

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 09:53:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617483.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_SRR617483 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617483_1.fastq.gz SRR617483_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 09:53:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617483.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,517,873 / 95.37%
Unmapped reads	1,482,127 / 4.63%
Mapped paired reads	30,517,873 / 95.37%
Mapped reads, first in pair	15,427,594 / 48.21%
Mapped reads, second in pair	15,090,279 / 47.16%
Mapped reads, both in pair	29,929,776 / 93.53%
Mapped reads, singletons	588,097 / 1.84%
Secondary alignments	0
Supplementary alignments	135,725 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	6,314,099 / 19.73%
Duplication rate	10.02%
Clipped reads	5,865,883 / 18.33%

2.2. ACGT Content

Number/percentage of A's	875,336,648 / 29.45%
Number/percentage of C's	600,879,000 / 20.21%
Number/percentage of T's	875,633,774 / 29.46%
Number/percentage of G's	615,710,813 / 20.71%
Number/percentage of N's	5,206,052 / 0.18%

GC Percentage	40.92%
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2.3. Coverage

Mean	0.9609
Standard Deviation	9.6897

2.4. Mapping Quality

Mean Mapping Quality	52.78
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2.5. Insert size

Mean	29,550.47
Standard Deviation	1,585,614.77
P25/Median/P75	176 / 224 / 297

2.6. Mismatches and indels

General error rate	1.15%
Mismatches	33,282,067
Insertions	441,760
Mapped reads with at least one insertion	1.42%
Deletions	1,038,416
Mapped reads with at least one deletion	3.33%
Homopolymer indels	47.51%

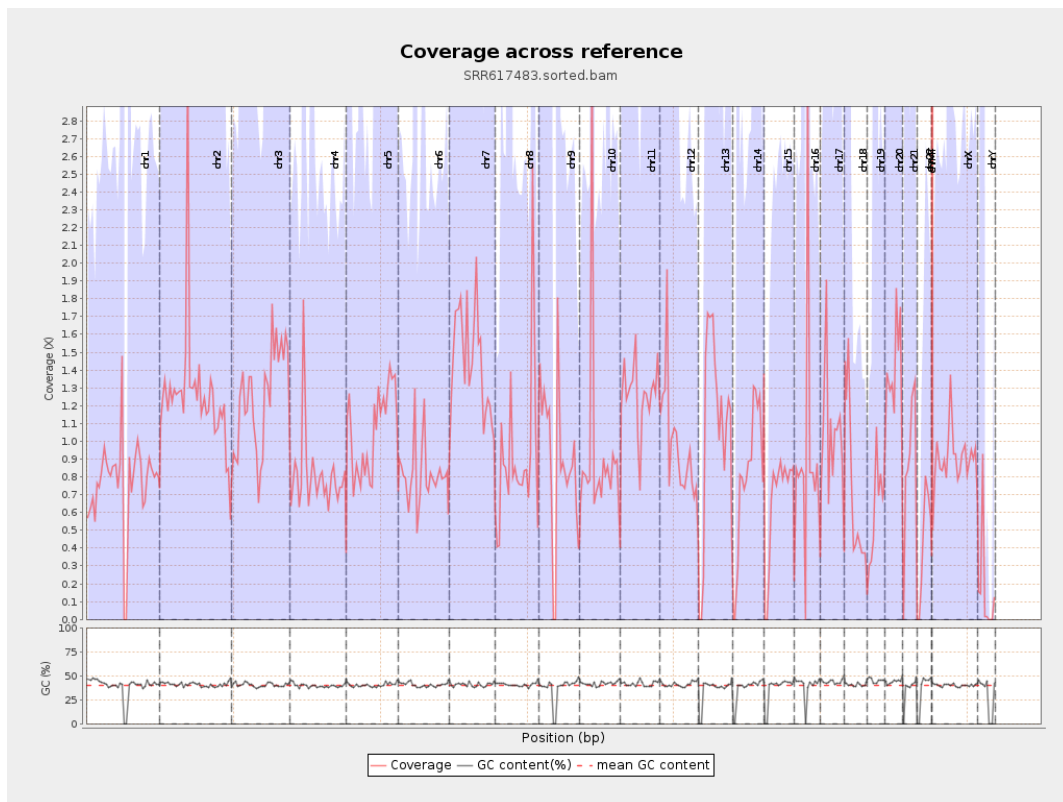
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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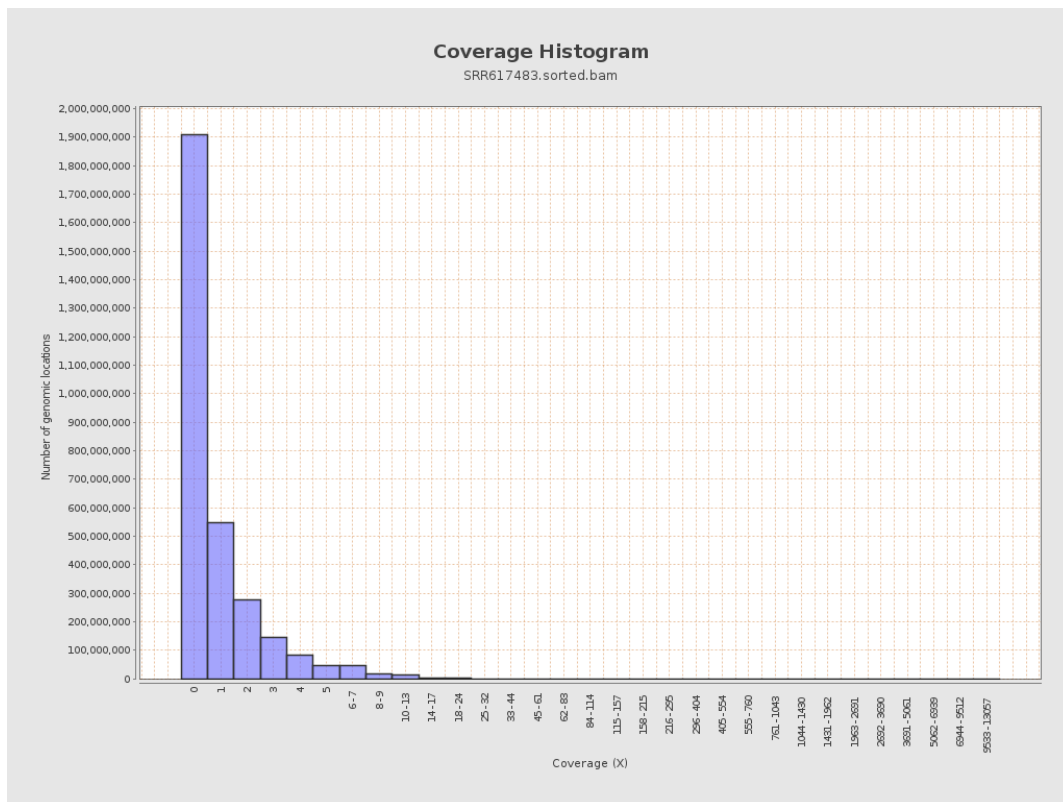
		bases	coverage	deviation
chr1	249250621	191586382	0.7686	9.4415
chr2	243199373	307455407	1.2642	11.4267
chr3	198022430	246109513	1.2428	2.2318
chr4	191154276	153824810	0.8047	6.1782
chr5	180915260	190465404	1.0528	2.0701
chr6	171115067	140386590	0.8204	5.3871
chr7	159138663	229330512	1.4411	13.1458
chr8	146364022	132129729	0.9027	3.8242
chr9	141213431	123055918	0.8714	18.4364
chr10	135534747	125711039	0.9275	18.5423
chr11	135006516	167899022	1.2436	12.536
chr12	133851895	129929820	0.9707	1.9756
chr13	115169878	126050180	1.0945	2.1066
chr14	107349540	86568897	0.8064	2.2158
chr15	102531392	67041970	0.6539	1.4437
chr16	90354753	80182728	0.8874	14.7788
chr17	81195210	82893347	1.0209	13.6047
chr18	78077248	53372000	0.6836	17.1373
chr19	59128983	35609351	0.6022	5.971
chr20	63025520	87910531	1.3948	2.784
chr21	48129895	42857027	0.8904	3.8068
chr22	51304566	22228771	0.4333	1.2459
chrMT	16571	2110136	127.3391	91.5832
chrX	155270560	139586480	0.899	4.0359

chrY	59373566	10243413	0.1725	13.7526
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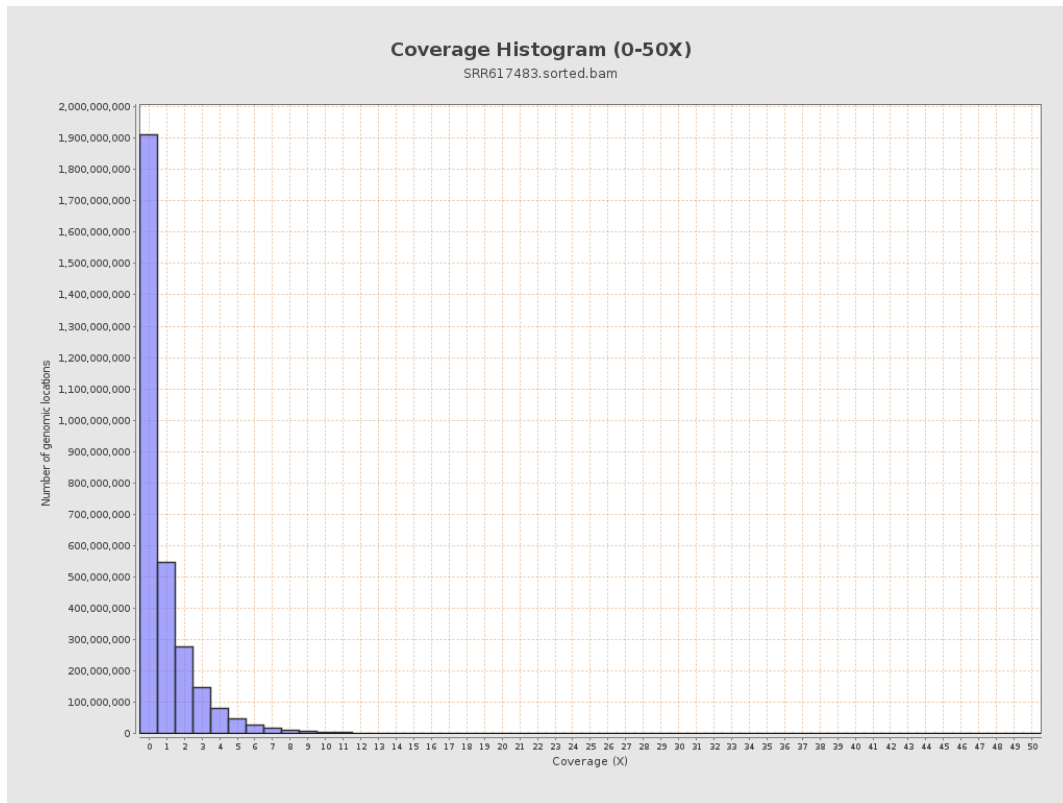
3. Results : Coverage across reference



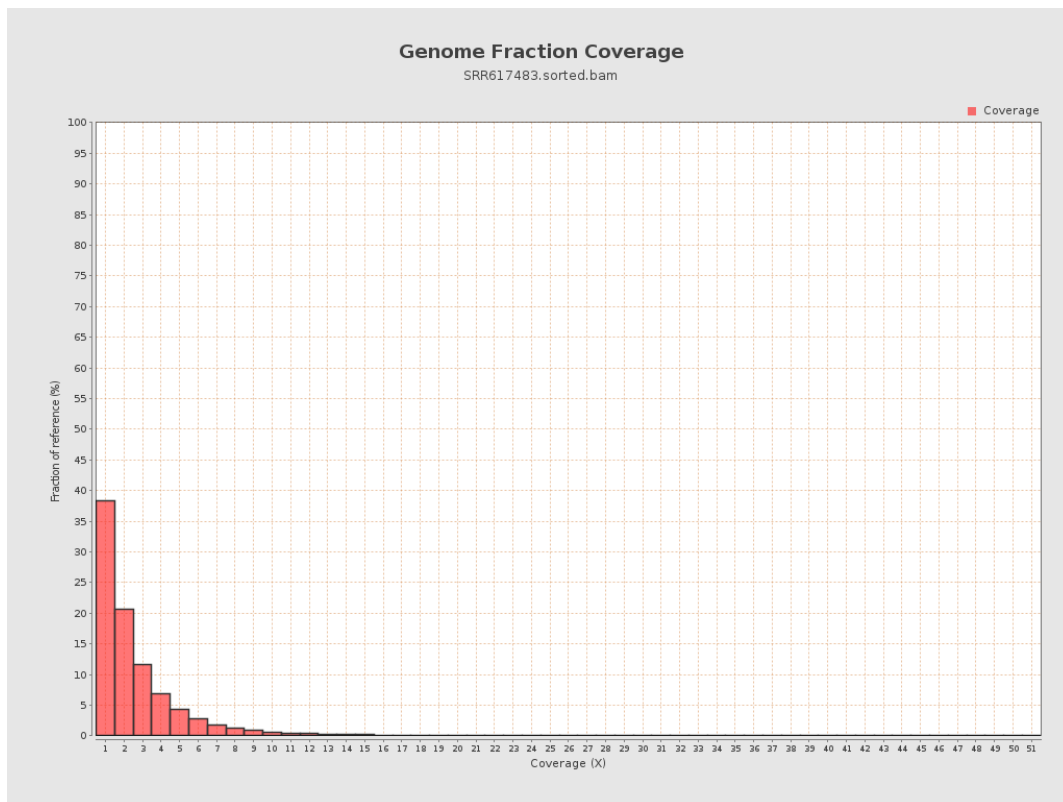
4. Results : Coverage Histogram



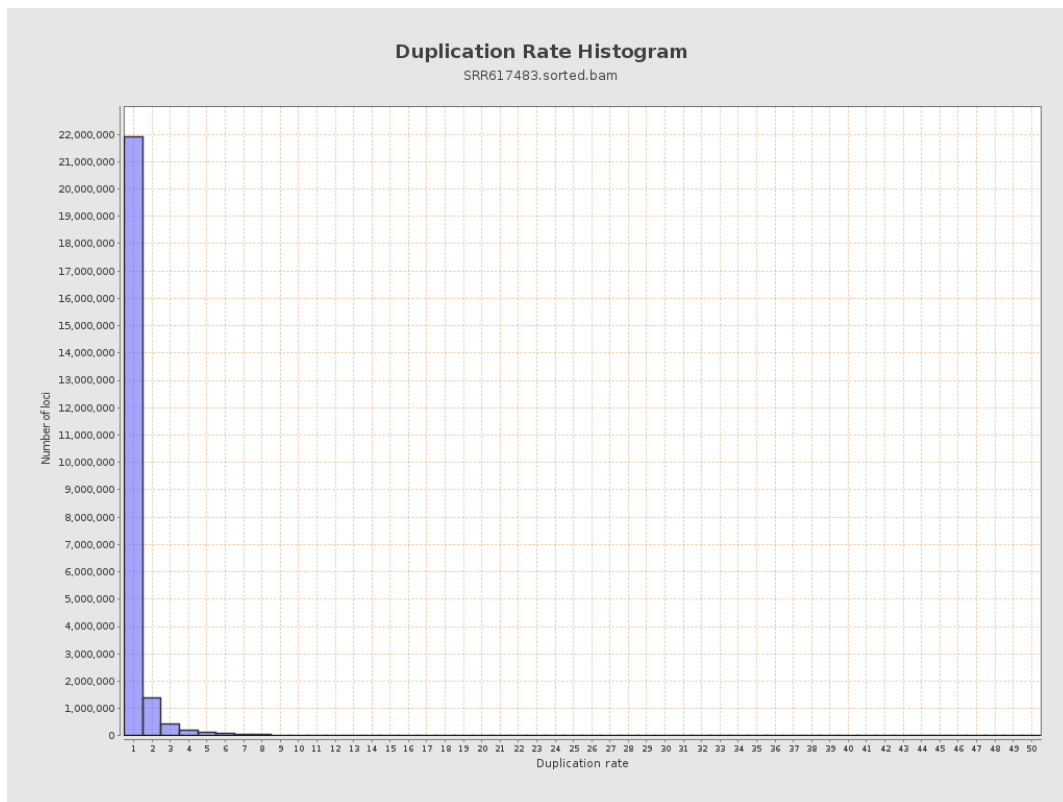
5. Results : Coverage Histogram (0-50X)



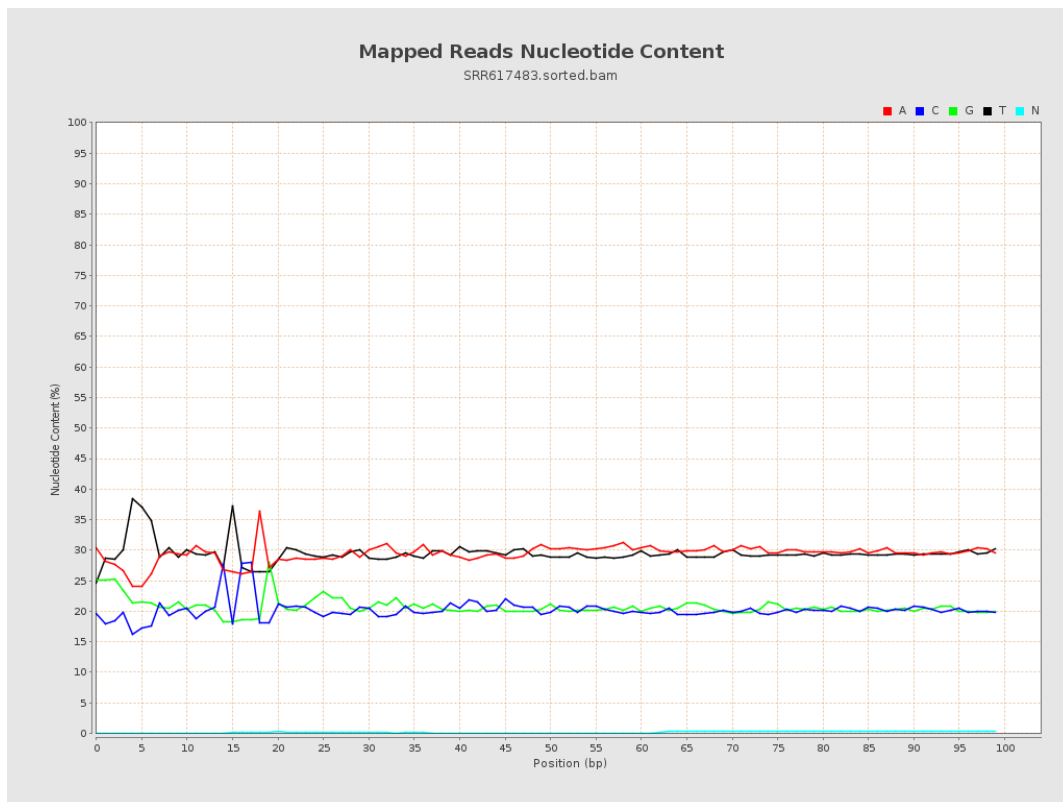
6. Results : Genome Fraction Coverage



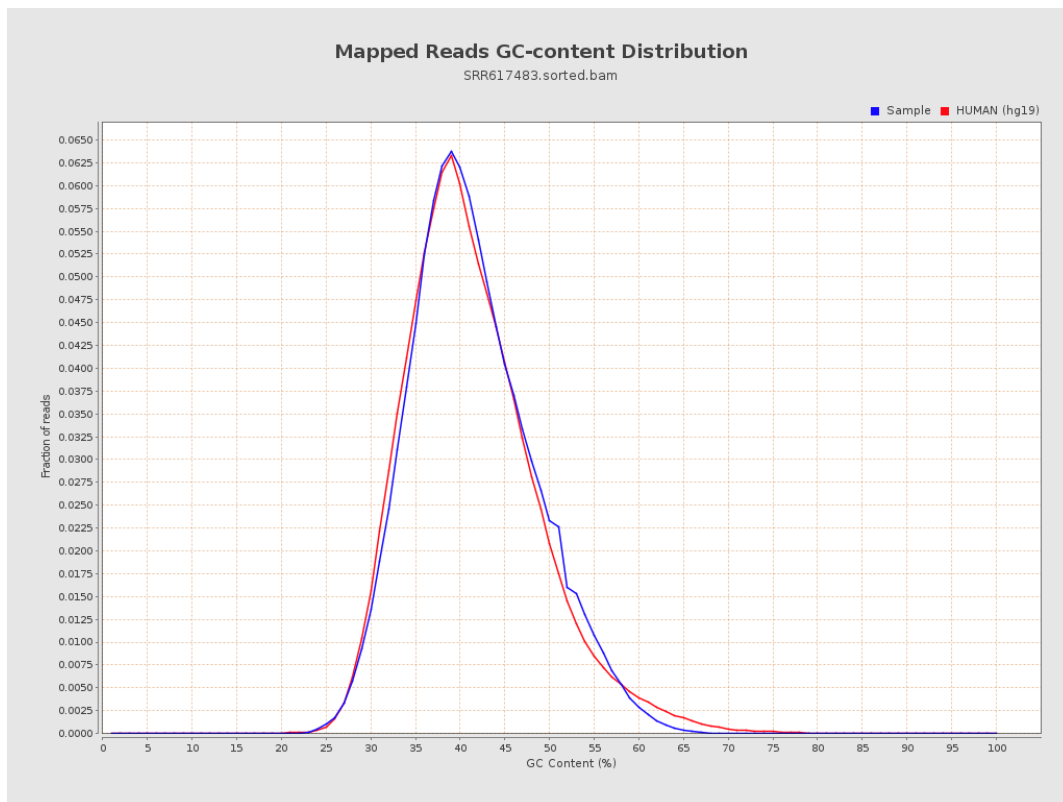
7. Results : Duplication Rate Histogram



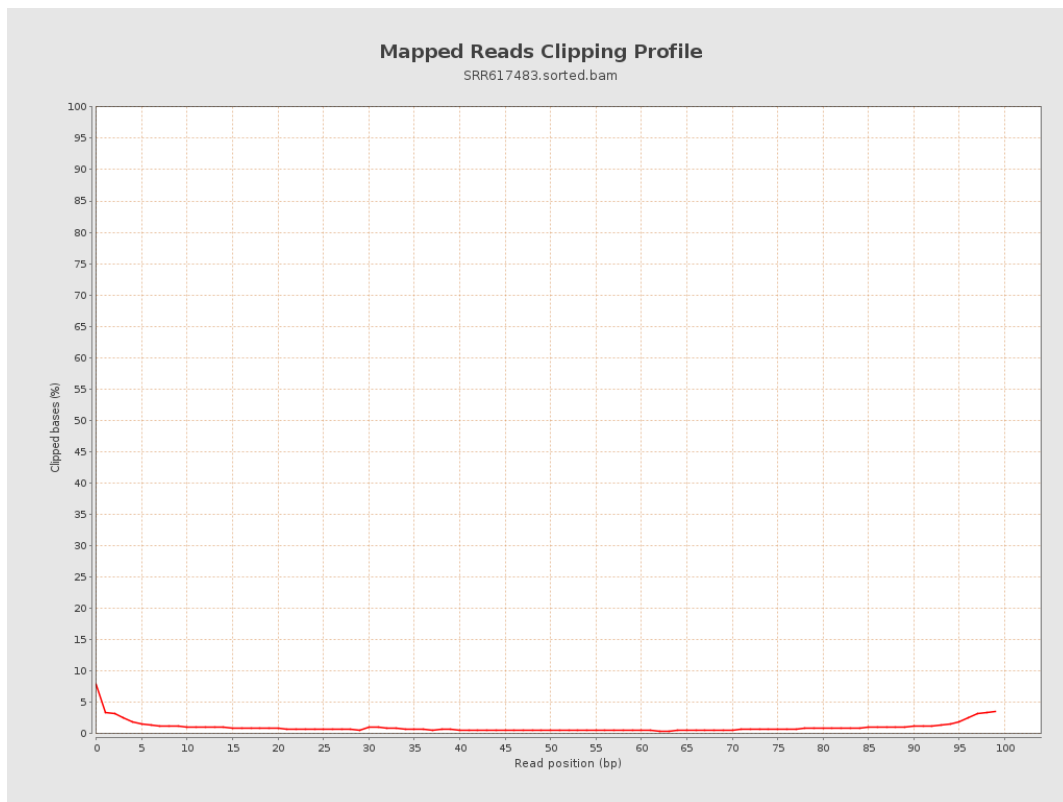
8. Results : Mapped Reads Nucleotide Content



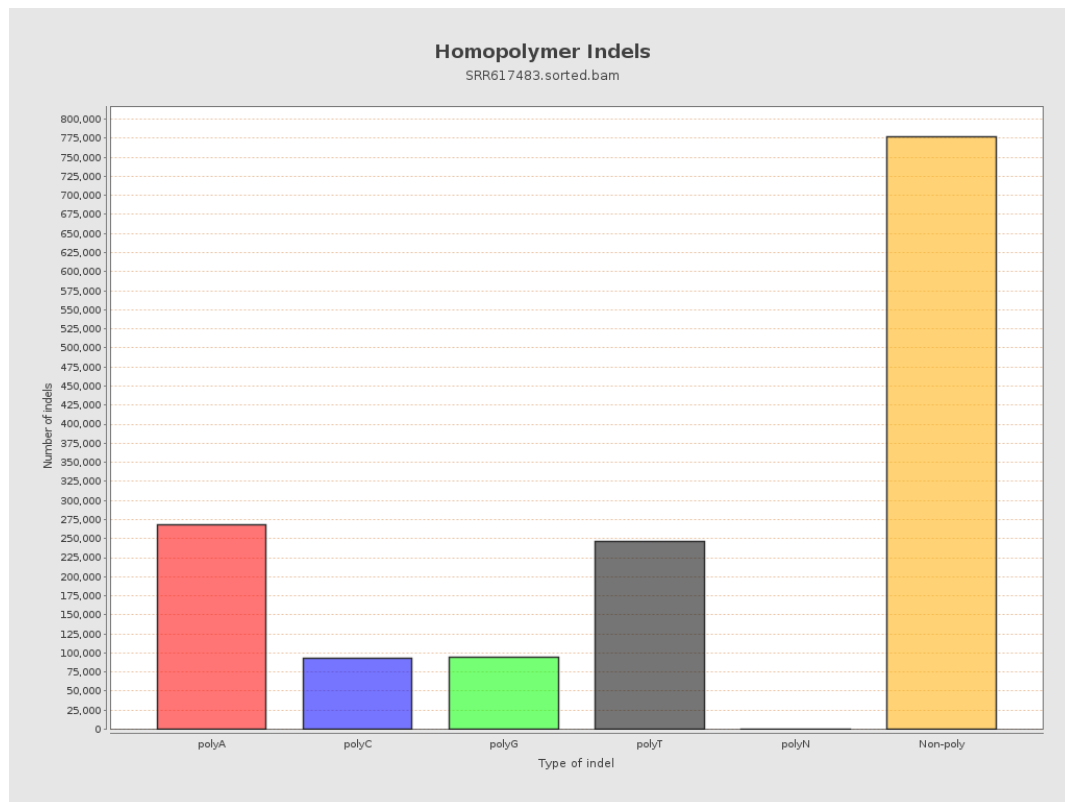
9. Results : Mapped Reads GC-content Distribution



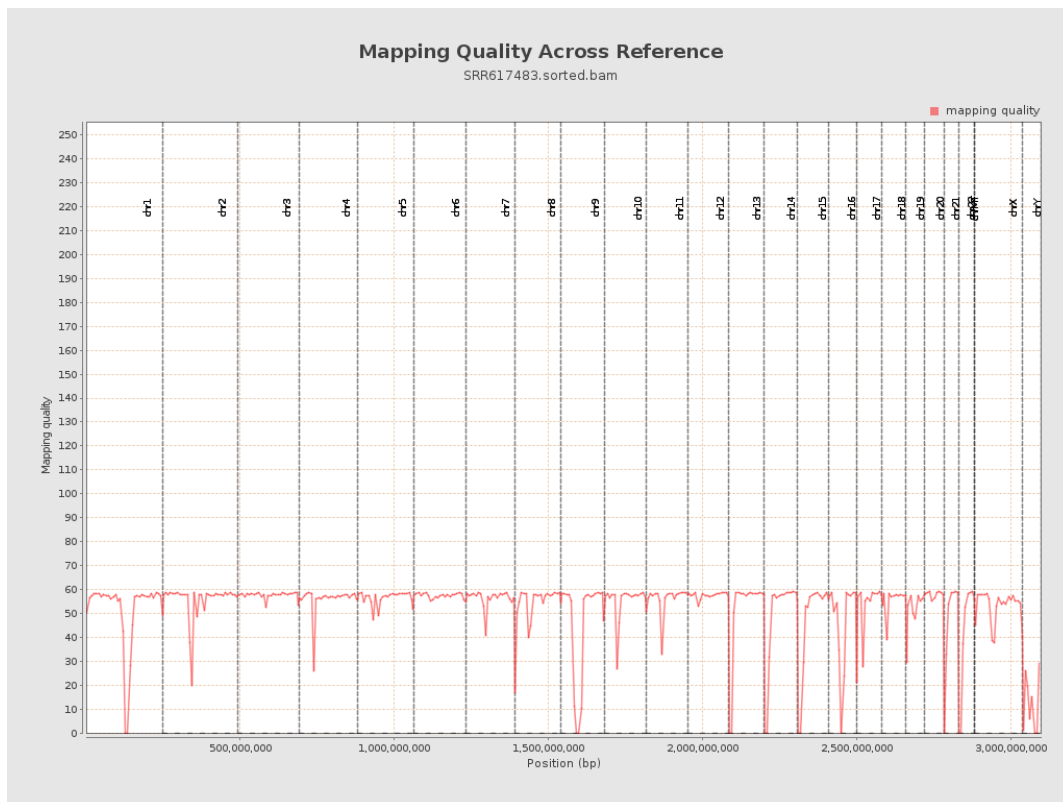
10. Results : Mapped Reads Clipping Profile



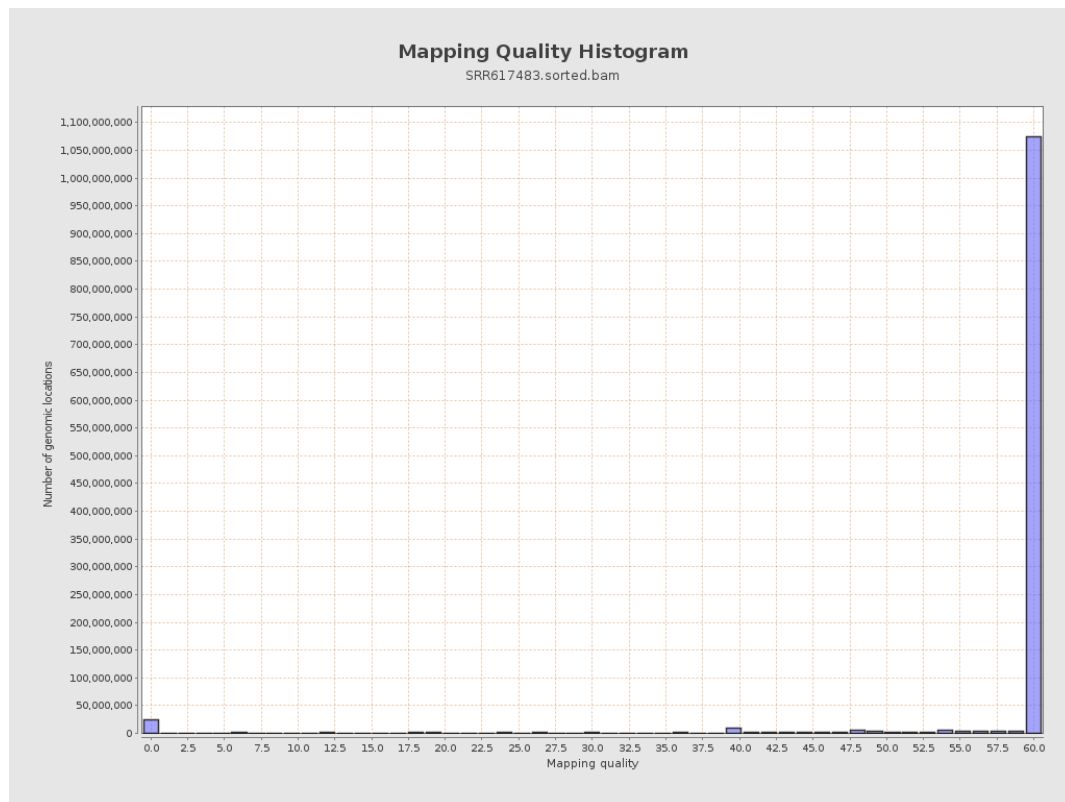
11. Results : Homopolymer Indels



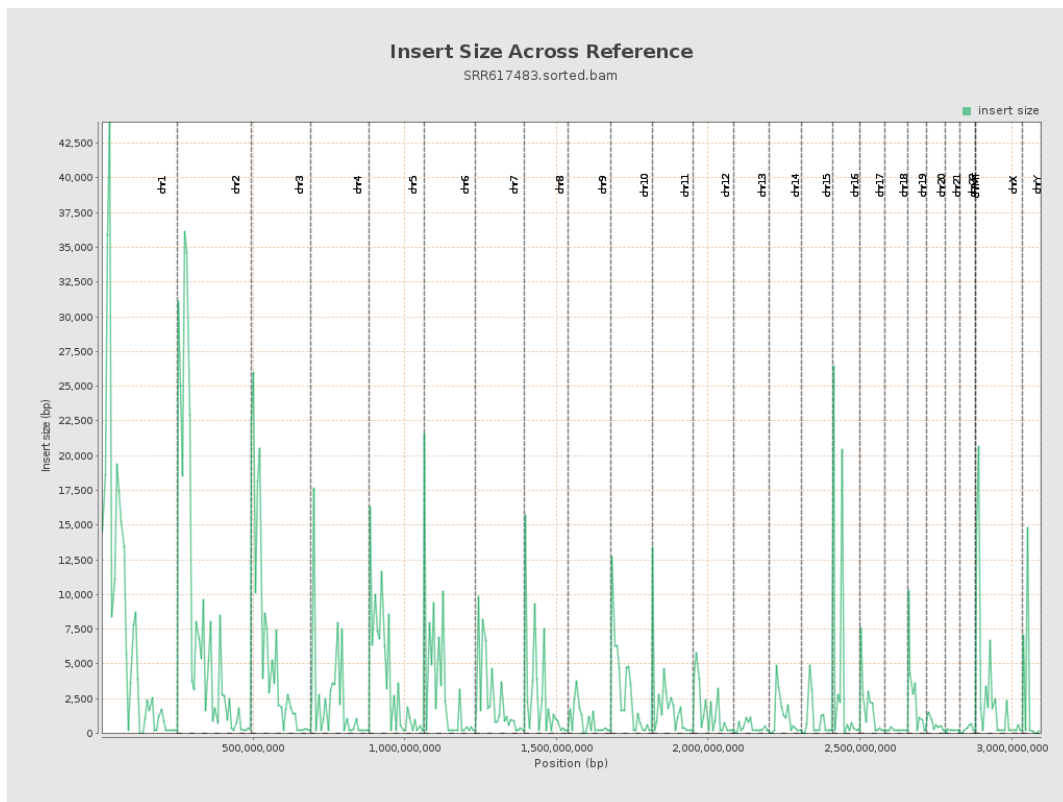
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

