

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/27 00:47:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432717.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_SRR6432717 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432717_1.fastq.gz SRR6432717_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 27 00:47:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432717.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	367,188,438
Mapped reads	367,054,179 / 99.96%
Unmapped reads	134,259 / 0.04%
Mapped paired reads	367,054,179 / 99.96%
Mapped reads, first in pair	183,529,510 / 49.98%
Mapped reads, second in pair	183,524,669 / 49.98%
Mapped reads, both in pair	367,004,126 / 99.95%
Mapped reads, singletons	50,053 / 0.01%
Secondary alignments	0
Supplementary alignments	2,672,236 / 0.73%
Read min/max/mean length	30 / 150 / 142.83
Duplicated reads (estimated)	184,083,392 / 50.13%
Duplication rate	34.26%
Clipped reads	72,431,462 / 19.73%

2.2. ACGT Content

Number/percentage of A's	14,482,589,413 / 28.01%
Number/percentage of C's	10,967,899,908 / 21.21%
Number/percentage of T's	14,322,097,980 / 27.7%
Number/percentage of G's	11,919,341,476 / 23.05%
Number/percentage of N's	7,876,923 / 0.02%

GC Percentage	44.27%
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2.3. Coverage

Mean	16.718
Standard Deviation	54.5817

2.4. Mapping Quality

Mean Mapping Quality	57.31
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2.5. Insert size

Mean	38,838.75
Standard Deviation	1,979,655.12
P25/Median/P75	302 / 322 / 340

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	380,348,971
Insertions	11,263,895
Mapped reads with at least one insertion	3.01%
Deletions	38,416,986
Mapped reads with at least one deletion	9.94%
Homopolymer indels	53.58%

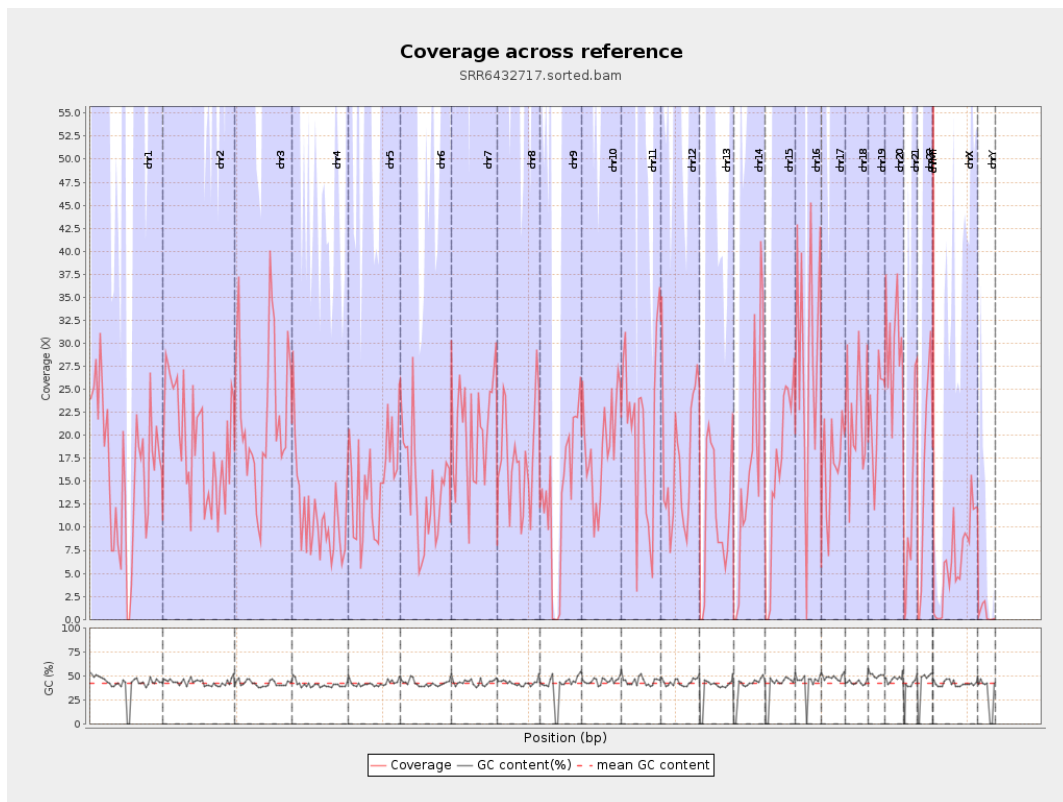
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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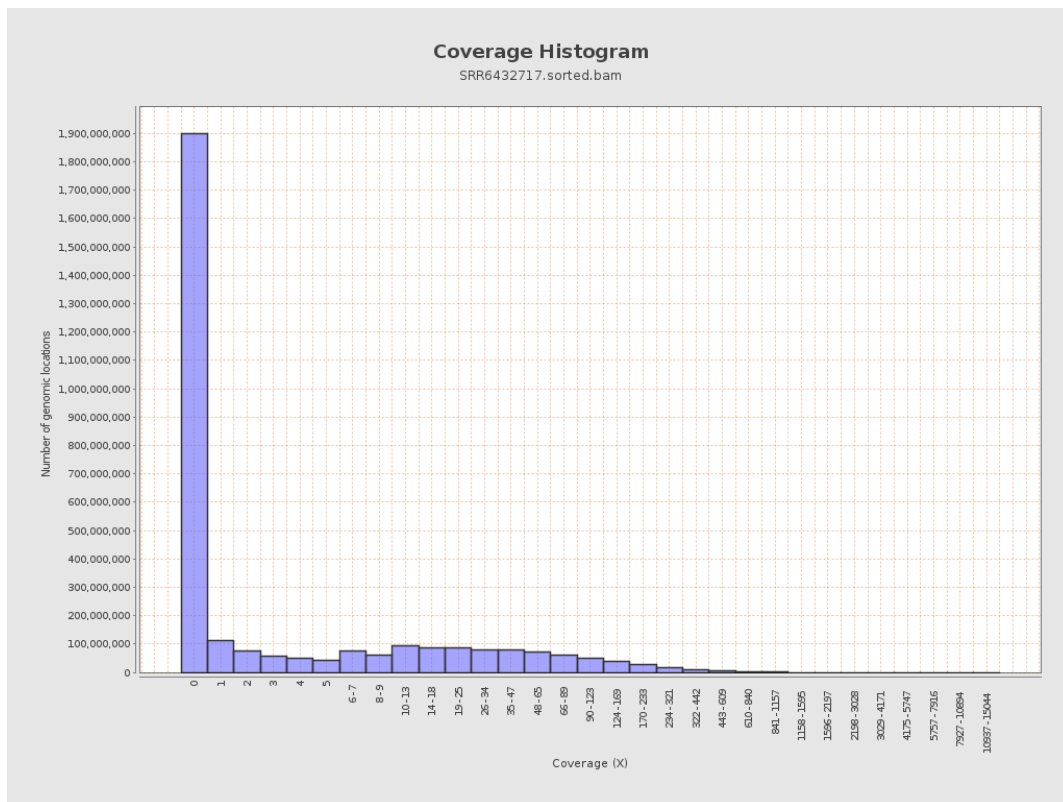
		bases	coverage	deviation
chr1	249250621	4042223719	16.2175	52.6734
chr2	243199373	4666805829	19.1892	60.723
chr3	198022430	4333567138	21.8842	63.129
chr4	191154276	2145421471	11.2235	39.0856
chr5	180915260	2694323555	14.8927	47.0463
chr6	171115067	2387286114	13.9513	45.8355
chr7	159138663	3313466897	20.8213	61.6199
chr8	146364022	2582045882	17.6413	52.8178
chr9	141213431	1898439622	13.4438	46.3213
chr10	135534747	2515064367	18.5566	54.5834
chr11	135006516	2790430454	20.6689	62.5381
chr12	133851895	2352114758	17.5725	53.7635
chr13	115169878	1286057377	11.1666	41.0036
chr14	107349540	1768318288	16.4725	55.5428
chr15	102531392	1655704478	16.1483	52.9245
chr16	90354753	2588967321	28.6534	85.0235
chr17	81195210	1374466350	16.9279	53.0481
chr18	78077248	1698555610	21.7548	62.8316
chr19	59128983	1304991976	22.0703	66.9858
chr20	63025520	1874575753	29.7431	78.3651
chr21	48129895	604007346	12.5495	47.2095
chr22	51304566	838120937	16.3362	56.1473
chrMT	16571	5660034	341.5626	526.438
chrX	155270560	992744334	6.3936	29.0372

chrY	59373566	40478730	0.6818	15.1179
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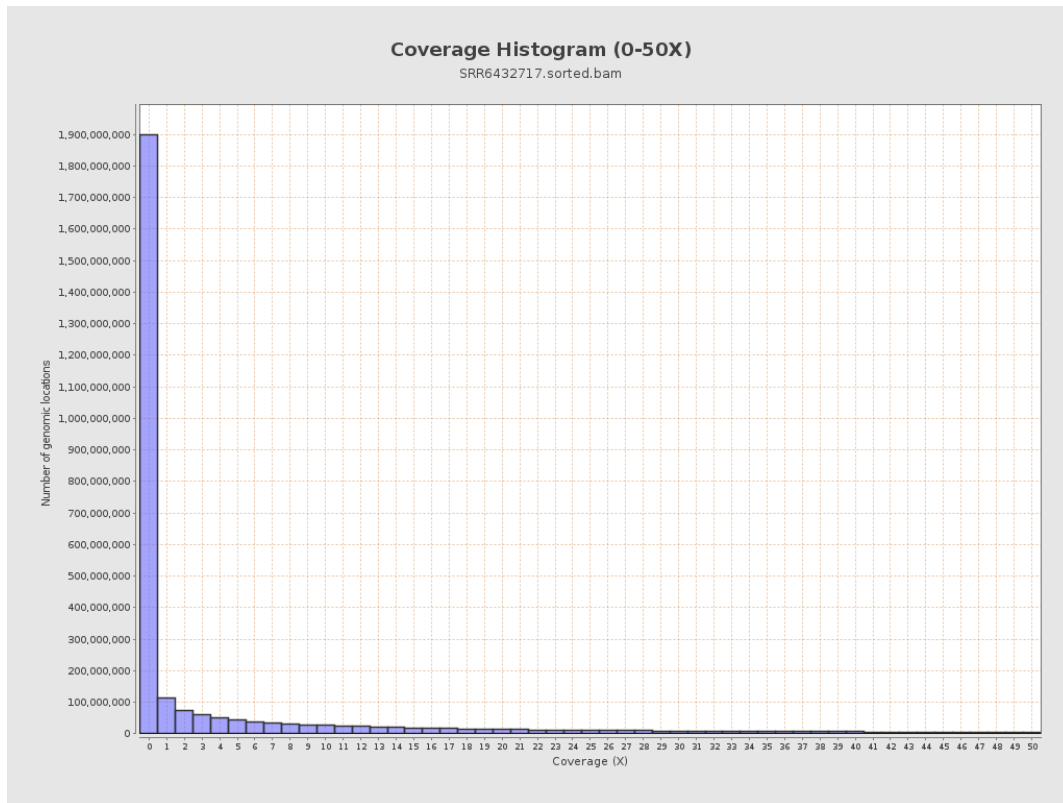
3. Results : Coverage across reference



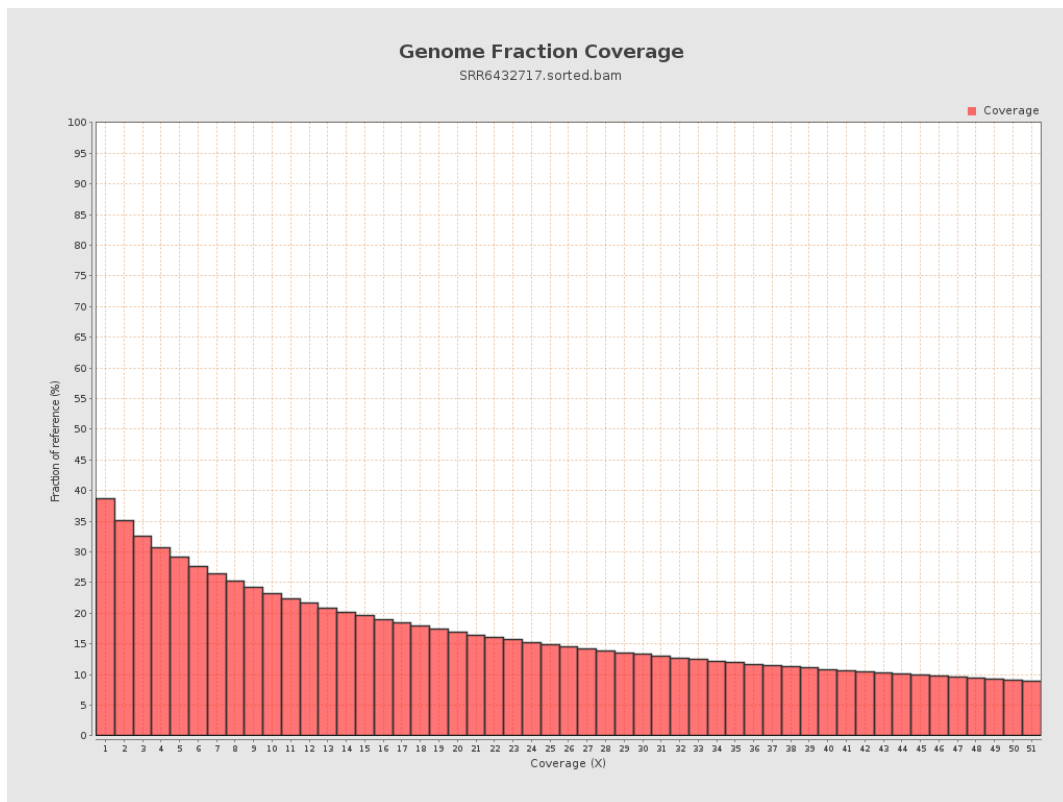
4. Results : Coverage Histogram



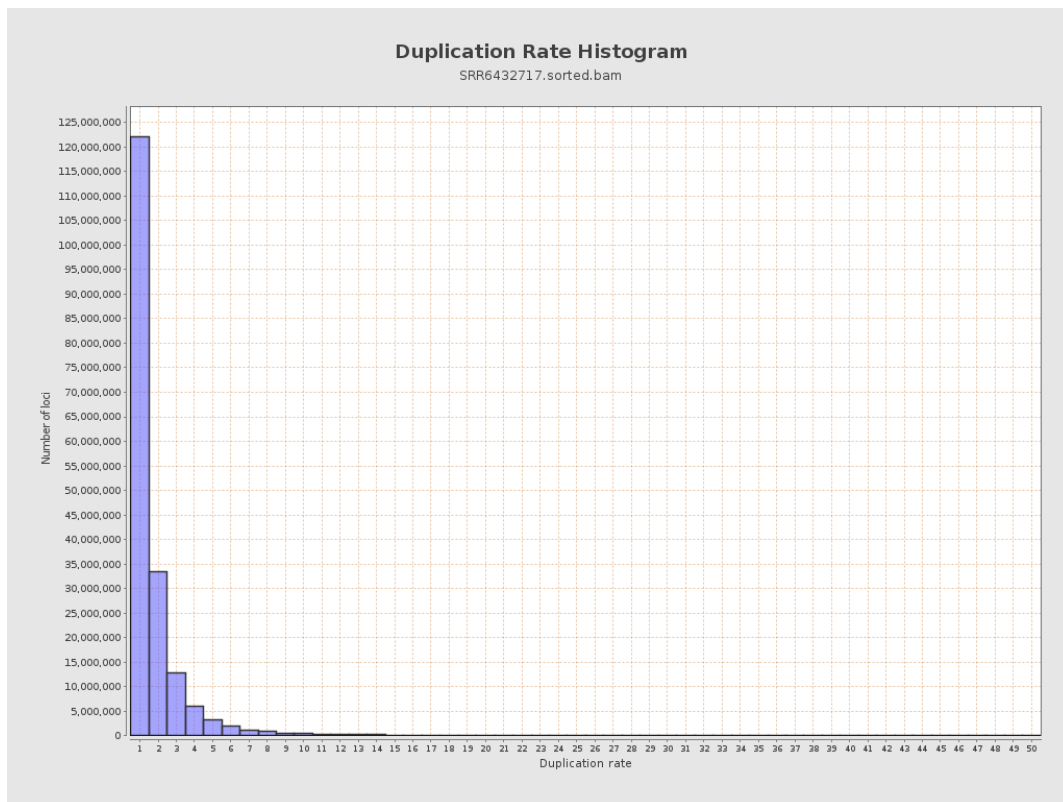
5. Results : Coverage Histogram (0-50X)



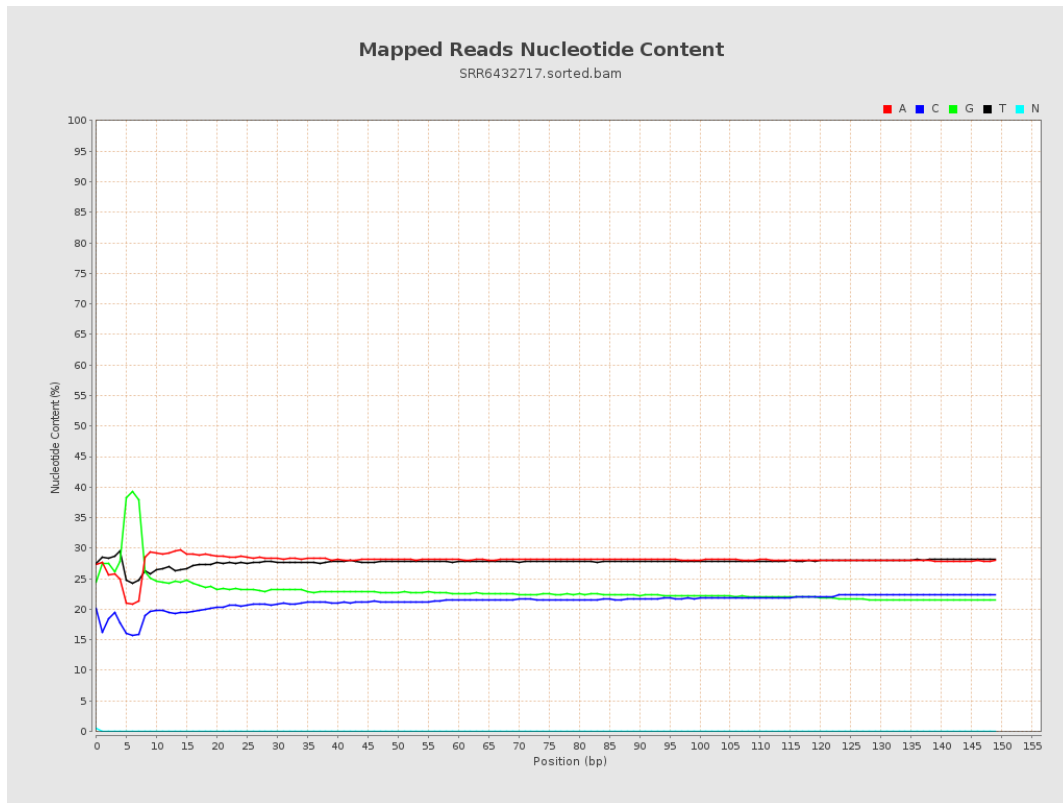
6. Results : Genome Fraction Coverage



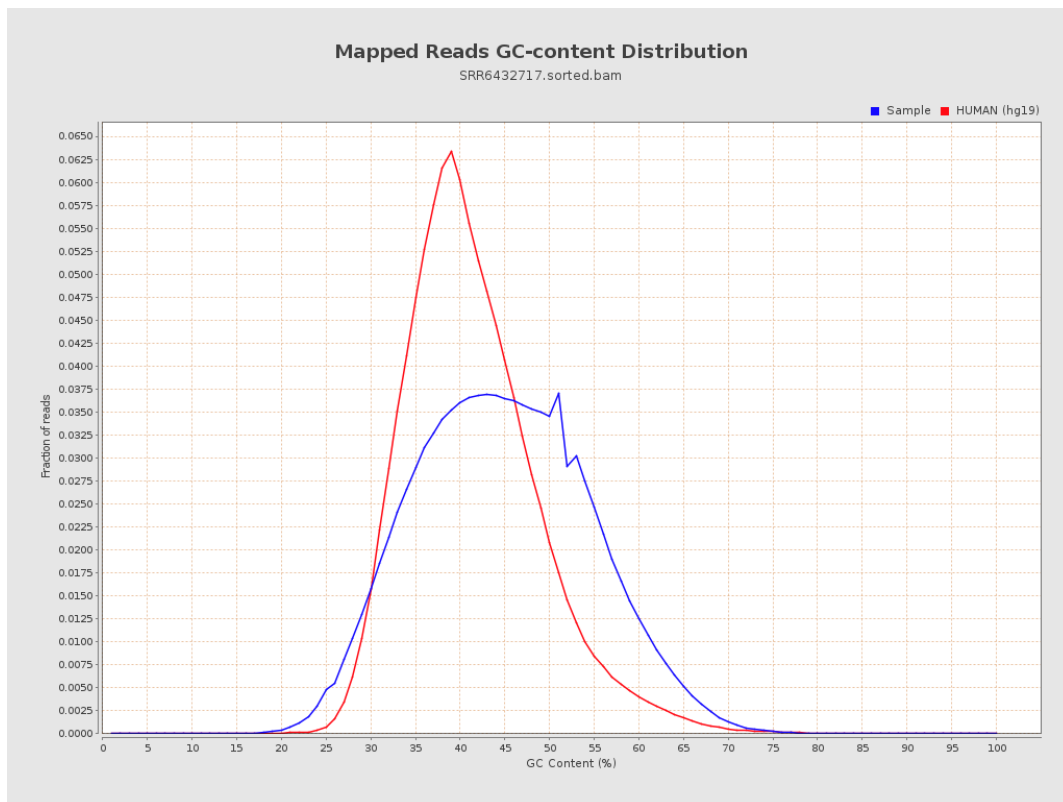
7. Results : Duplication Rate Histogram



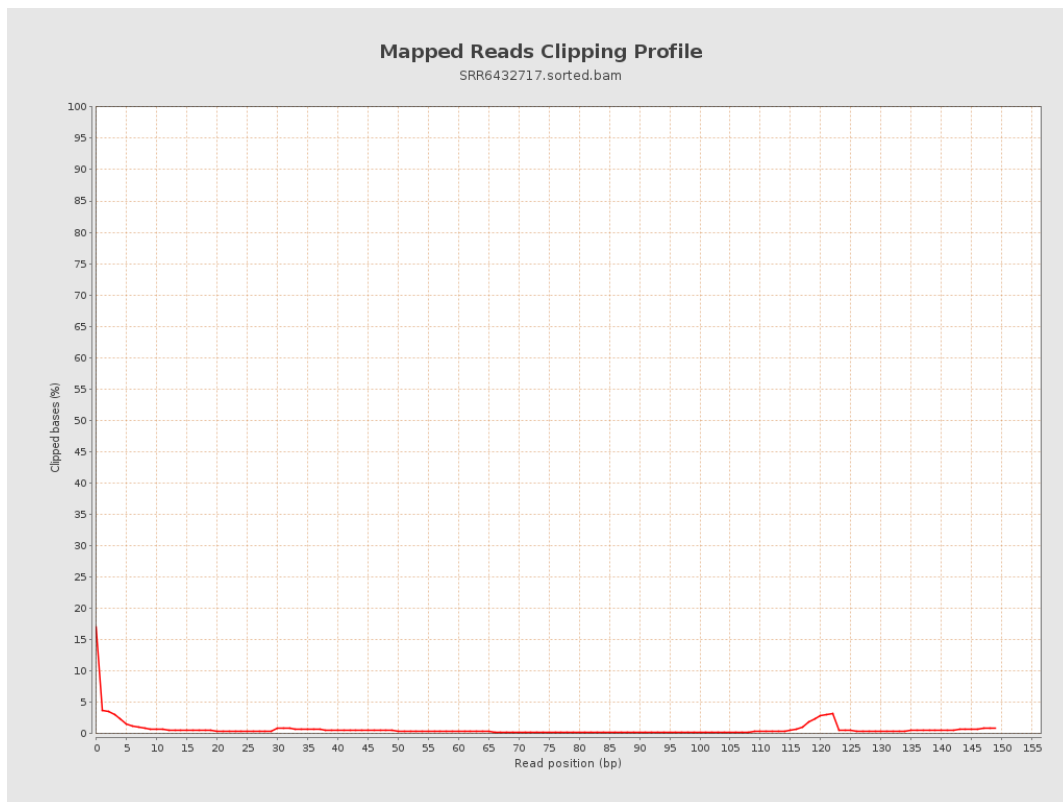
8. Results : Mapped Reads Nucleotide Content



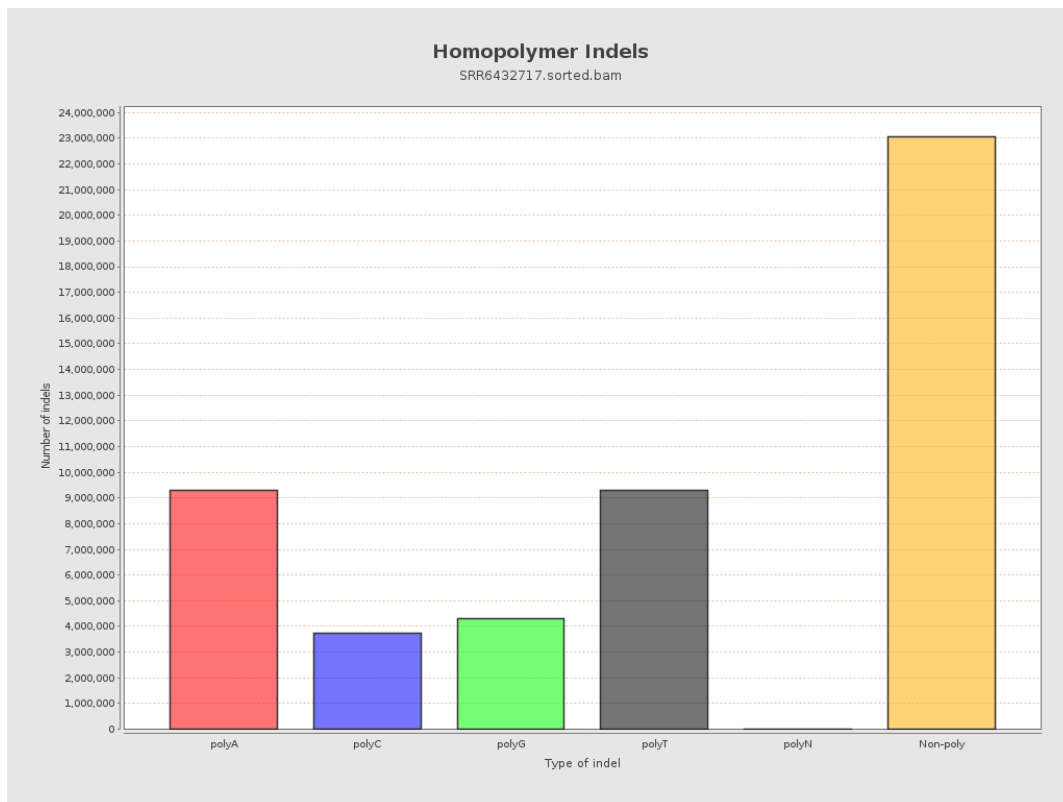
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



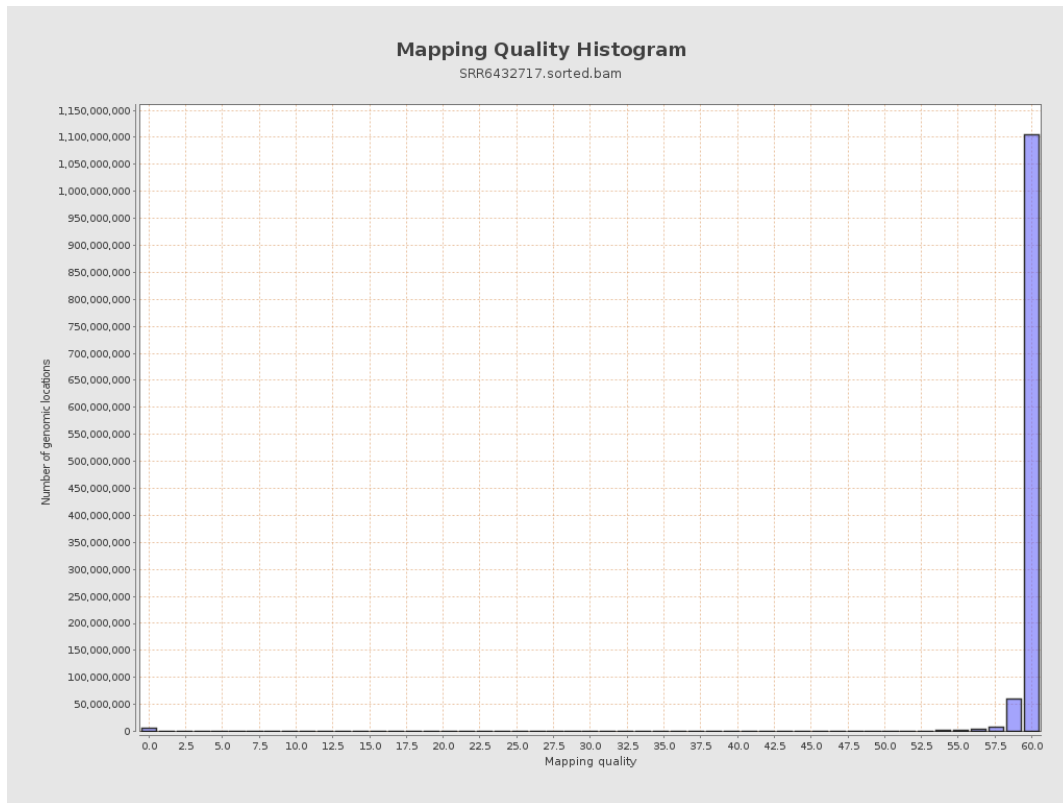
11. Results : Homopolymer Indels



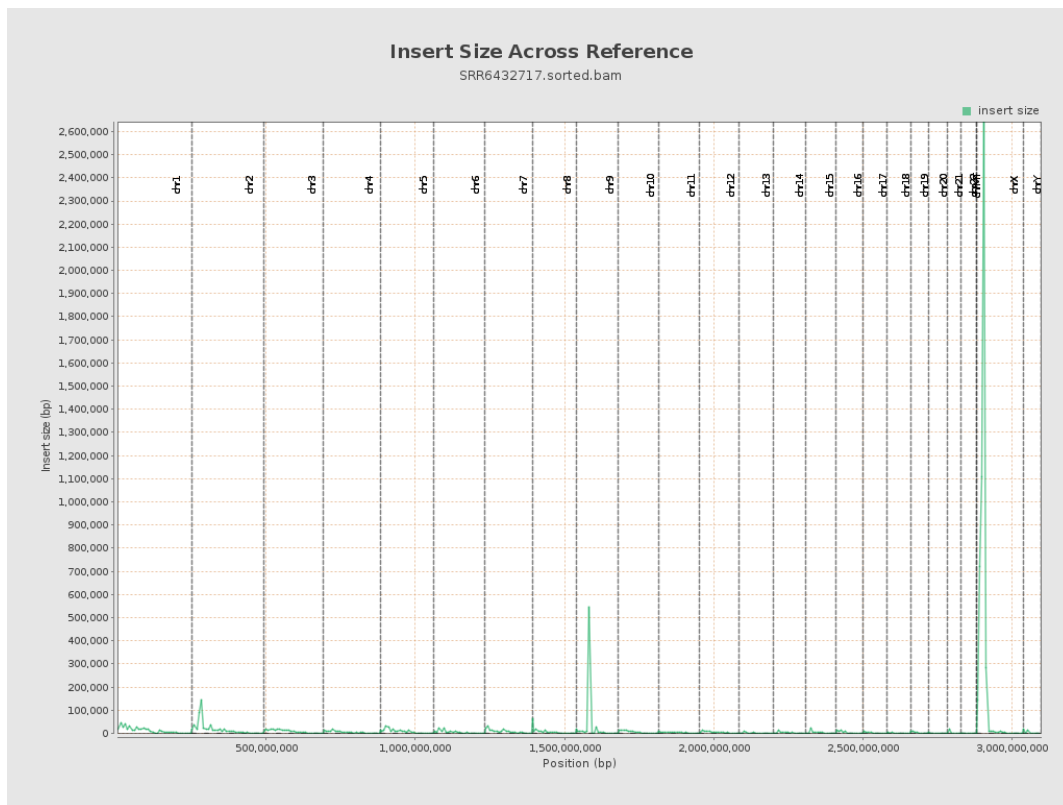
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

