

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 02:56:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472583.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_SRR3472583 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472583_1.fastq.gz SRR3472583_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 02:56:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472583.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,266,670
Mapped reads	9,369,521 / 91.26%
Unmapped reads	897,149 / 8.74%
Mapped paired reads	9,369,521 / 91.26%
Mapped reads, first in pair	4,724,488 / 46.02%
Mapped reads, second in pair	4,645,033 / 45.24%
Mapped reads, both in pair	9,154,932 / 89.17%
Mapped reads, singletons	214,589 / 2.09%
Secondary alignments	0
Supplementary alignments	286,326 / 2.79%
Read min/max/mean length	30 / 100 / 101.08
Duplicated reads (estimated)	1,597,882 / 15.56%
Duplication rate	14.72%
Clipped reads	7,250,994 / 70.63%

2.2. ACGT Content

Number/percentage of A's	195,155,907 / 25.8%
Number/percentage of C's	151,419,616 / 20.02%
Number/percentage of T's	224,935,583 / 29.73%
Number/percentage of G's	184,488,479 / 24.39%
Number/percentage of N's	503,612 / 0.07%

GC Percentage	44.4%
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2.3. Coverage

Mean	0.2445
Standard Deviation	2.3737

2.4. Mapping Quality

Mean Mapping Quality	50.49
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2.5. Insert size

Mean	217,045.61
Standard Deviation	4,492,447.93
P25/Median/P75	88 / 126 / 173

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	9,023,889
Insertions	71,969
Mapped reads with at least one insertion	0.75%
Deletions	171,939
Mapped reads with at least one deletion	1.8%
Homopolymer indels	42.56%

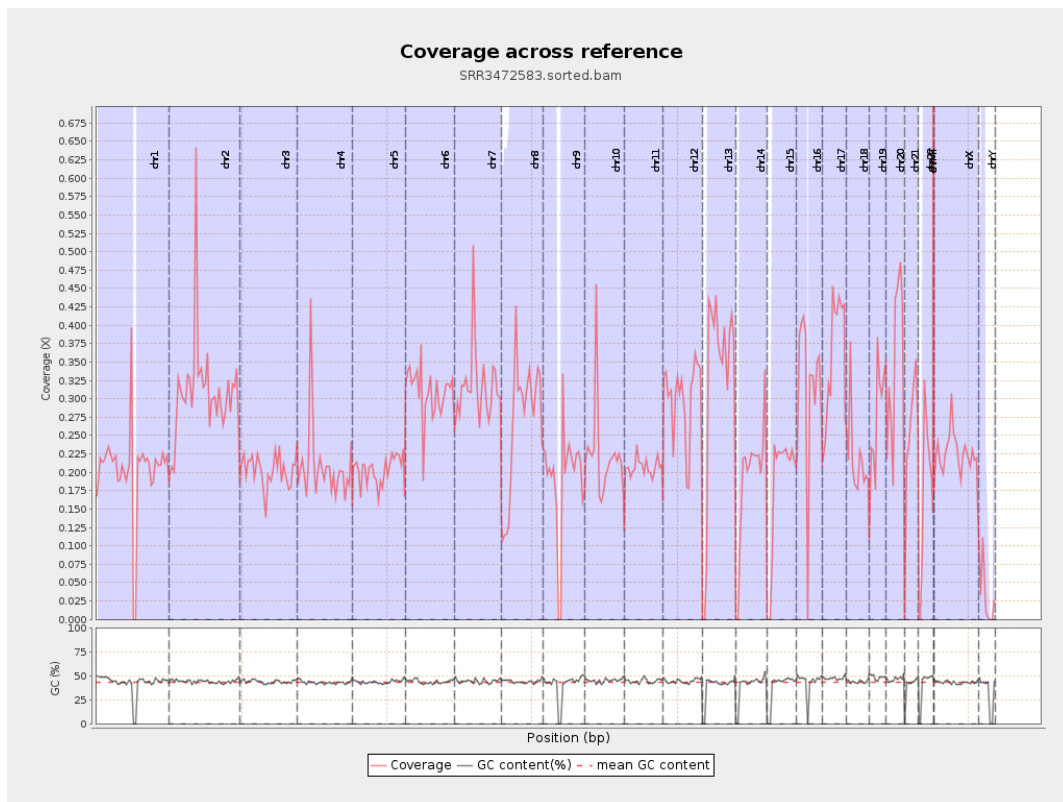
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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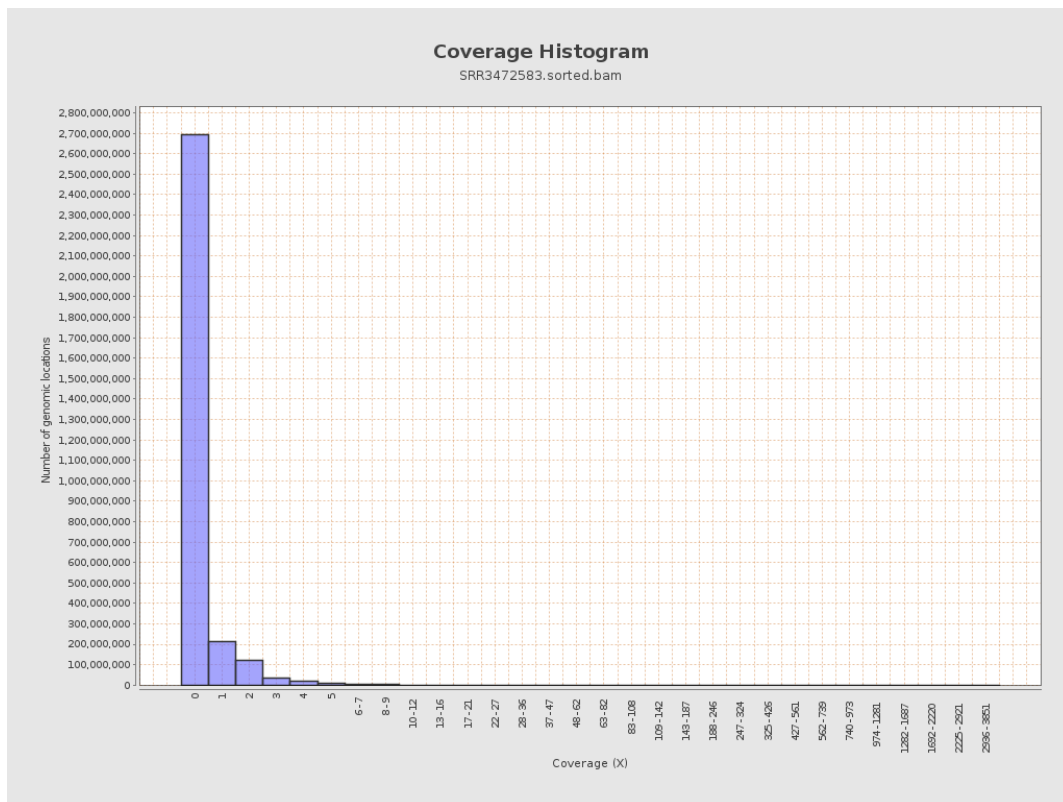
		bases	coverage	deviation
chr1	249250621	50634039	0.2031	3.5265
chr2	243199373	75101160	0.3088	2.75
chr3	198022430	40040487	0.2022	0.6931
chr4	191154276	39425964	0.2063	1.3519
chr5	180915260	36697713	0.2028	0.7488
chr6	171115067	52869453	0.309	1.3911
chr7	159138663	50739716	0.3188	3.7124
chr8	146364022	38995484	0.2664	2.0954
chr9	141213431	26877796	0.1903	2.5537
chr10	135534747	30066184	0.2218	2.4383
chr11	135006516	27704678	0.2052	1.7574
chr12	133851895	40070575	0.2994	0.8912
chr13	115169878	37225748	0.3232	0.9314
chr14	107349540	20507745	0.191	5.6085
chr15	102531392	18721970	0.1826	0.6685
chr16	90354753	28518583	0.3156	1.3611
chr17	81195210	29424405	0.3624	2.0416
chr18	78077248	17304276	0.2216	4.6177
chr19	59128983	16459943	0.2784	2.4338
chr20	63025520	21839287	0.3465	1.4706
chr21	48129895	12140506	0.2522	1.0512
chr22	51304566	8610817	0.1678	0.6564
chrMT	16571	25165	1.5186	4.6411
chrX	155270560	35009834	0.2255	1.1315

chrY	59373566	1813505	0.0305	1.1183
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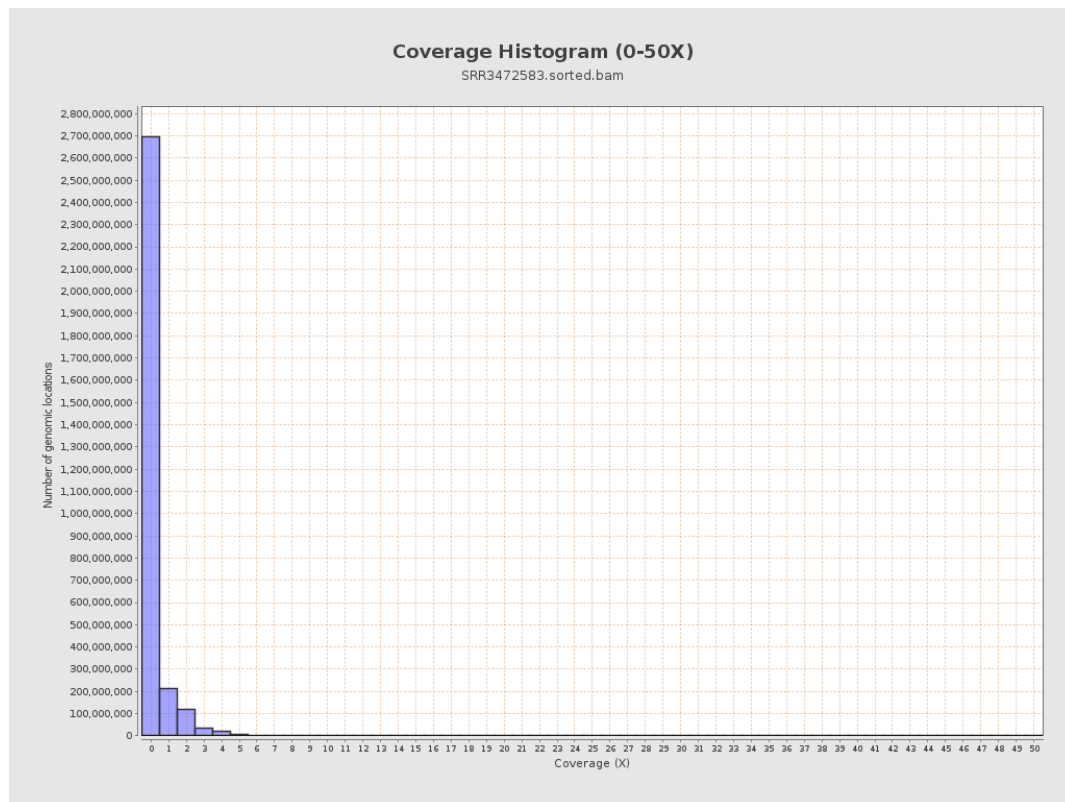
3. Results : Coverage across reference



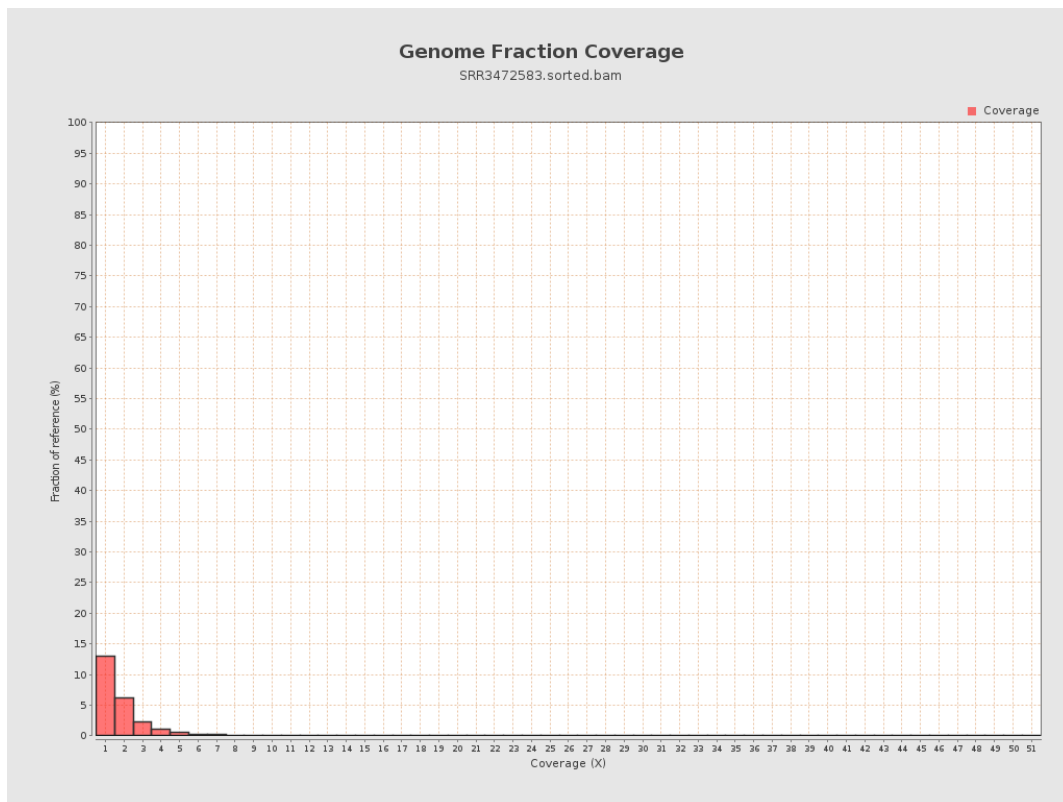
4. Results : Coverage Histogram



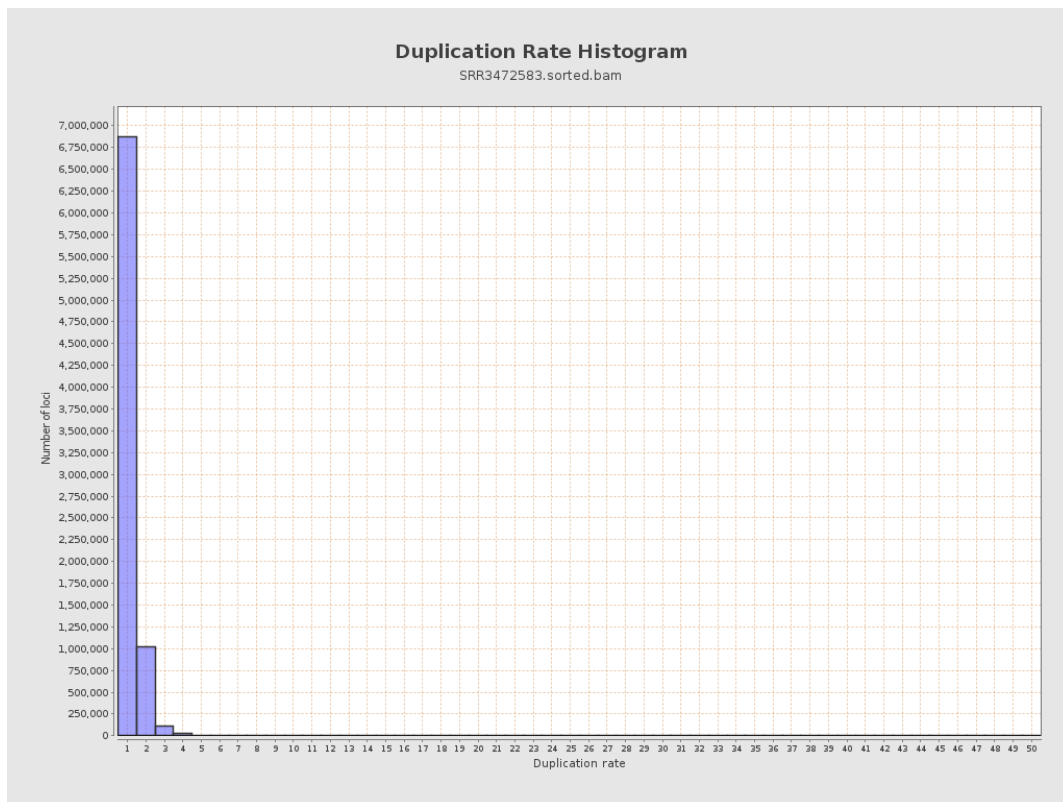
5. Results : Coverage Histogram (0-50X)



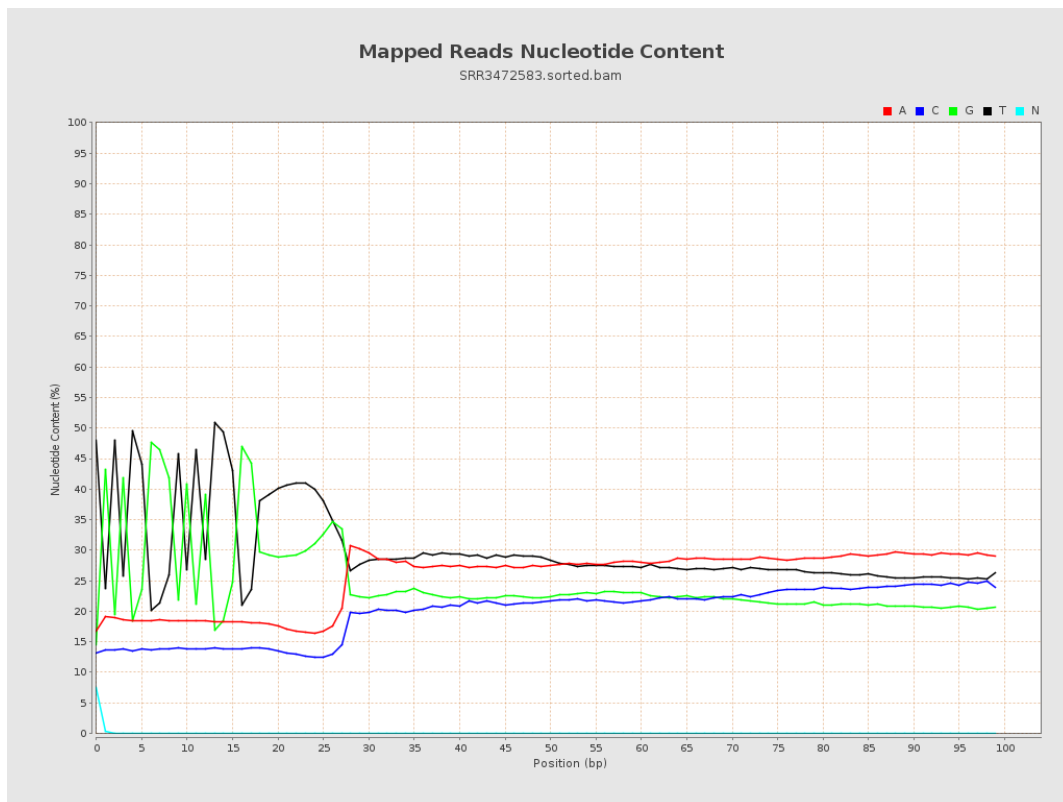
6. Results : Genome Fraction Coverage



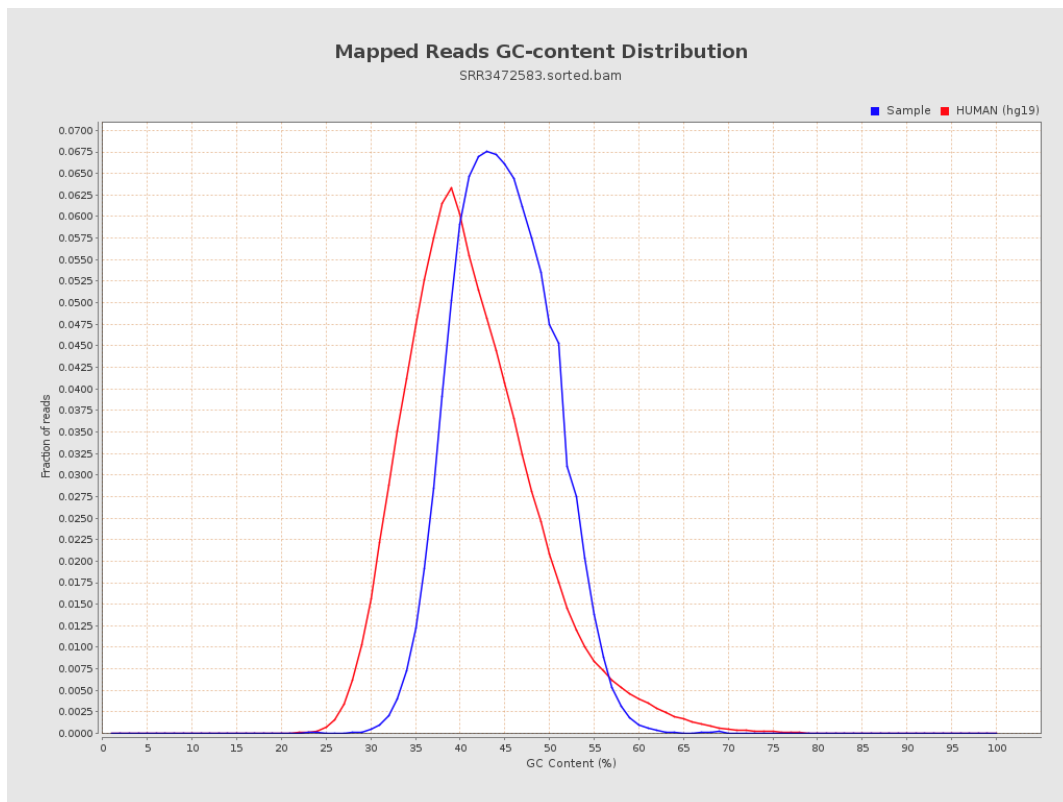
7. Results : Duplication Rate Histogram



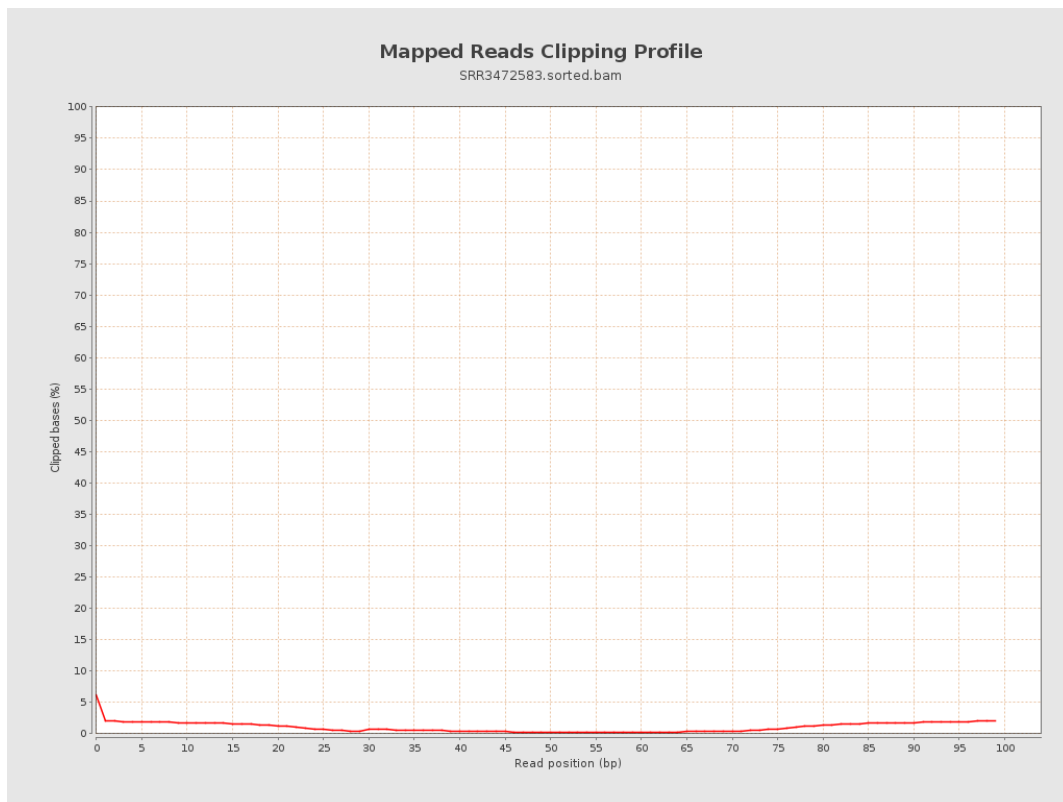
8. Results : Mapped Reads Nucleotide Content



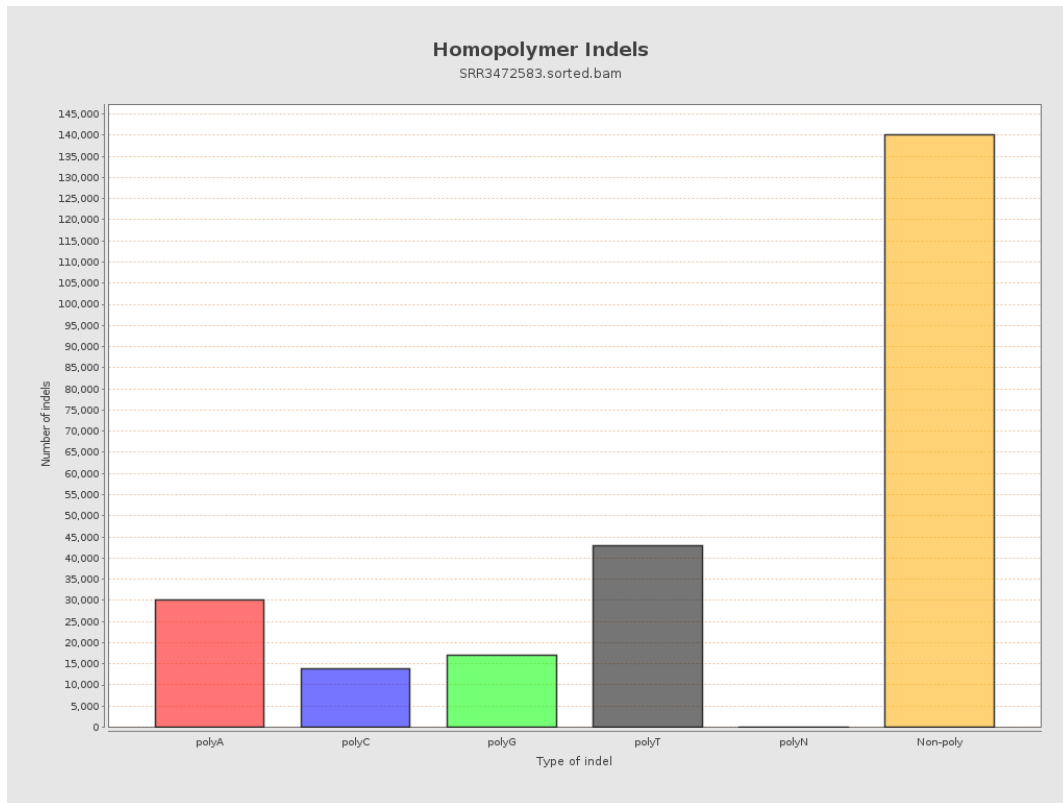
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



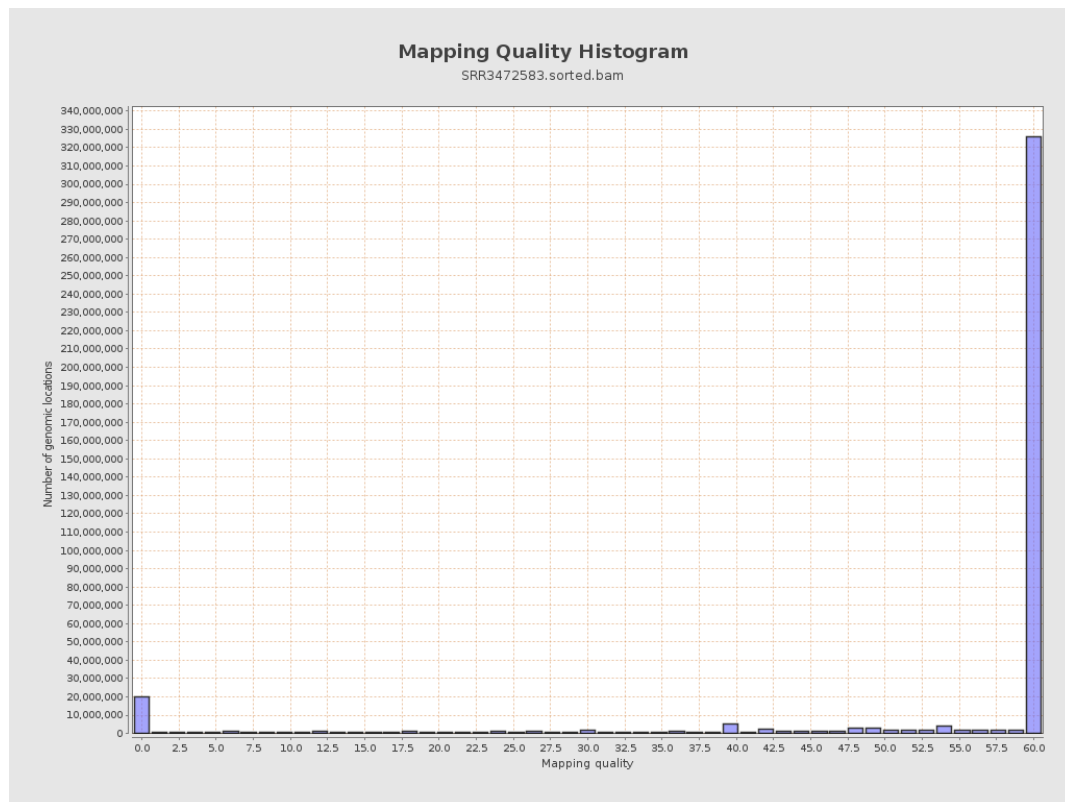
11. Results : Homopolymer Indels



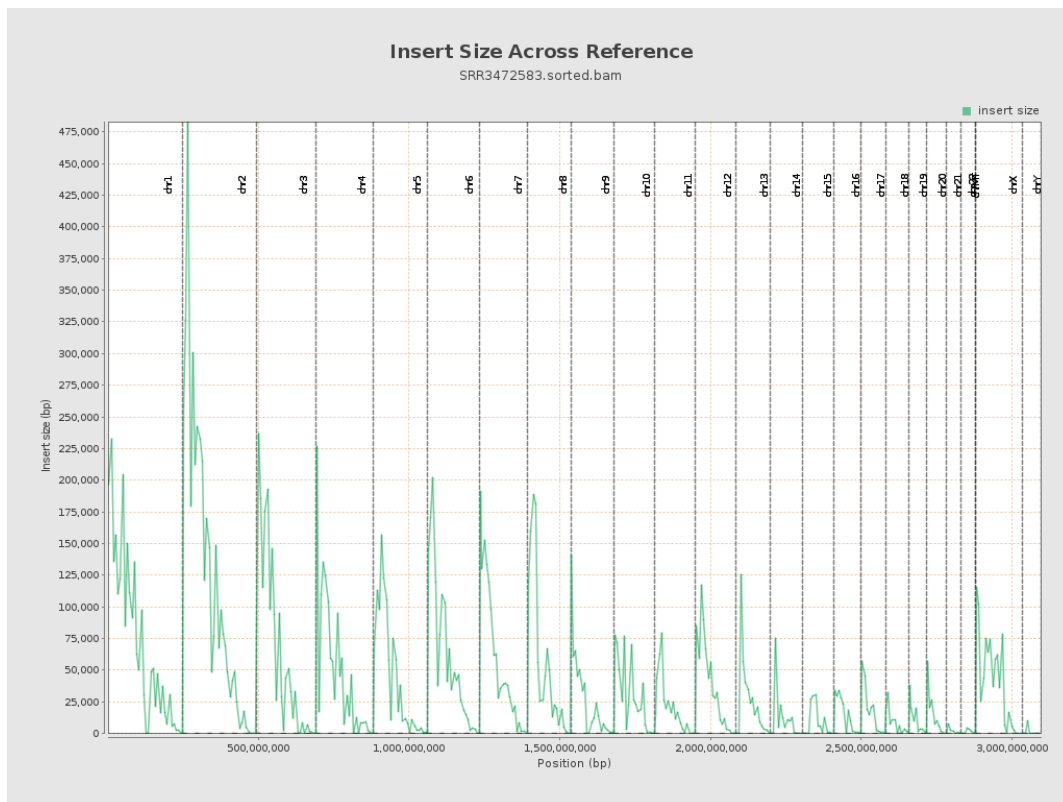
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

