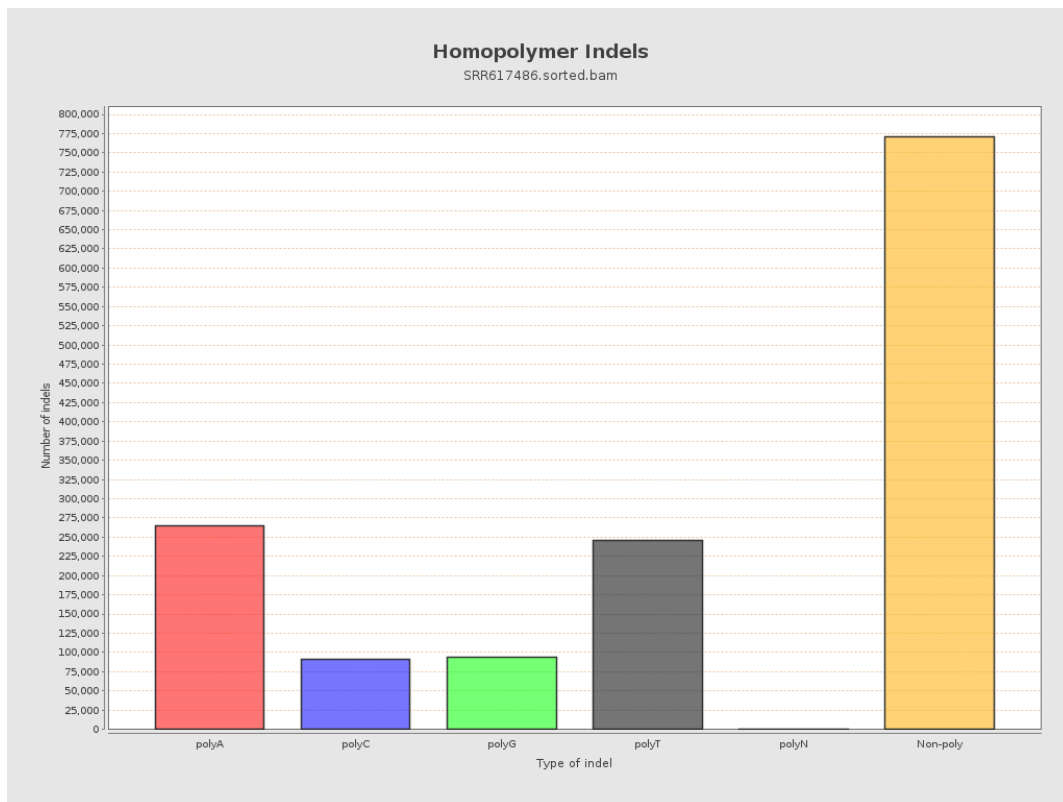
9. Results : Mapped Reads GC-content Distribution



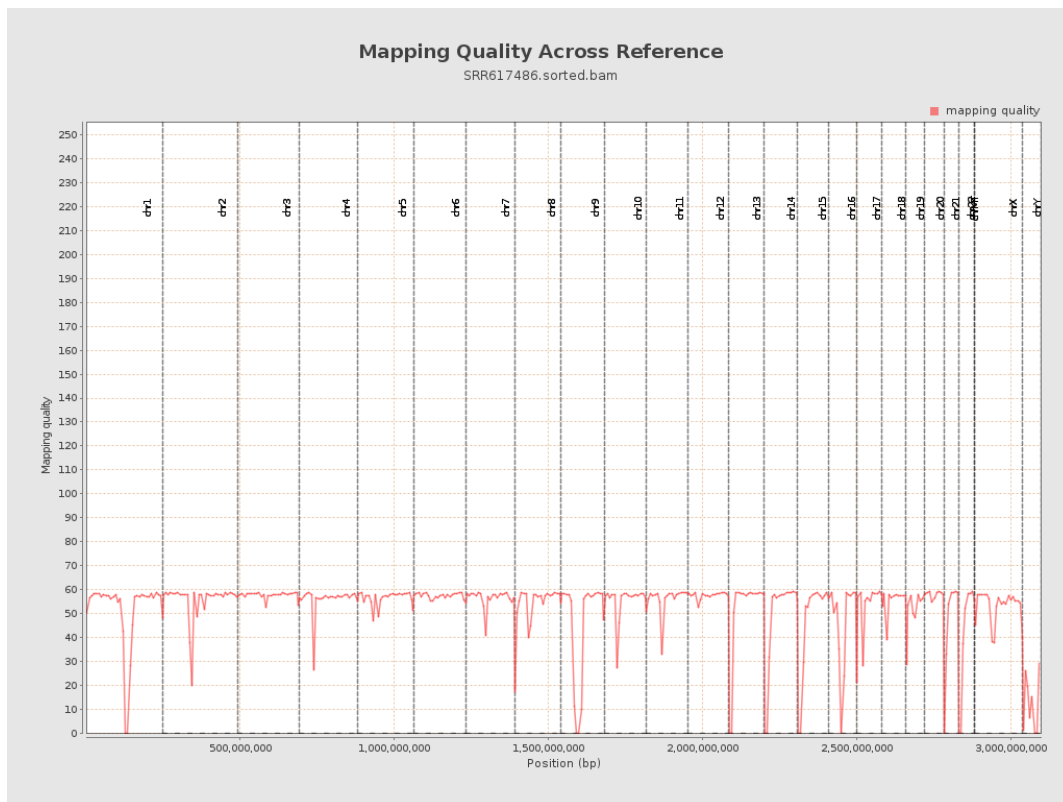
10. Results : Mapped Reads Clipping Profile



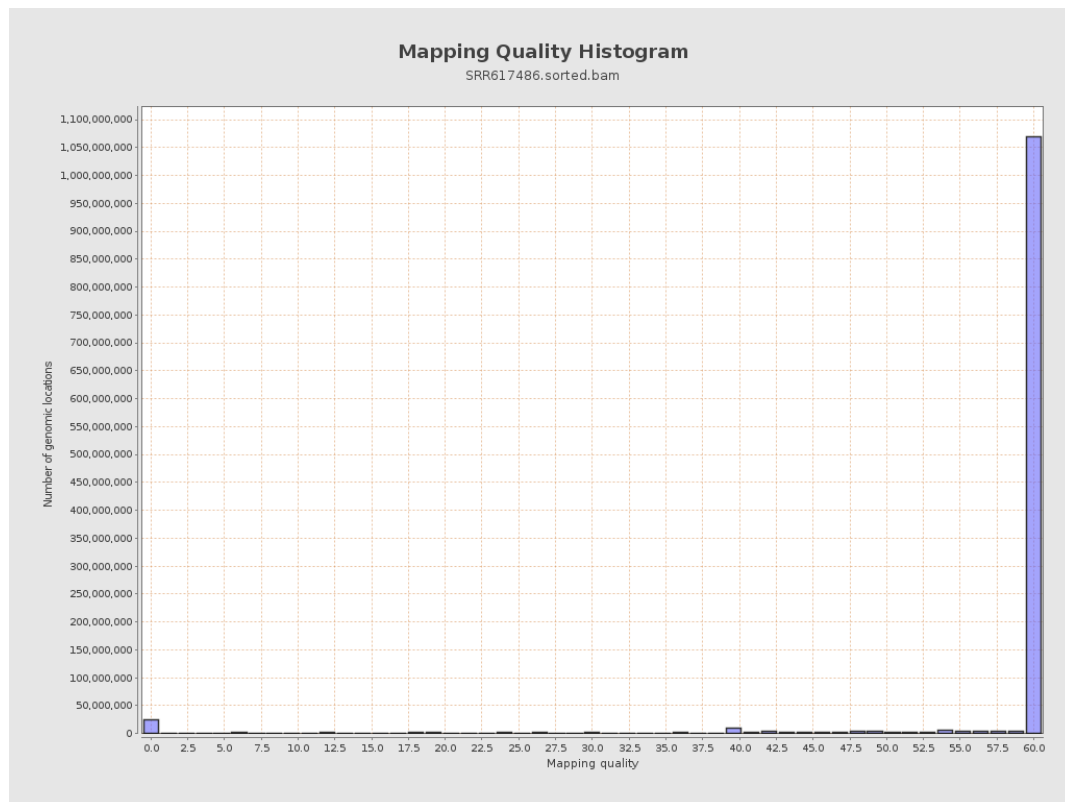
11. Results : Homopolymer Indels



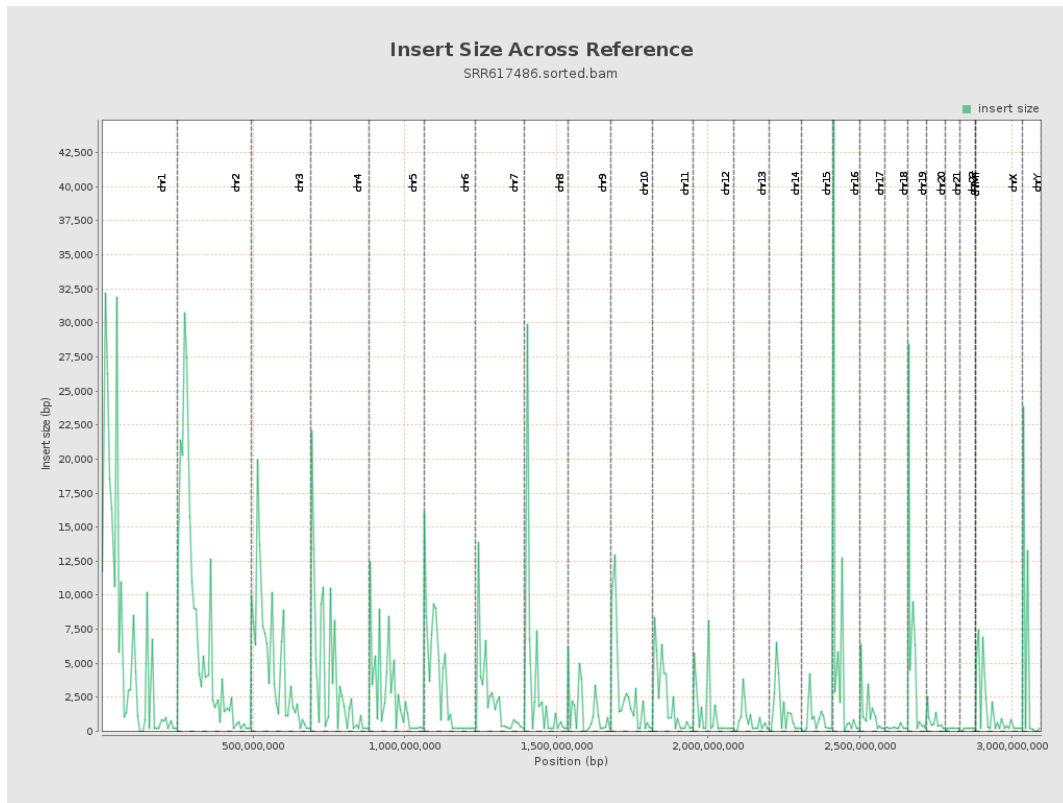
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

