

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/27 17:01:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432719.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_SRR6432719 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432719_1.fastq.gz SRR6432719_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 27 17:01:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432719.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	382,970,880
Mapped reads	382,837,886 / 99.97%
Unmapped reads	132,994 / 0.03%
Mapped paired reads	382,837,886 / 99.97%
Mapped reads, first in pair	191,422,159 / 49.98%
Mapped reads, second in pair	191,415,727 / 49.98%
Mapped reads, both in pair	382,789,018 / 99.95%
Mapped reads, singletons	48,868 / 0.01%
Secondary alignments	0
Supplementary alignments	161,075 / 0.04%
Read min/max/mean length	30 / 150 / 140.24
Duplicated reads (estimated)	184,752,394 / 48.24%
Duplication rate	31.84%
Clipped reads	99,682,109 / 26.03%

2.2. ACGT Content

Number/percentage of A's	14,462,318,217 / 27.42%
Number/percentage of C's	11,405,623,235 / 21.63%
Number/percentage of T's	14,266,570,868 / 27.05%
Number/percentage of G's	12,596,865,324 / 23.89%
Number/percentage of N's	2,892,576 / 0.01%

GC Percentage	45.52%
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2.3. Coverage

Mean	17.0514
Standard Deviation	48.8972

2.4. Mapping Quality

Mean Mapping Quality	55.47
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2.5. Insert size

Mean	72,594.06
Standard Deviation	2,724,582.59
P25/Median/P75	291 / 307 / 323

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	467,630,699
Insertions	10,718,717
Mapped reads with at least one insertion	2.74%
Deletions	35,805,678
Mapped reads with at least one deletion	8.92%
Homopolymer indels	51.87%

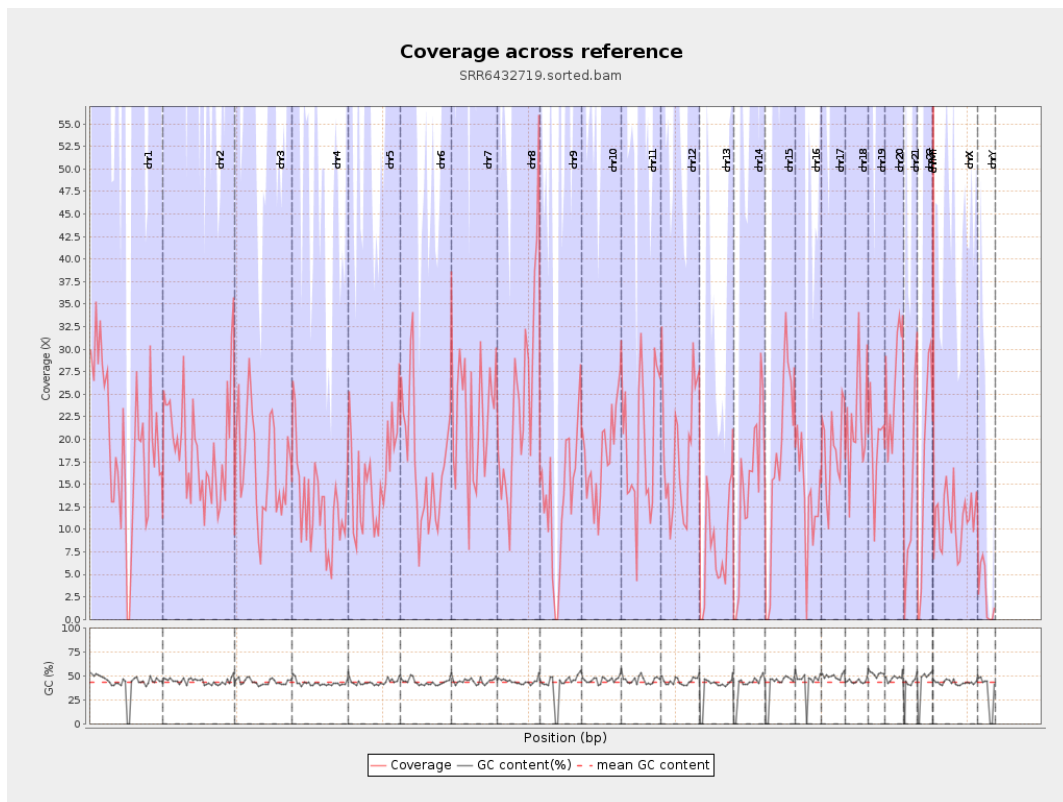
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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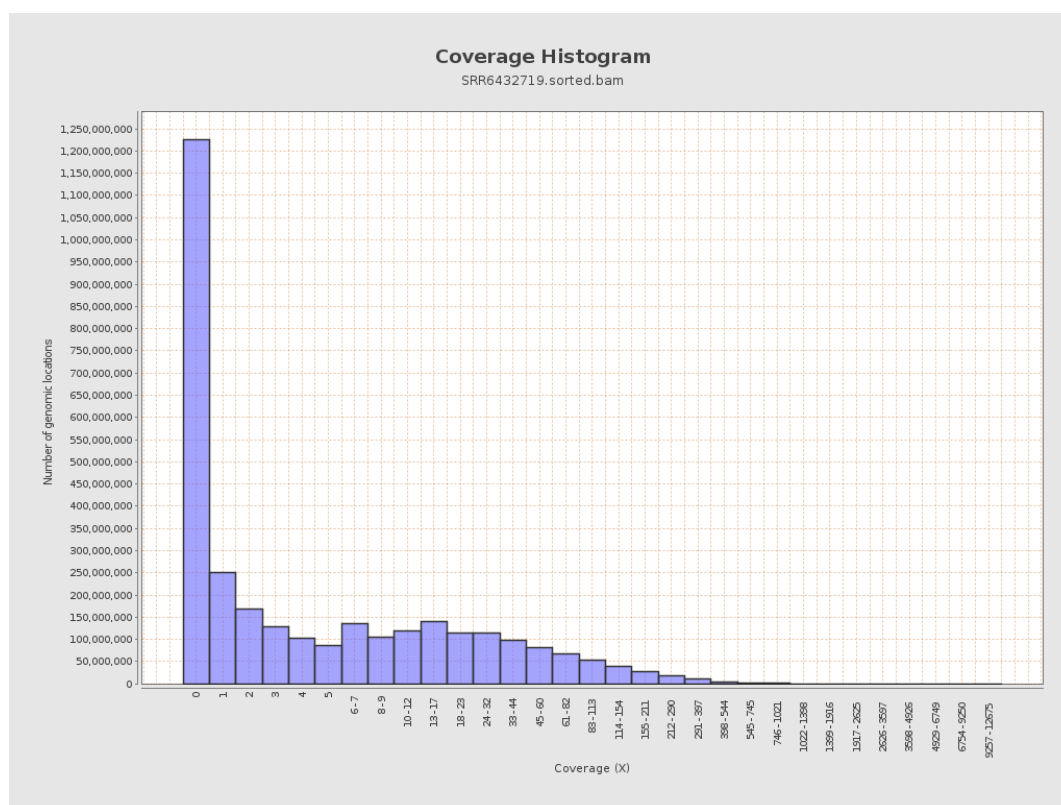
		bases	coverage	deviation
chr1	249250621	4843914891	19.4339	53.9452
chr2	243199373	4634721064	19.0573	54.0789
chr3	198022430	3354252357	16.9387	45.1795
chr4	191154276	2449809247	12.8159	37.7761
chr5	180915260	2908902389	16.0788	44.2005
chr6	171115067	2907349594	16.9906	46.5983
chr7	159138663	3589362553	22.5549	58.7132
chr8	146364022	3553884418	24.2811	65.3014
chr9	141213431	1877267124	13.2938	44.2873
chr10	135534747	2461129117	18.1587	47.4159
chr11	135006516	2641927044	19.5689	51.7119
chr12	133851895	2516529427	18.8009	50.191
chr13	115169878	934073065	8.1104	27.268
chr14	107349540	1586934193	14.7829	43.129
chr15	102531392	1820404846	17.7546	51.0459
chr16	90354753	1242470538	13.751	44.3271
chr17	81195210	1525538055	18.7885	49.3189
chr18	78077248	1685363608	21.5858	58.3456
chr19	59128983	1138584032	19.2559	53.4835
chr20	63025520	1666765667	26.4459	63.6779
chr21	48129895	657436623	13.6596	48.4914
chr22	51304566	877662585	17.1069	50.4281
chrMT	16571	5205735	314.1473	573.4846
chrX	155270560	1730907267	11.1477	31.9456

chrY	59373566	175519654	2.9562	20.6696
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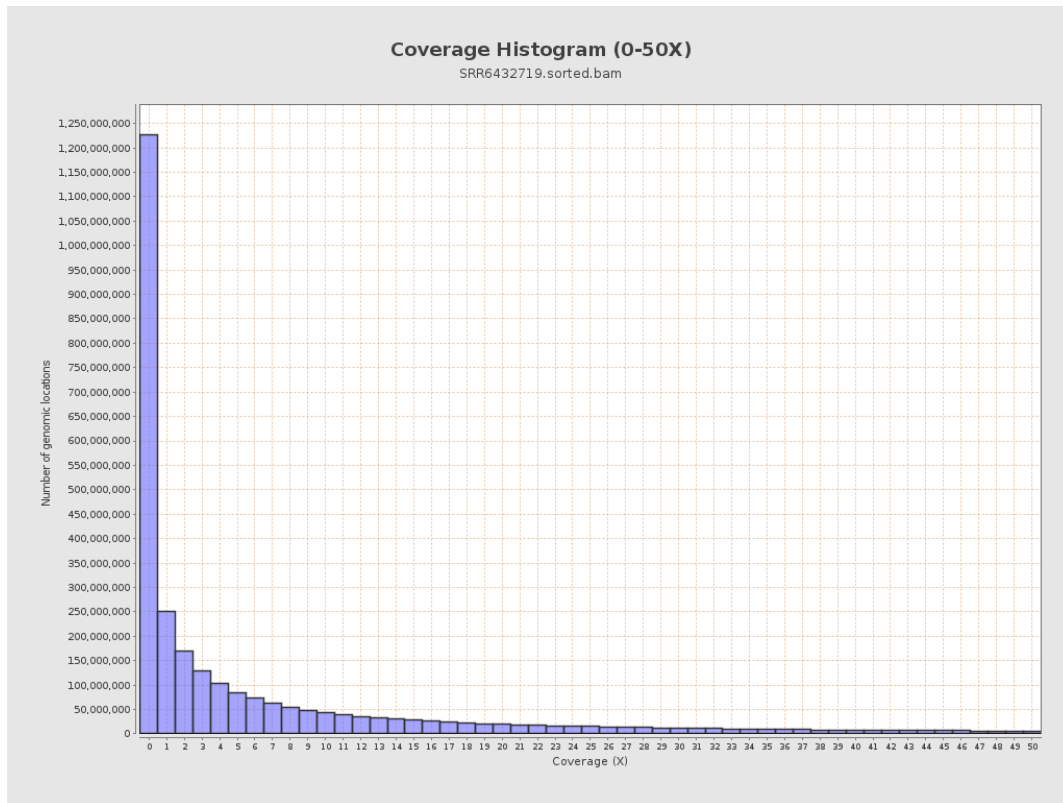
3. Results : Coverage across reference



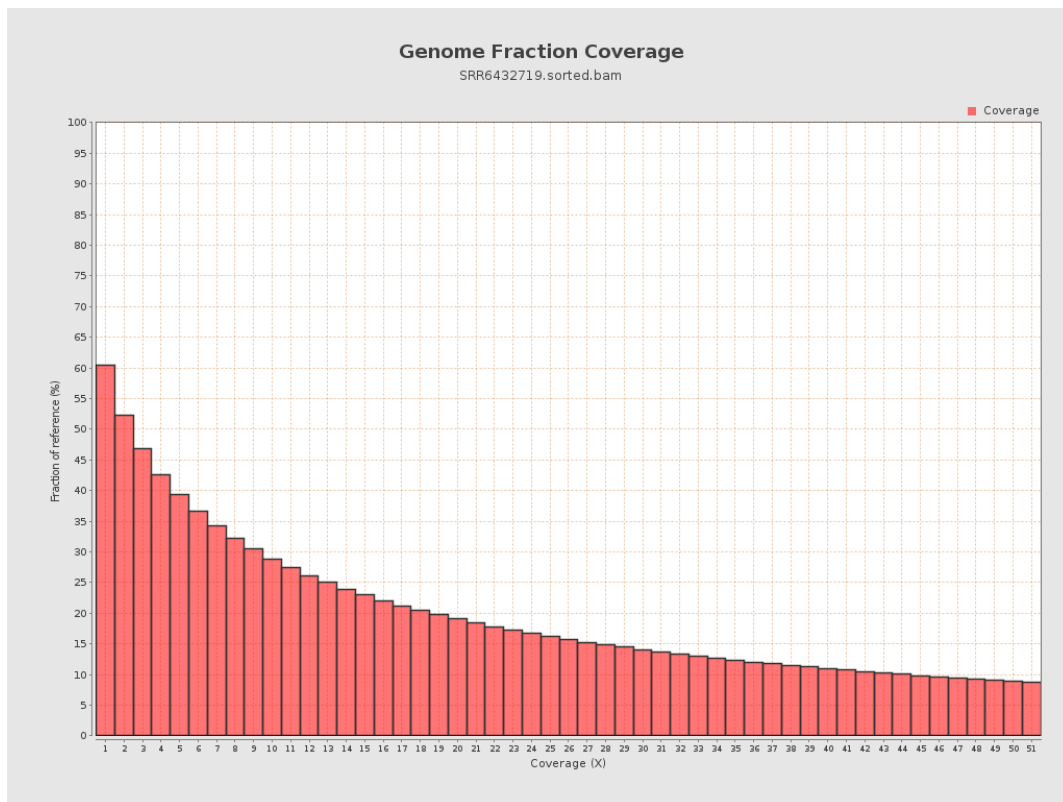
4. Results : Coverage Histogram



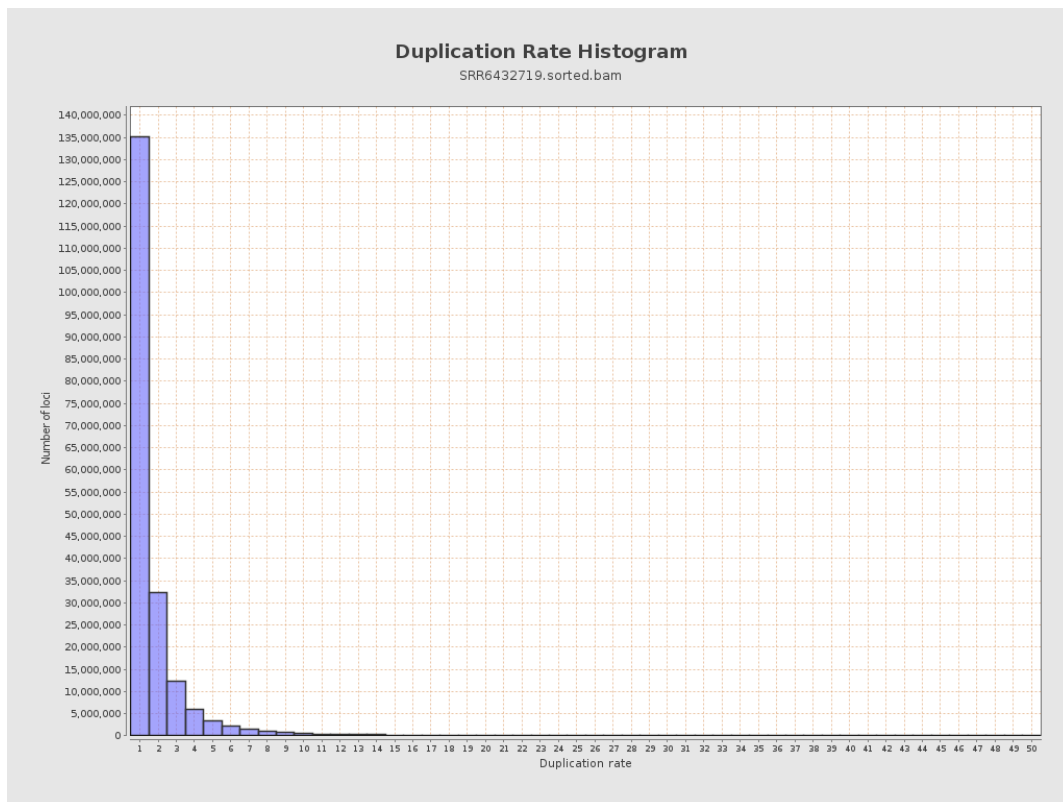
5. Results : Coverage Histogram (0-50X)



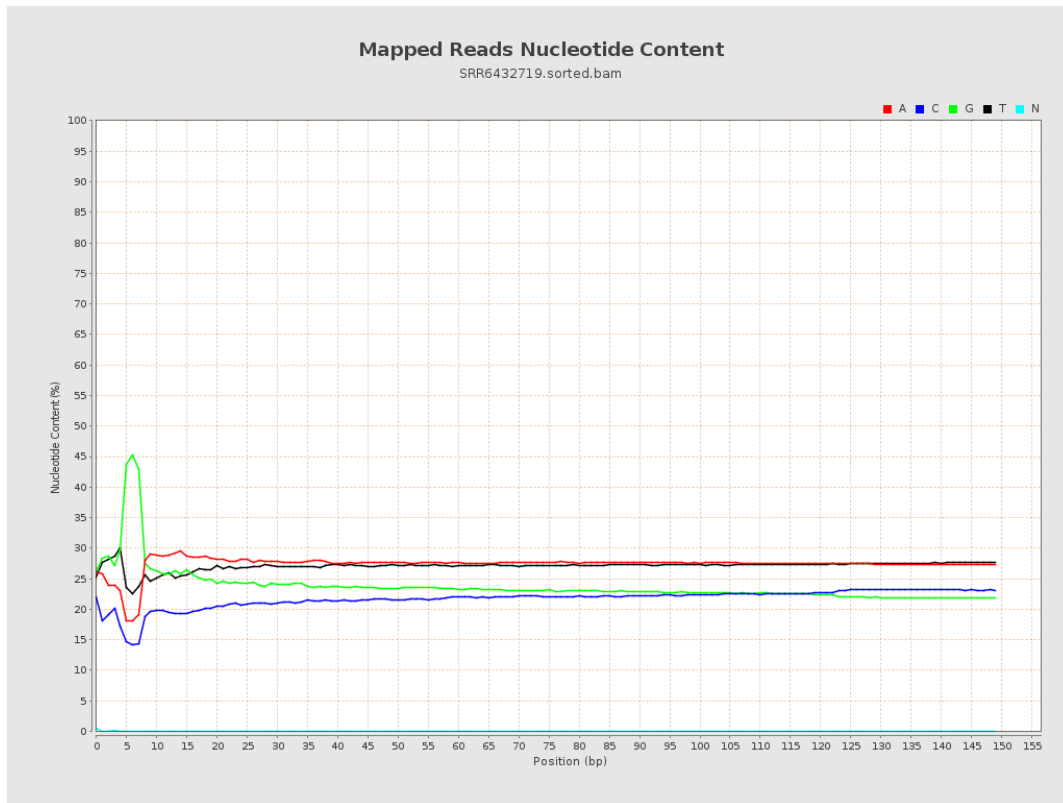
6. Results : Genome Fraction Coverage



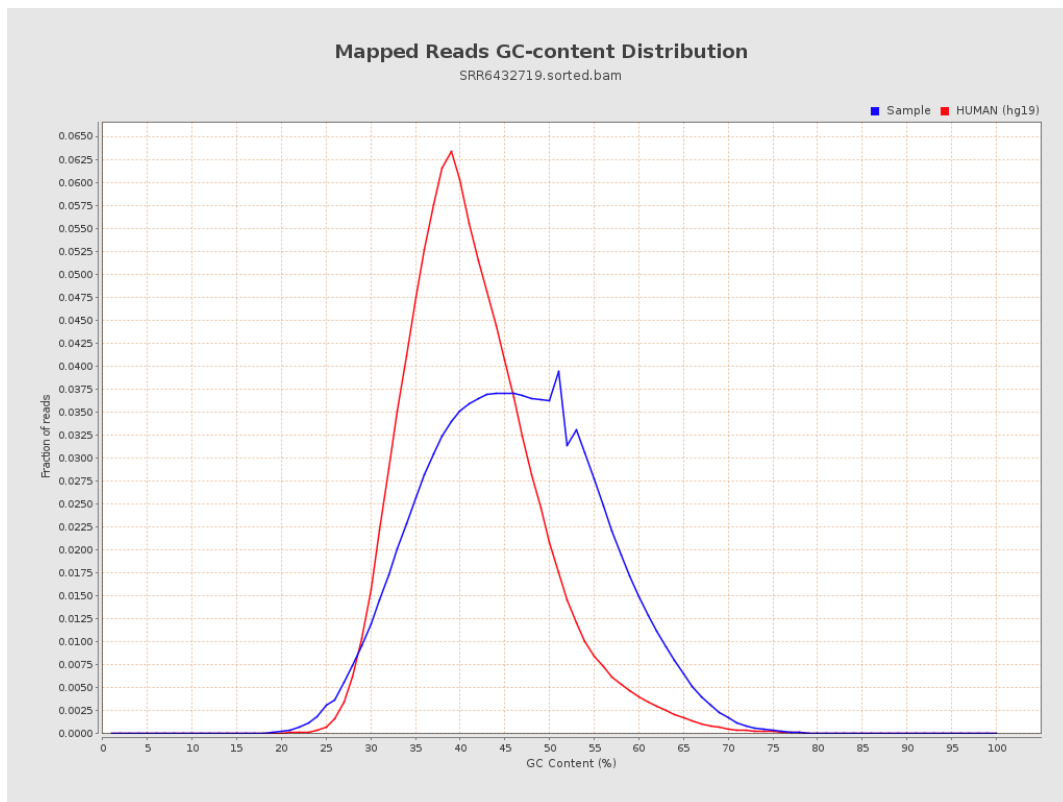
7. Results : Duplication Rate Histogram



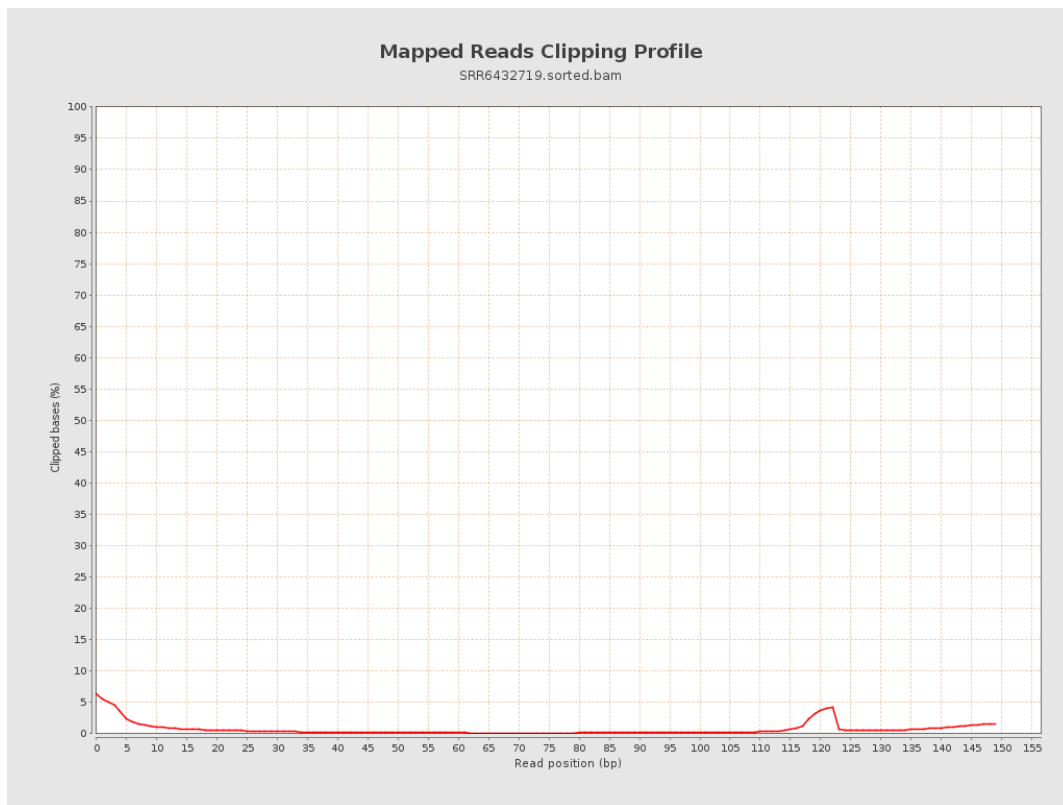
8. Results : Mapped Reads Nucleotide Content



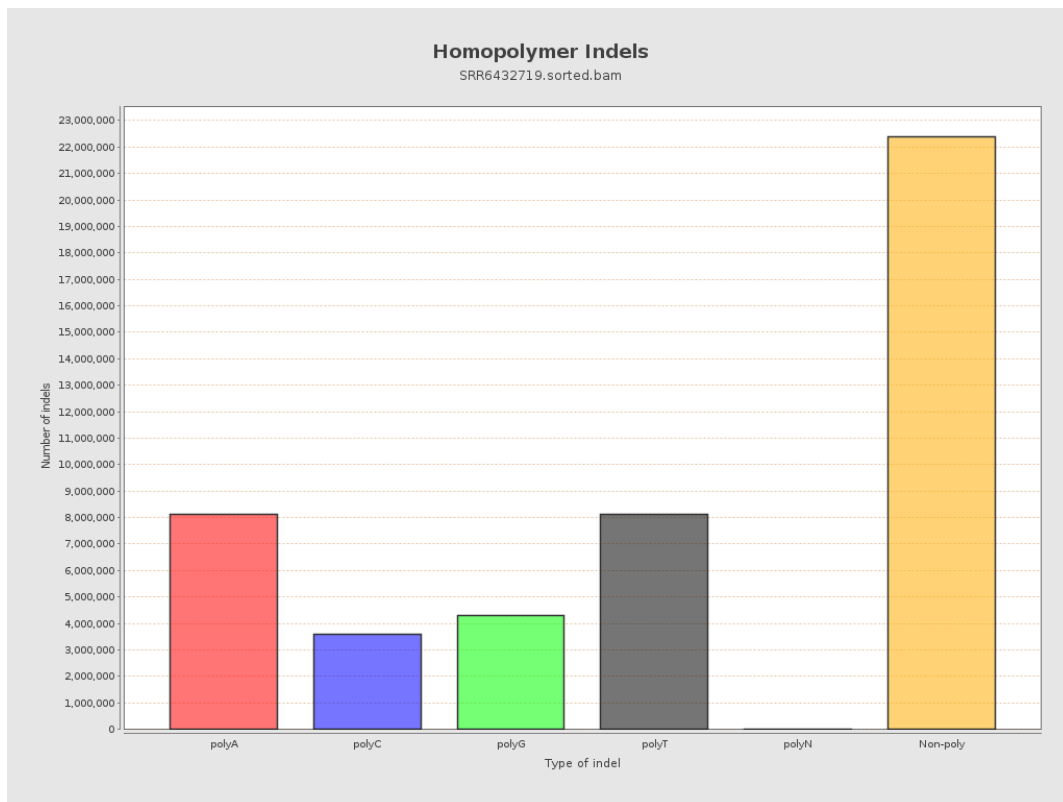
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



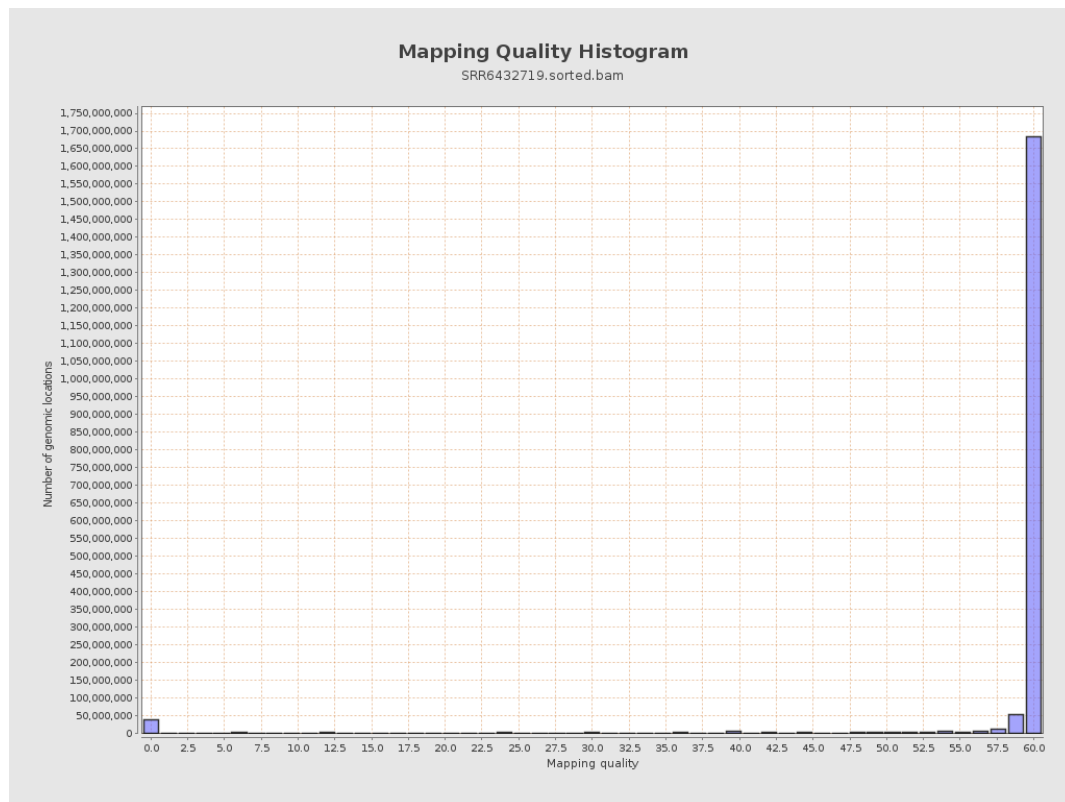
11. Results : Homopolymer Indels



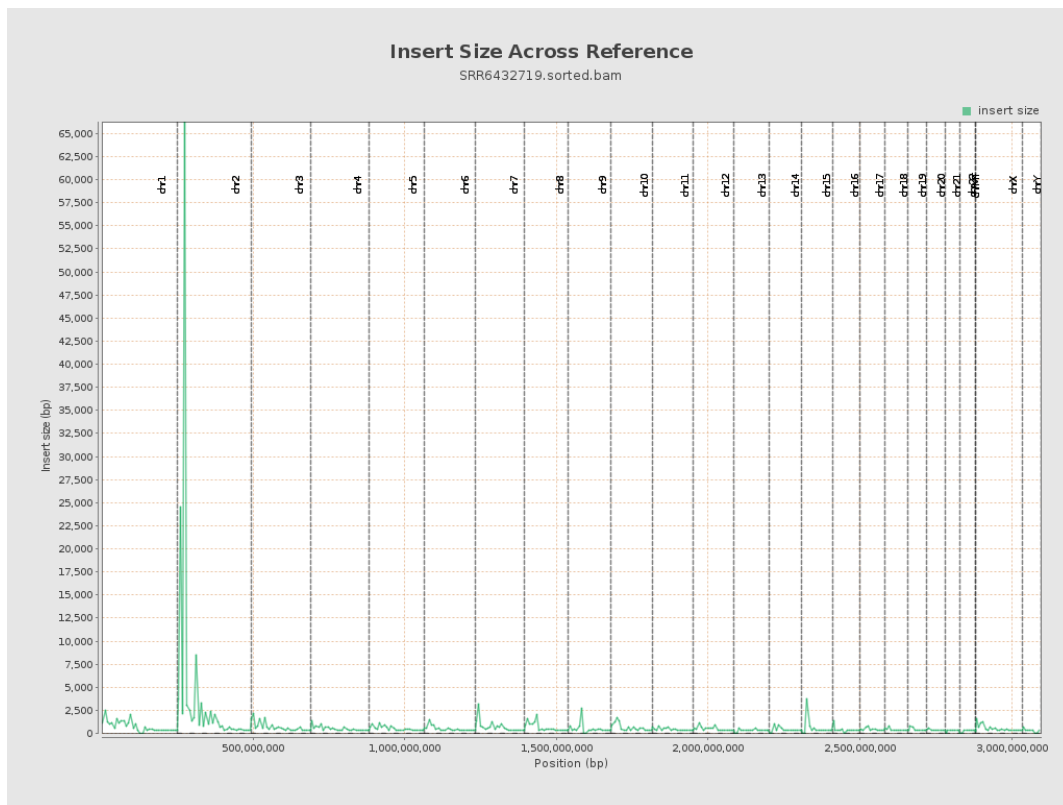
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

