

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 23:45:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432723.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_SRR6432723 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432723_1.fastq.gz SRR6432723_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 23:44:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432723.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	408,567,090
Mapped reads	408,411,285 / 99.96%
Unmapped reads	155,805 / 0.04%
Mapped paired reads	408,411,285 / 99.96%
Mapped reads, first in pair	204,209,931 / 49.98%
Mapped reads, second in pair	204,201,354 / 49.98%
Mapped reads, both in pair	408,354,920 / 99.95%
Mapped reads, singletons	56,365 / 0.01%
Secondary alignments	0
Supplementary alignments	3,053,422 / 0.75%
Read min/max/mean length	30 / 150 / 140
Duplicated reads (estimated)	211,320,590 / 51.72%
Duplication rate	32.67%
Clipped reads	109,986,075 / 26.92%

2.2. ACGT Content

Number/percentage of A's	15,543,982,748 / 27.69%
Number/percentage of C's	11,869,996,855 / 21.15%
Number/percentage of T's	15,321,771,118 / 27.3%
Number/percentage of G's	13,385,769,542 / 23.85%
Number/percentage of N's	9,991,549 / 0.02%

GC Percentage	44.99%
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2.3. Coverage

Mean	18.1498
Standard Deviation	51.7193

2.4. Mapping Quality

Mean Mapping Quality	57.42
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2.5. Insert size

Mean	76,362.02
Standard Deviation	2,747,215.61
P25/Median/P75	302 / 321 / 340

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	491,865,989
Insertions	11,738,387
Mapped reads with at least one insertion	2.82%
Deletions	38,504,616
Mapped reads with at least one deletion	8.99%
Homopolymer indels	52.59%

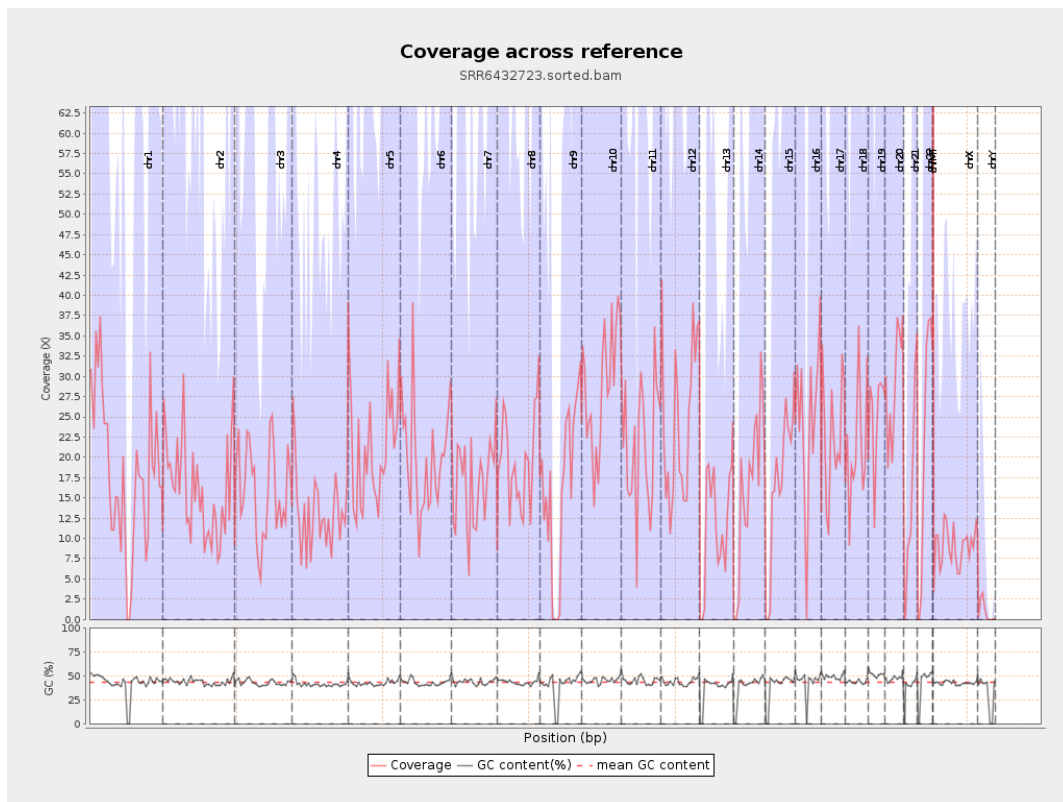
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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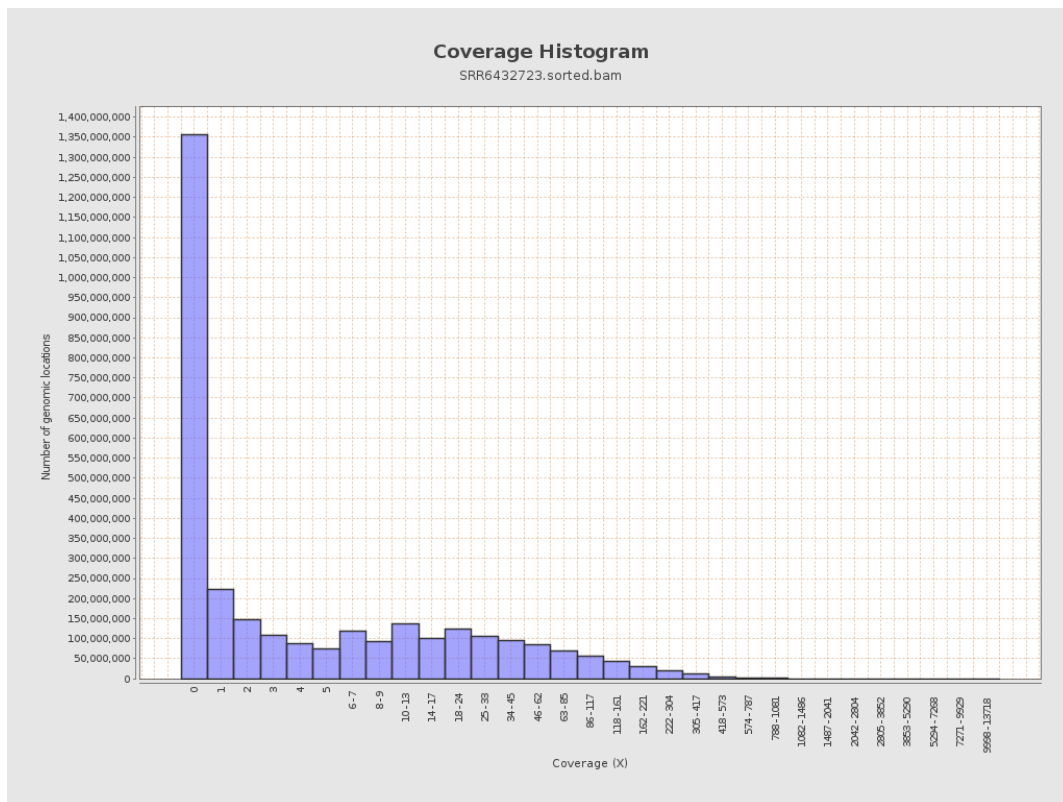
		bases	coverage	deviation
chr1	249250621	4501979241	18.0621	51.2664
chr2	243199373	3899089084	16.0325	48.4098
chr3	198022430	3121057626	15.7611	43.2756
chr4	191154276	2515243606	13.1582	38.4939
chr5	180915260	3838690278	21.2182	55.9885
chr6	171115067	3391871860	19.8222	53.4298
chr7	159138663	2734335666	17.1821	47.3162
chr8	146364022	2874856398	19.6418	51.3601
chr9	141213431	2252911798	15.9539	47.7309
chr10	135534747	3876312376	28.6001	70.8839
chr11	135006516	2890553901	21.4105	56.4383
chr12	133851895	3274527000	24.4638	63.2299
chr13	115169878	1325950697	11.513	36.8851
chr14	107349540	1751556155	16.3164	47.1297
chr15	102531392	1674190909	16.3286	48.1261
chr16	90354753	2210580627	24.4656	66.9772
chr17	81195210	1849123880	22.7738	58.4336
chr18	78077248	1619541627	20.7428	55.7443
chr19	59128983	1475395247	24.9521	65.5364
chr20	63025520	1805679445	28.65	68.2033
chr21	48129895	734337196	15.2574	47.5959
chr22	51304566	1104502143	21.5283	62.1534
chrMT	16571	4428694	267.2557	432.4347
chrX	155270560	1398041878	9.0039	28.2154

chrY	59373566	61560914	1.0368	13.8041
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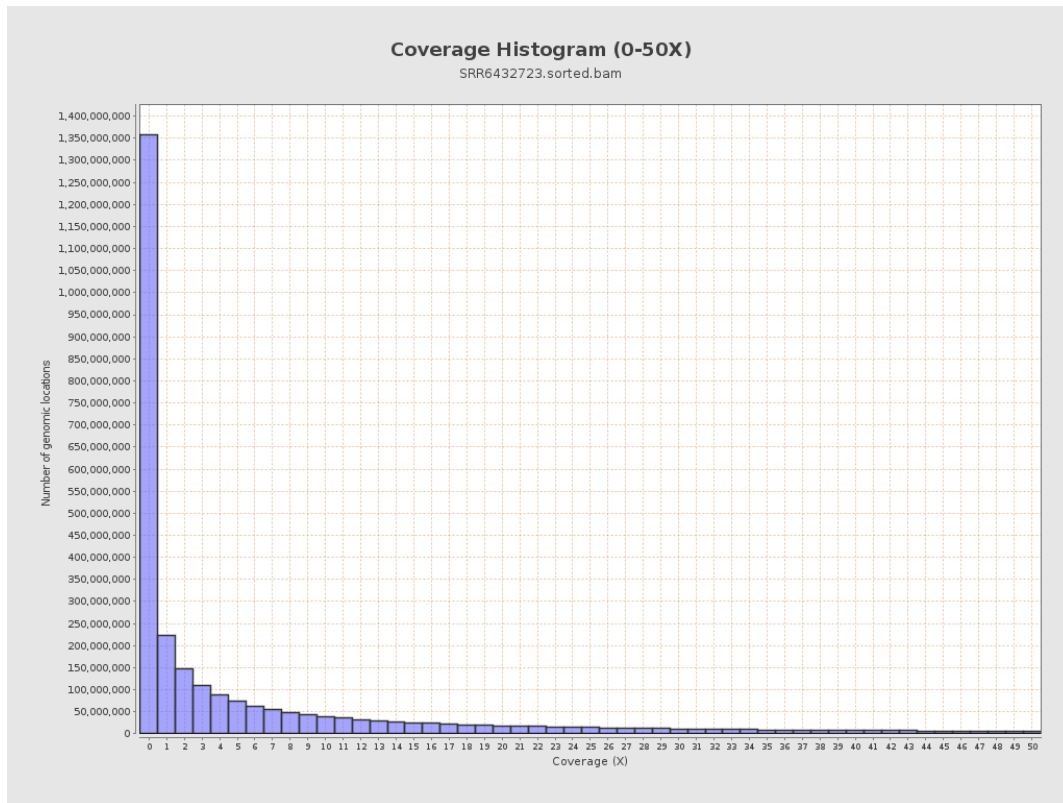
3. Results : Coverage across reference



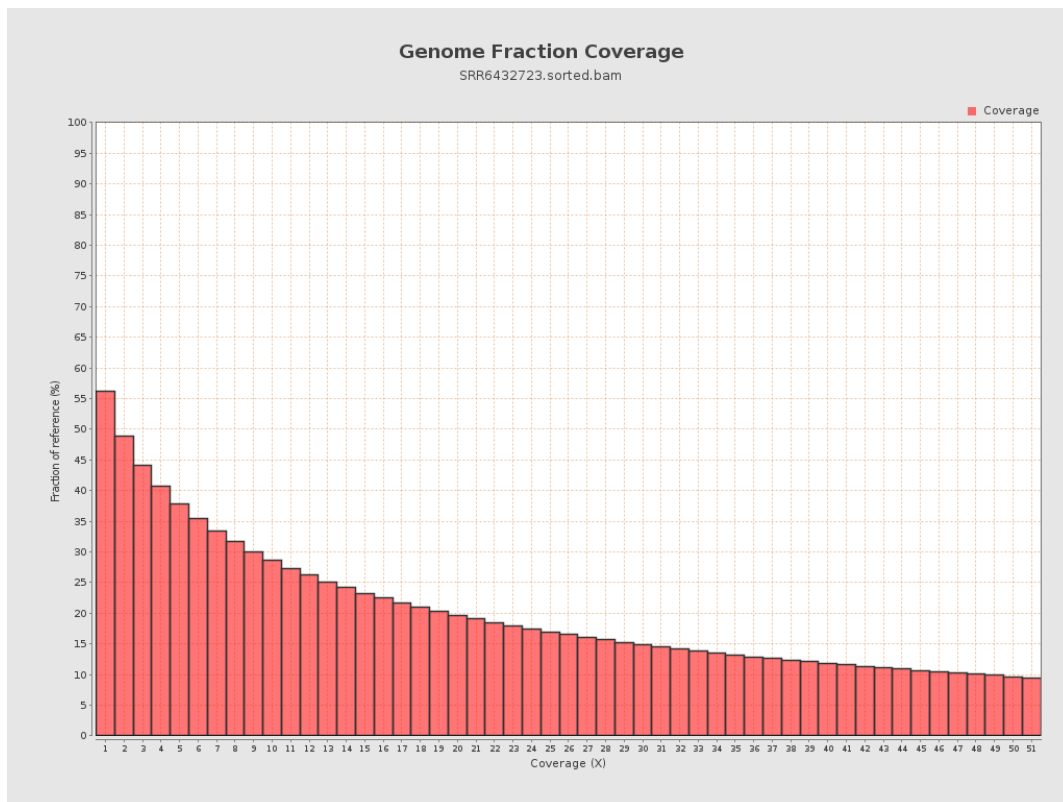
4. Results : Coverage Histogram



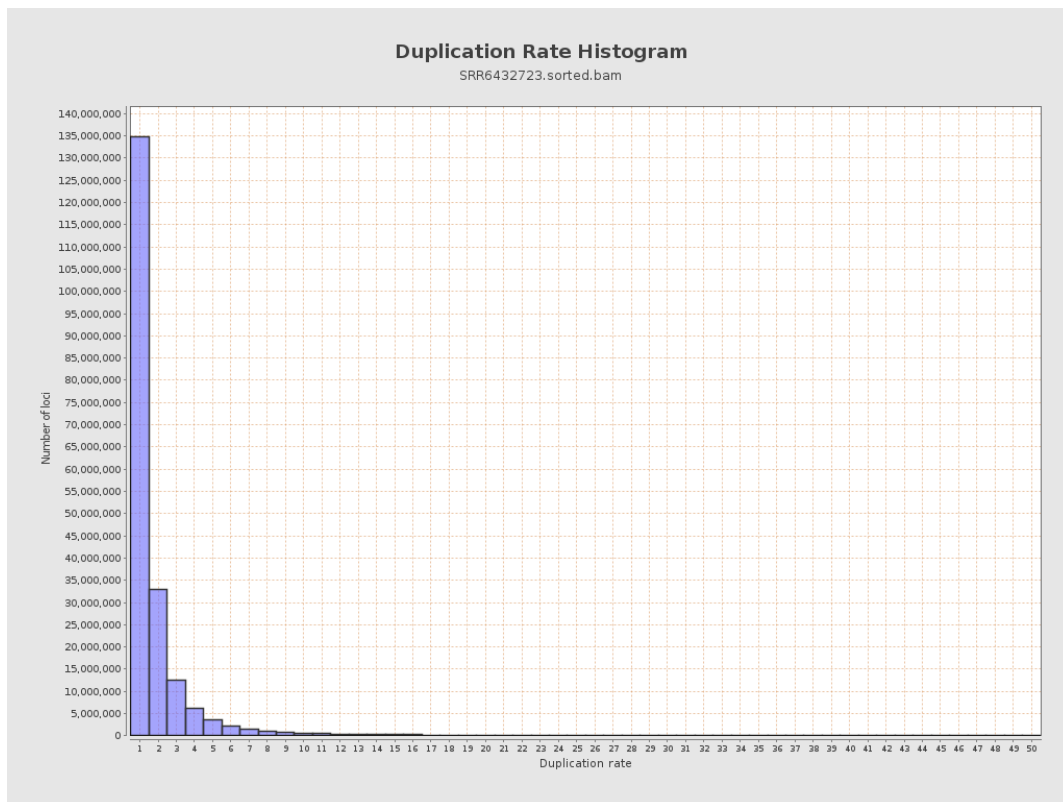
5. Results : Coverage Histogram (0-50X)



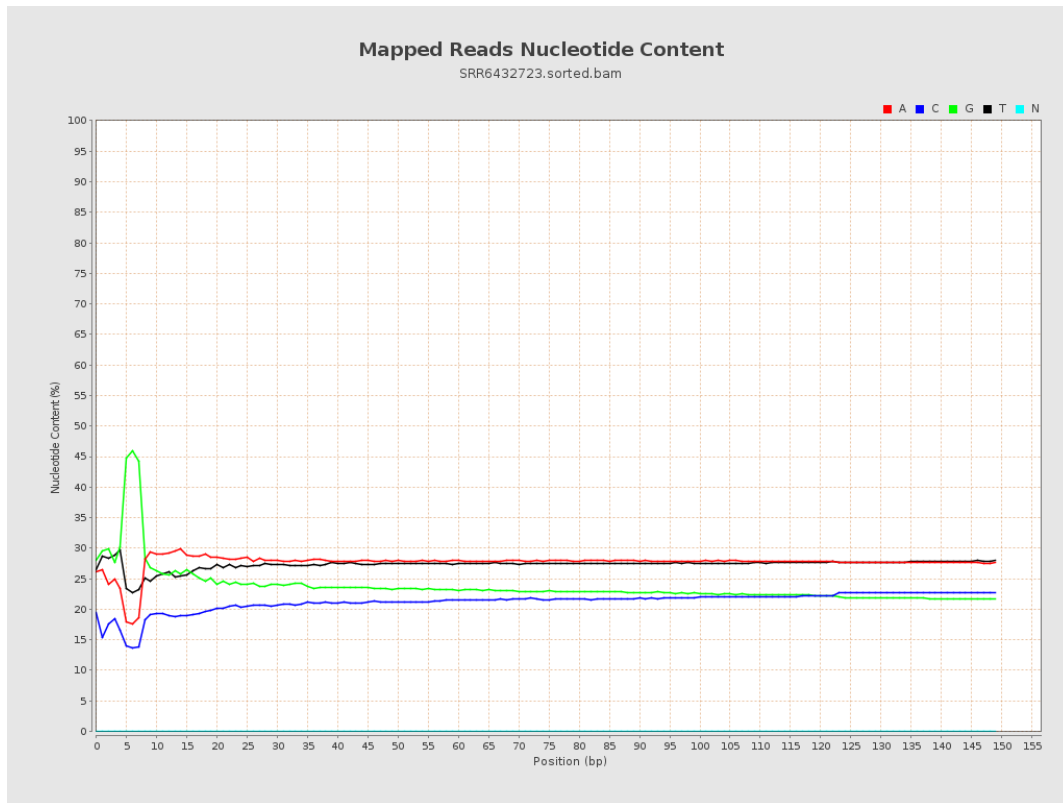
6. Results : Genome Fraction Coverage



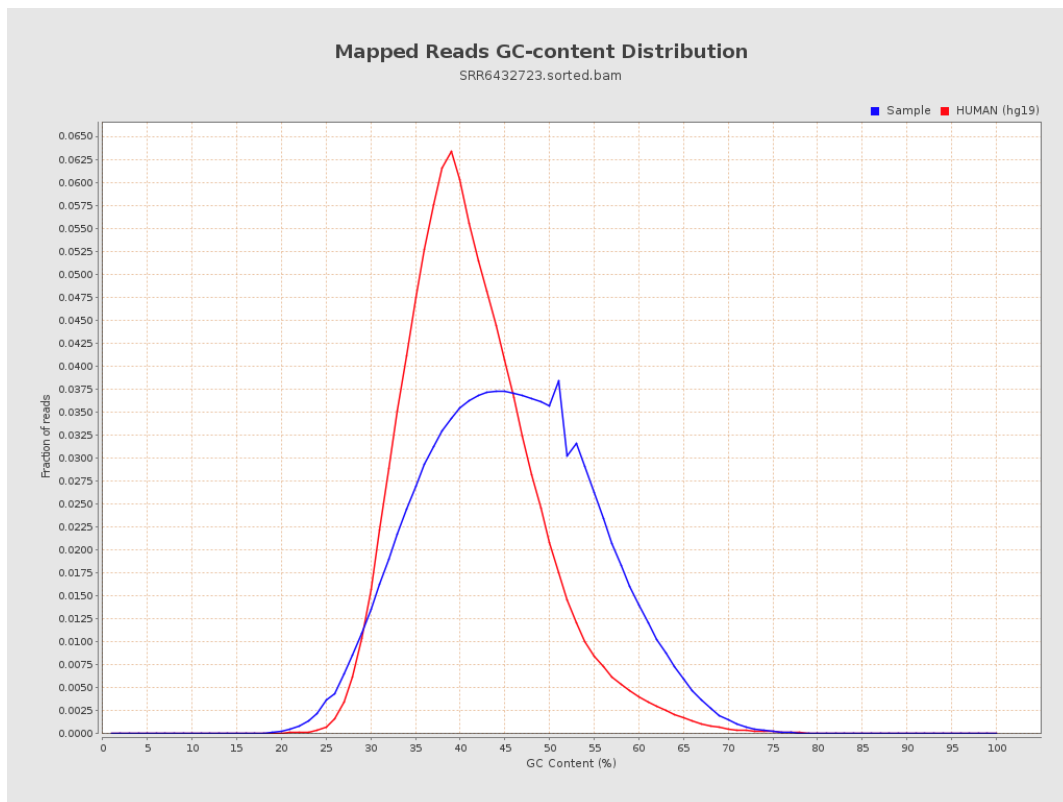
7. Results : Duplication Rate Histogram



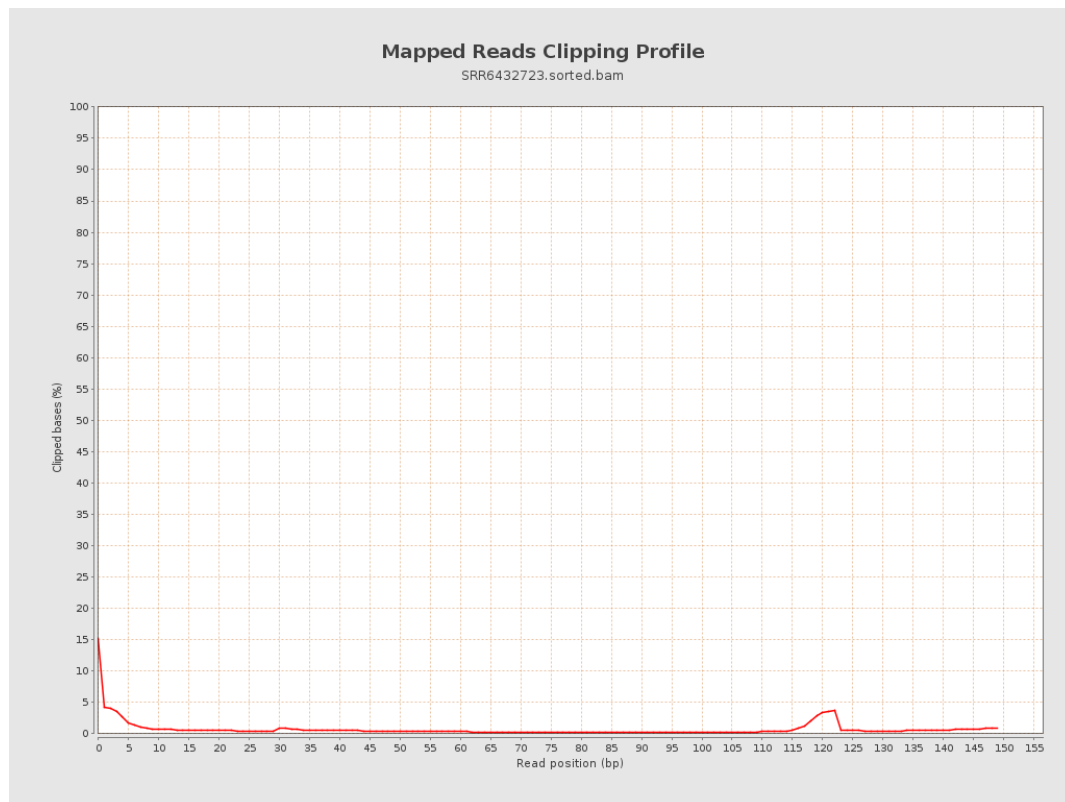
8. Results : Mapped Reads Nucleotide Content



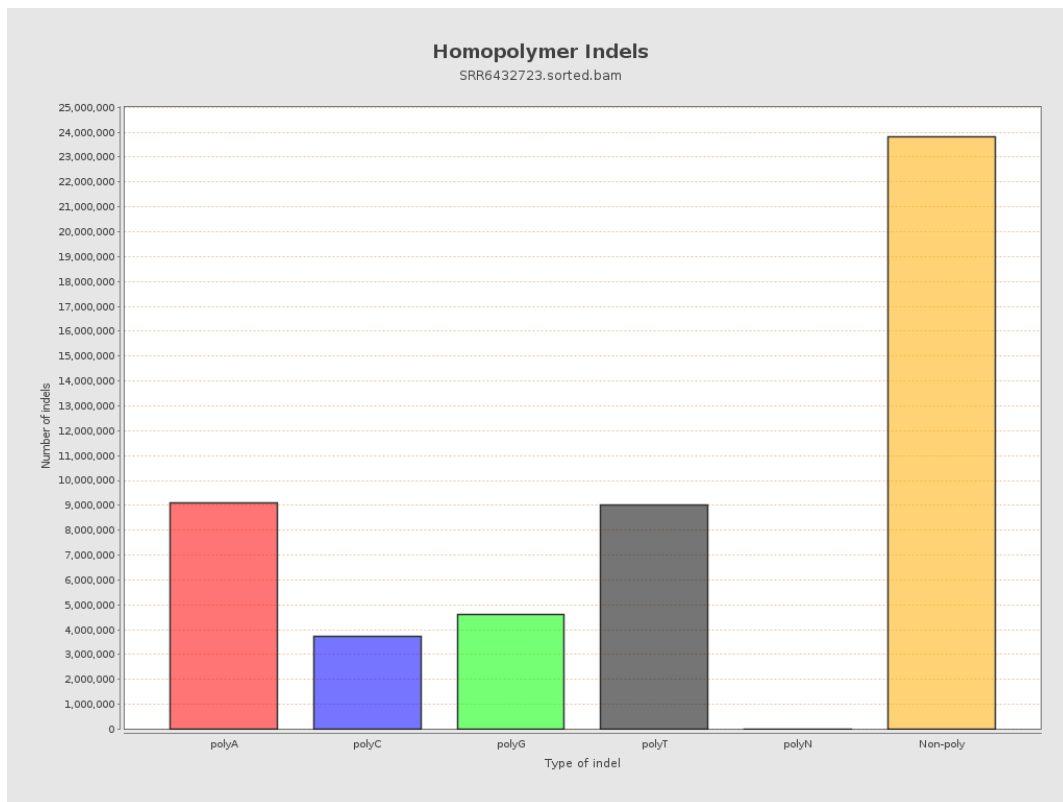
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



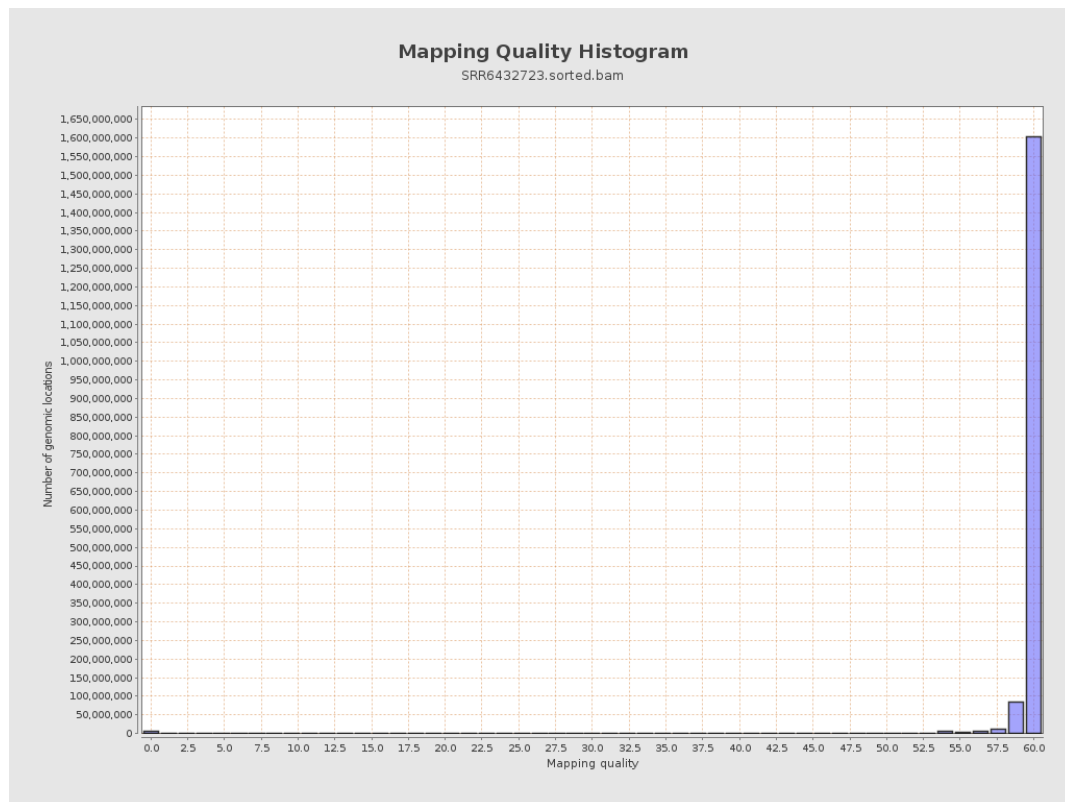
11. Results : Homopolymer Indels



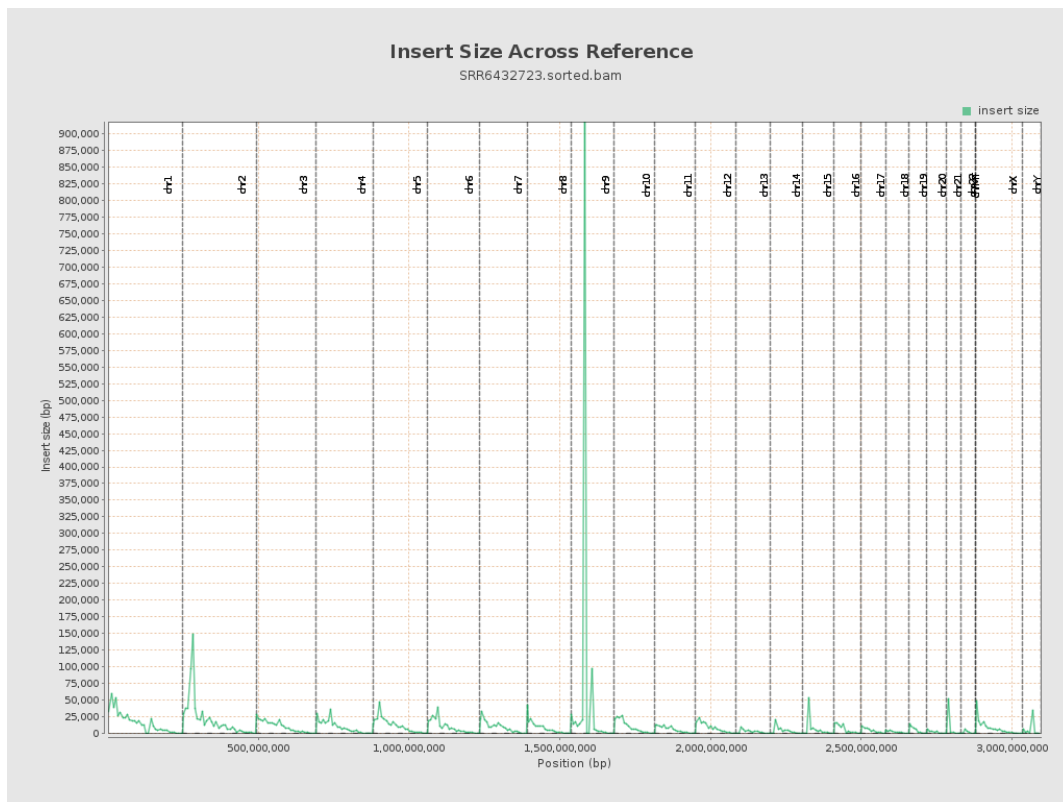
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

