

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 07:36:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432721.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_SRR6432721 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432721_1.fastq.gz SRR6432721_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 07:36:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432721.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	398,969,730
Mapped reads	398,809,161 / 99.96%
Unmapped reads	160,569 / 0.04%
Mapped paired reads	398,809,161 / 99.96%
Mapped reads, first in pair	199,408,831 / 49.98%
Mapped reads, second in pair	199,400,330 / 49.98%
Mapped reads, both in pair	398,748,002 / 99.94%
Mapped reads, singletons	61,159 / 0.02%
Secondary alignments	0
Supplementary alignments	5,153,462 / 1.29%
Read min/max/mean length	30 / 150 / 141.66
Duplicated reads (estimated)	199,410,197 / 49.98%
Duplication rate	32.87%
Clipped reads	101,351,807 / 25.4%

2.2. ACGT Content

Number/percentage of A's	15,451,231,573 / 27.9%
Number/percentage of C's	11,732,161,882 / 21.18%
Number/percentage of T's	15,250,560,581 / 27.53%
Number/percentage of G's	12,942,994,346 / 23.37%
Number/percentage of N's	10,522,890 / 0.02%

GC Percentage	44.55%
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2.3. Coverage

Mean	17.9101
Standard Deviation	51.8984

2.4. Mapping Quality

Mean Mapping Quality	57.4
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2.5. Insert size

Mean	63,150.27
Standard Deviation	2,540,178.7
P25/Median/P75	300 / 318 / 336

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	438,482,752
Insertions	12,269,677
Mapped reads with at least one insertion	3.01%
Deletions	39,399,227
Mapped reads with at least one deletion	9.4%
Homopolymer indels	53.06%

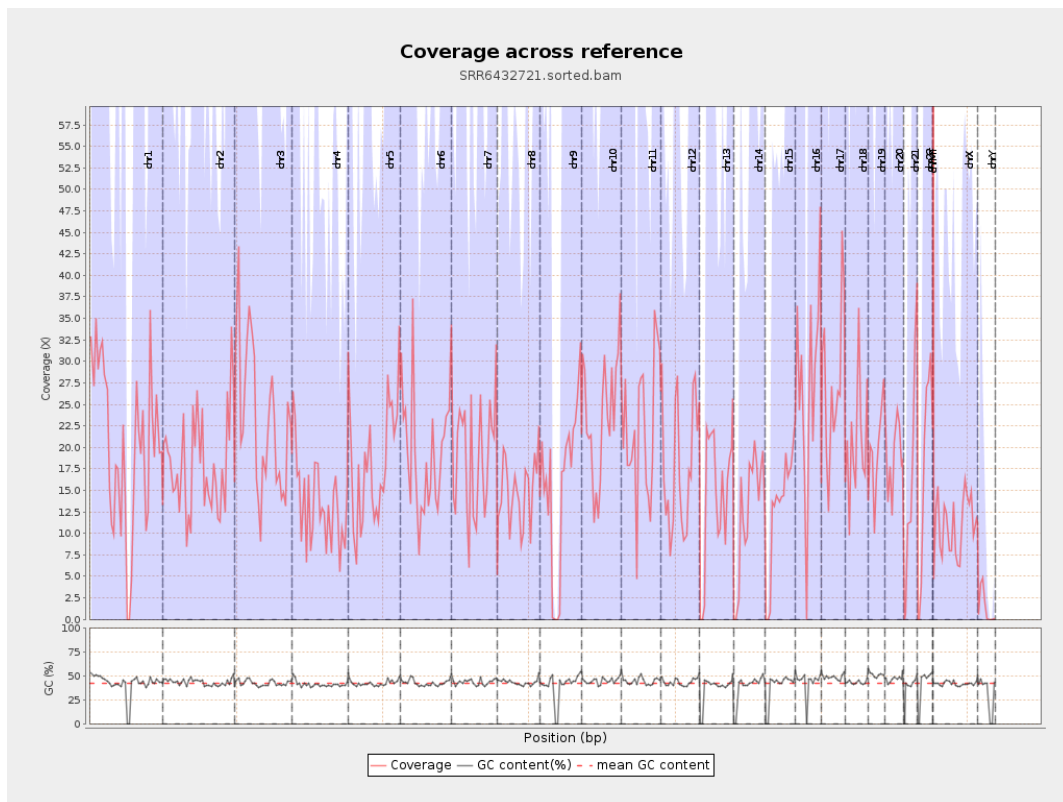
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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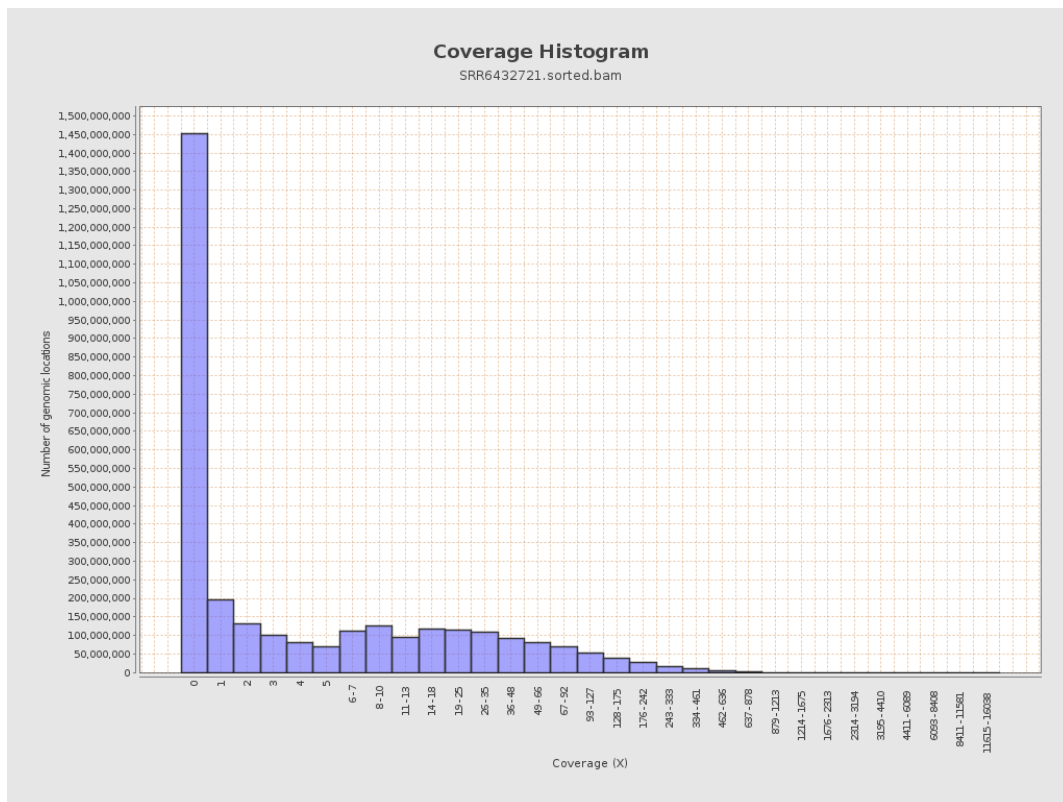
		bases	coverage	deviation
chr1	249250621	5008565234	20.0945	56.1109
chr2	243199373	4375186260	17.9901	54.0812
chr3	198022430	4533424911	22.8935	60.2624
chr4	191154276	2559331094	13.3888	39.6585
chr5	180915260	3307311799	18.281	51.0929
chr6	171115067	3259697197	19.0497	52.4555
chr7	159138663	3065790807	19.2649	53.4575
chr8	146364022	2179308819	14.8896	41.62
chr9	141213431	2212781317	15.6698	47.0584
chr10	135534747	3181251113	23.4718	60.4192
chr11	135006516	2988474456	22.1358	57.5894
chr12	133851895	2399636969	17.9276	50.3506
chr13	115169878	1634219951	14.1896	43.6844
chr14	107349540	1357116371	12.642	38.6745
chr15	102531392	1291262357	12.5938	39.4872
chr16	90354753	2450399373	27.1198	75.8463
chr17	81195210	2218031177	27.3173	69.4521
chr18	78077248	1587978530	20.3386	56.5478
chr19	59128983	1163992676	19.6857	55.4373
chr20	63025520	1183172006	18.7729	49.3841
chr21	48129895	783341714	16.2756	52.3467
chr22	51304566	902563652	17.5923	52.8268
chrMT	16571	5199138	313.7492	481.4545
chrX	155270560	1705934372	10.9869	33.5362

chrY	59373566	90120086	1.5178	17.8538
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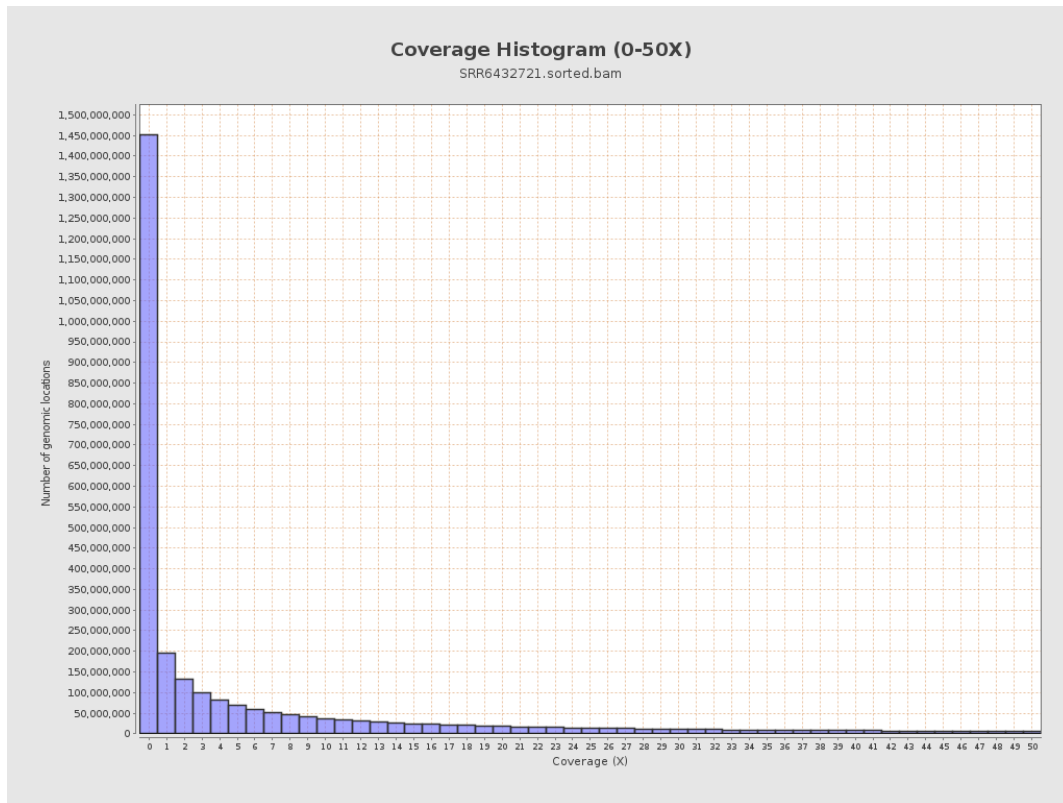
3. Results : Coverage across reference



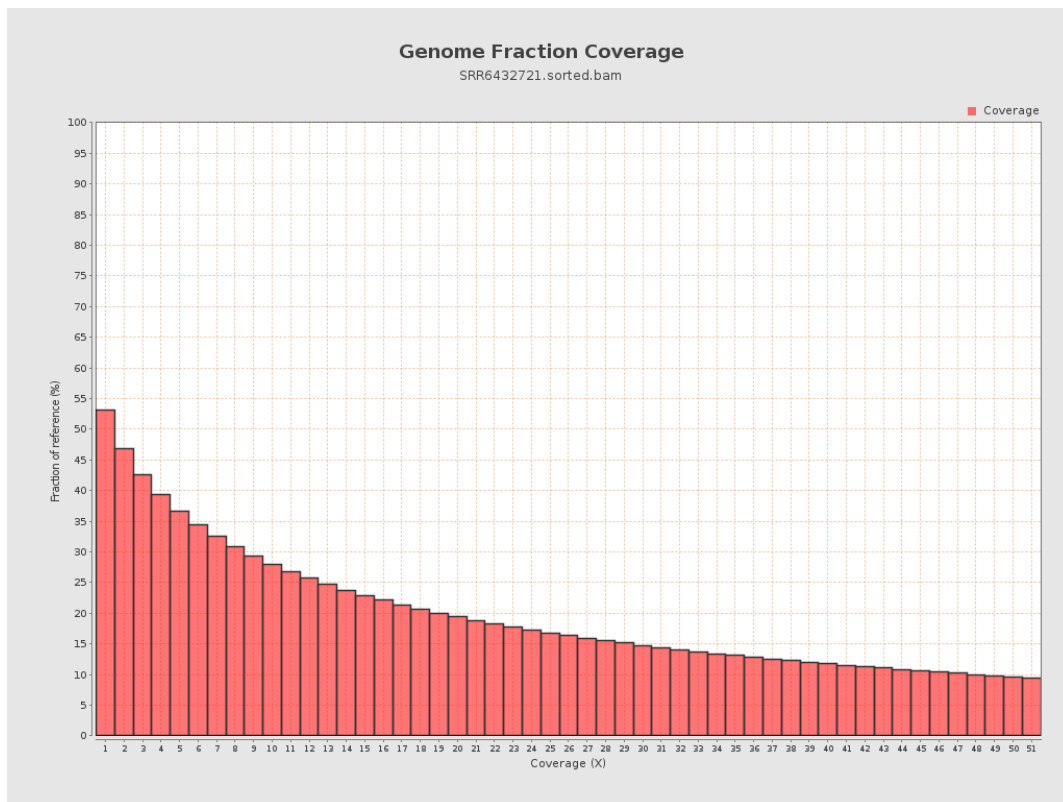
4. Results : Coverage Histogram



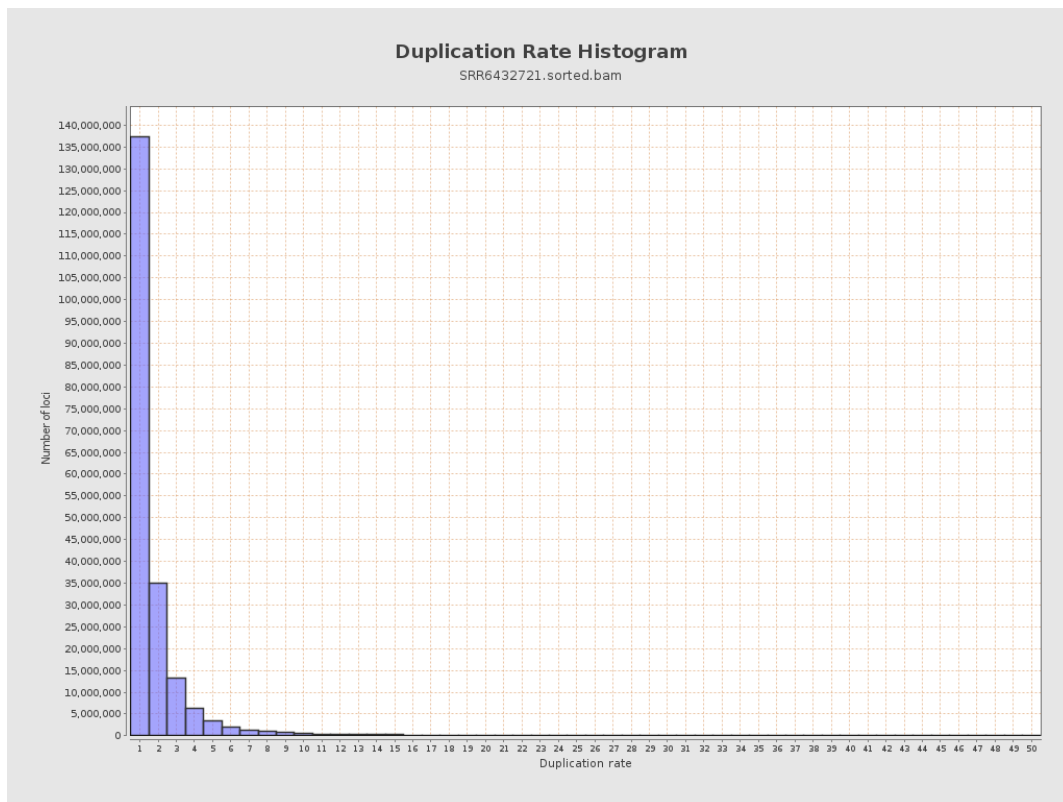
5. Results : Coverage Histogram (0-50X)



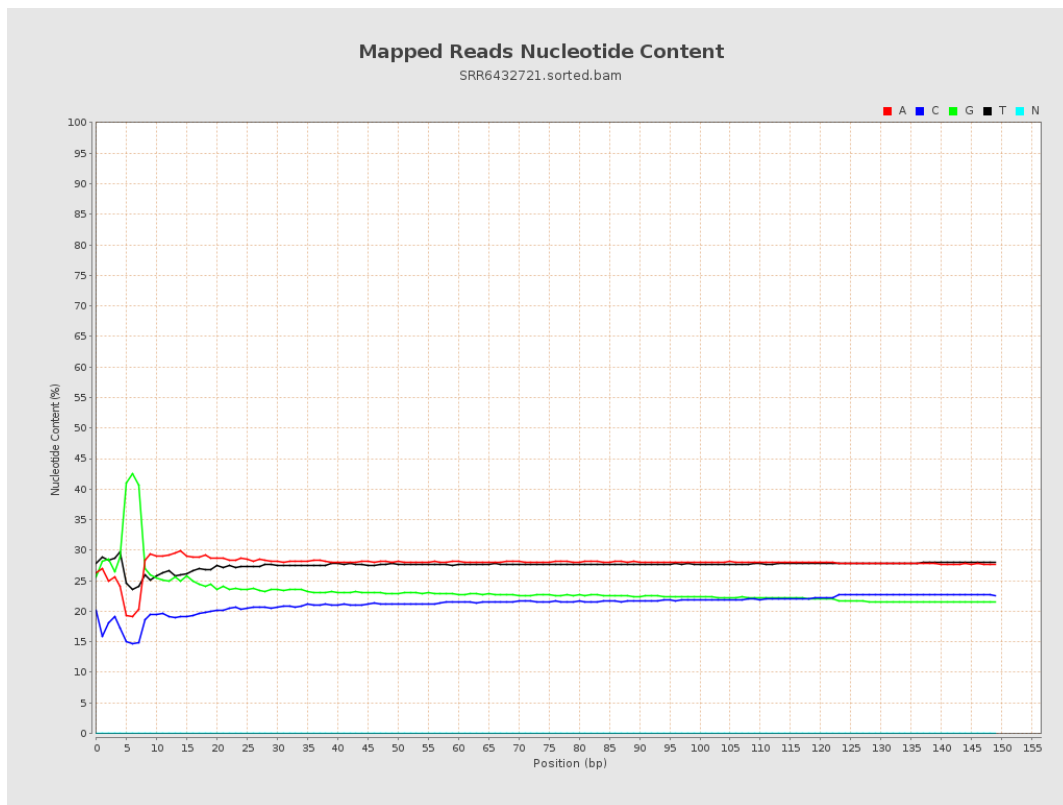
6. Results : Genome Fraction Coverage



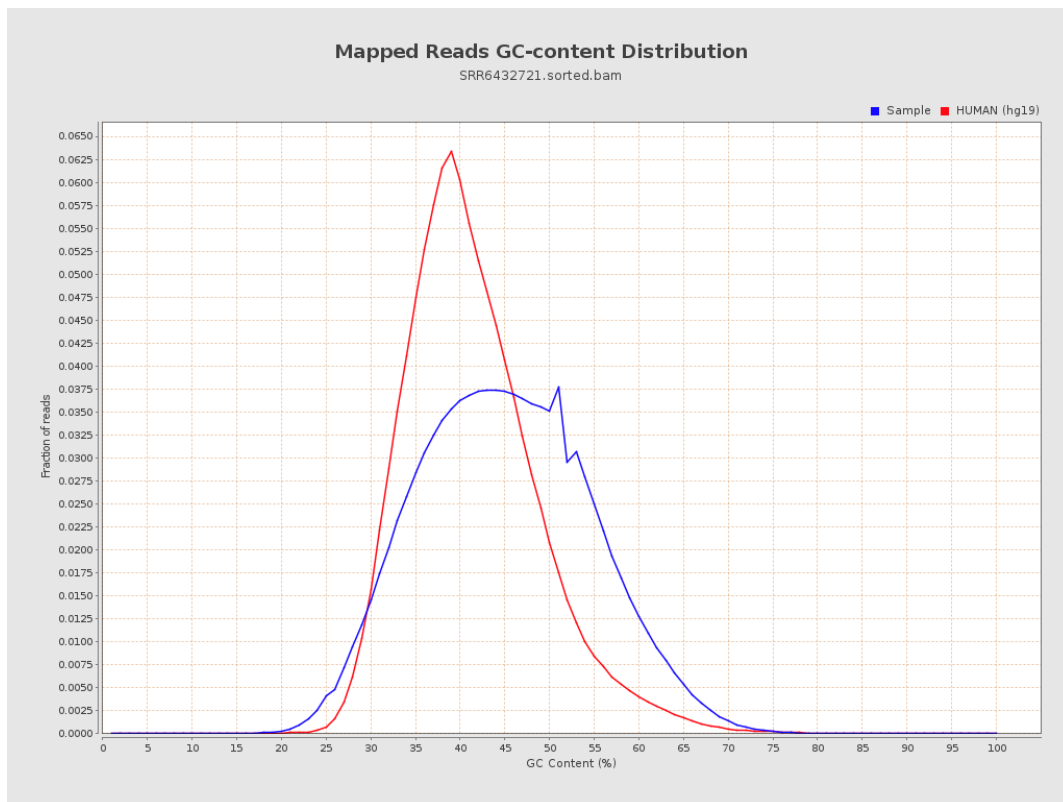
7. Results : Duplication Rate Histogram



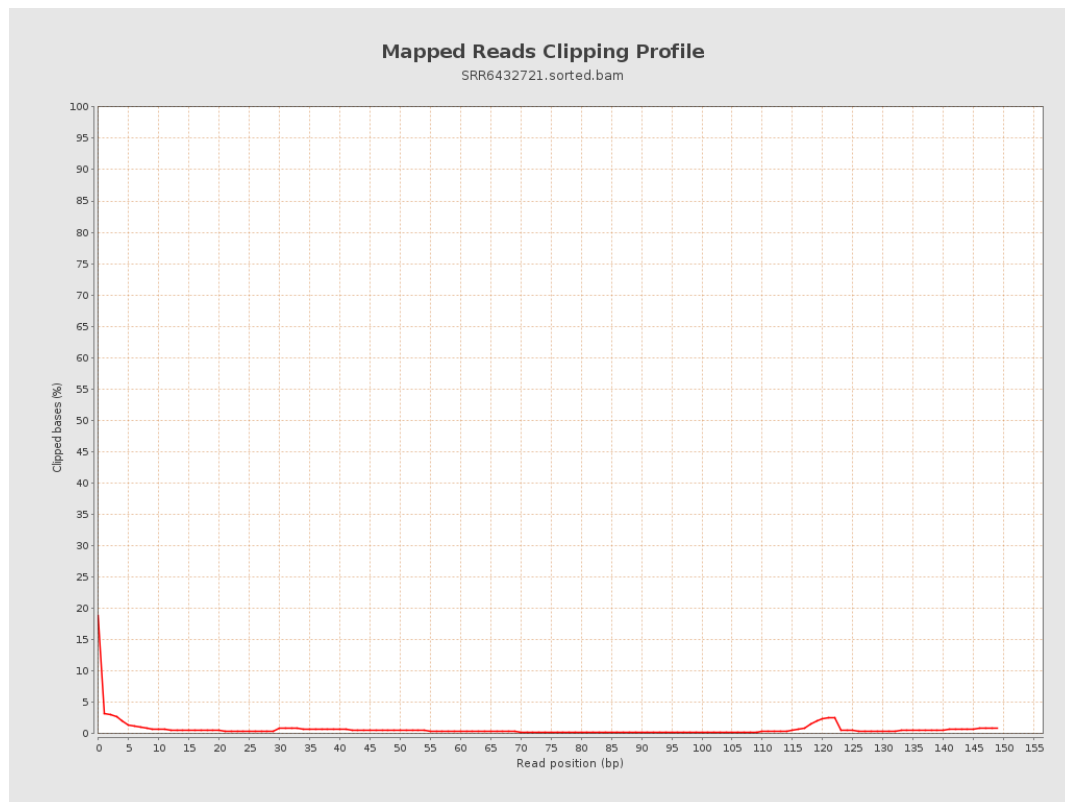
8. Results : Mapped Reads Nucleotide Content



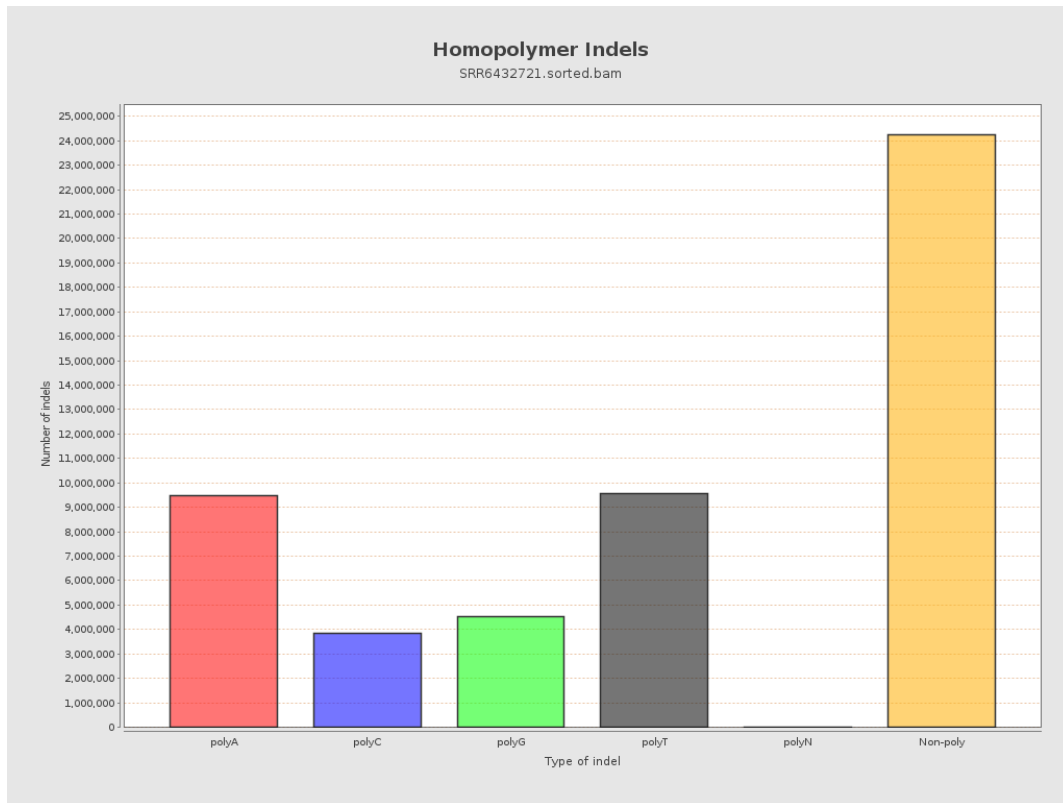
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



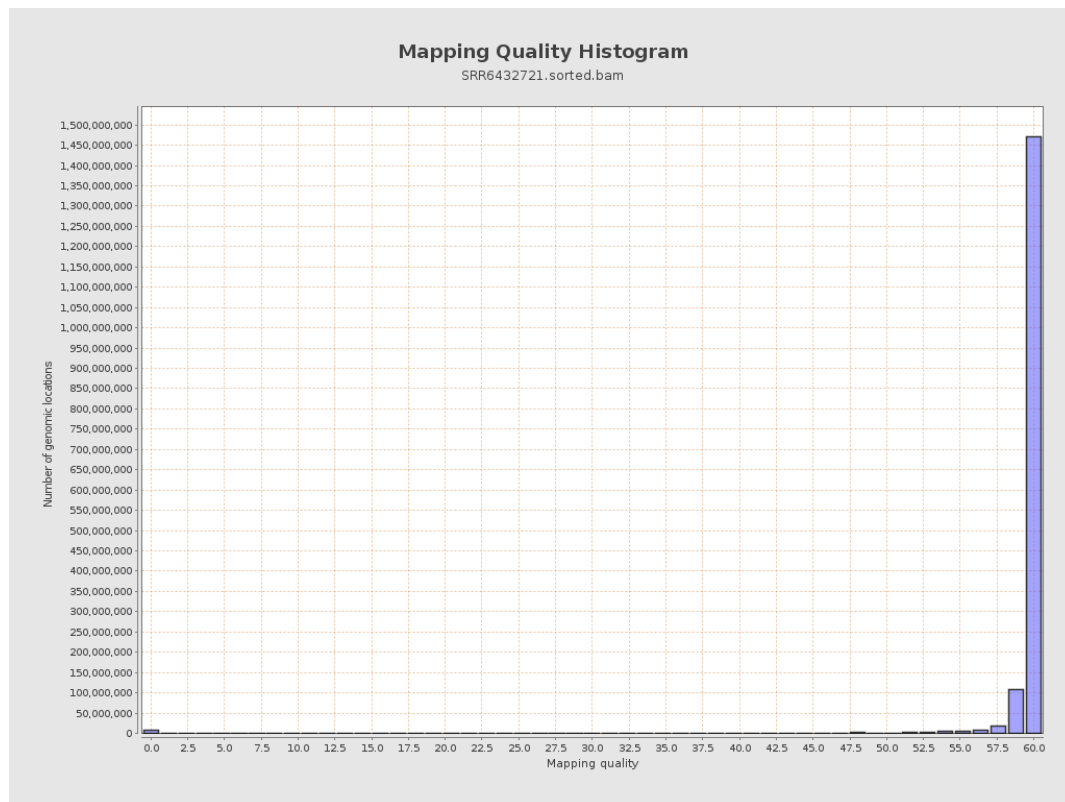
11. Results : Homopolymer Indels



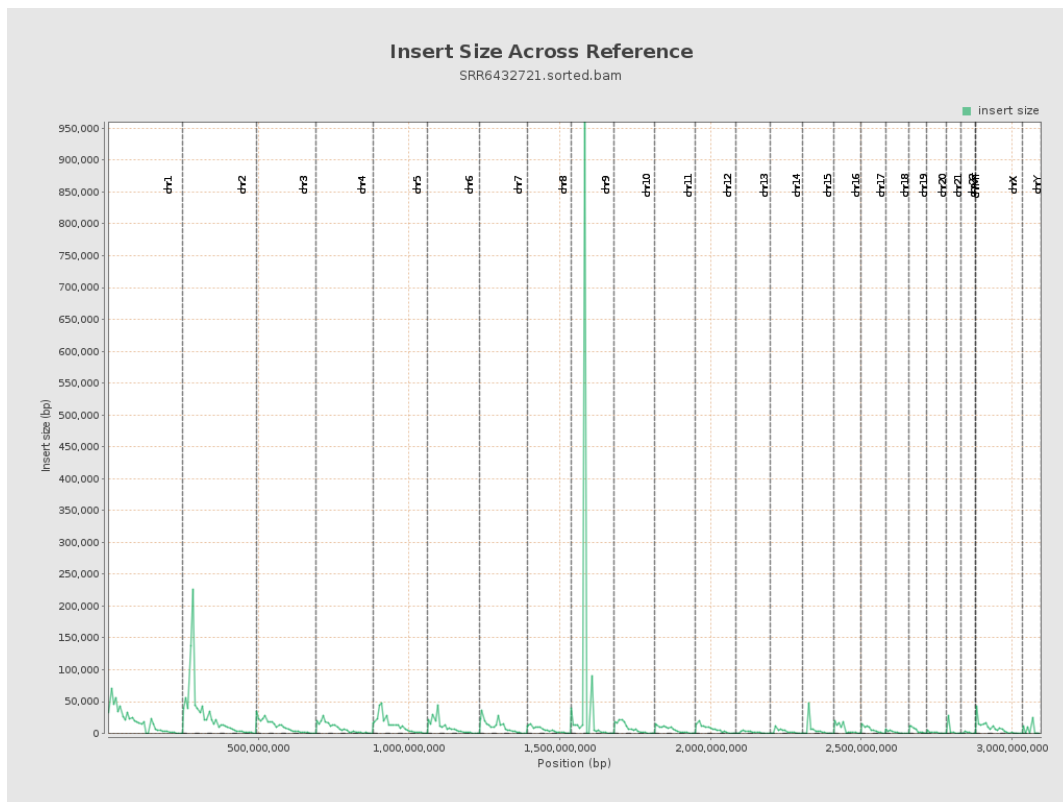
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

