

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 09:13:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432724.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_SRR6432724 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432724_1.fastq.gz SRR6432724_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 09:13:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432724.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	412,186,398
Mapped reads	411,997,641 / 99.95%
Unmapped reads	188,757 / 0.05%
Mapped paired reads	411,997,641 / 99.95%
Mapped reads, first in pair	206,004,064 / 49.98%
Mapped reads, second in pair	205,993,577 / 49.98%
Mapped reads, both in pair	411,931,492 / 99.94%
Mapped reads, singletons	66,149 / 0.02%
Secondary alignments	0
Supplementary alignments	219,282 / 0.05%
Read min/max/mean length	30 / 150 / 140.07
Duplicated reads (estimated)	201,423,620 / 48.87%
Duplication rate	32.3%
Clipped reads	110,845,466 / 26.89%

2.2. ACGT Content

Number/percentage of A's	15,440,469,268 / 27.27%
Number/percentage of C's	12,322,908,987 / 21.76%
Number/percentage of T's	15,264,892,051 / 26.96%
Number/percentage of G's	13,594,001,826 / 24.01%
Number/percentage of N's	279,671 / 0%

GC Percentage	45.77%
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2.3. Coverage

Mean	18.3086
Standard Deviation	53.1076

2.4. Mapping Quality

Mean Mapping Quality	55.39
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2.5. Insert size

Mean	71,066.22
Standard Deviation	2,681,279.94
P25/Median/P75	285 / 303 / 320

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	526,435,275
Insertions	11,584,354
Mapped reads with at least one insertion	2.75%
Deletions	37,979,111
Mapped reads with at least one deletion	8.79%
Homopolymer indels	51.49%

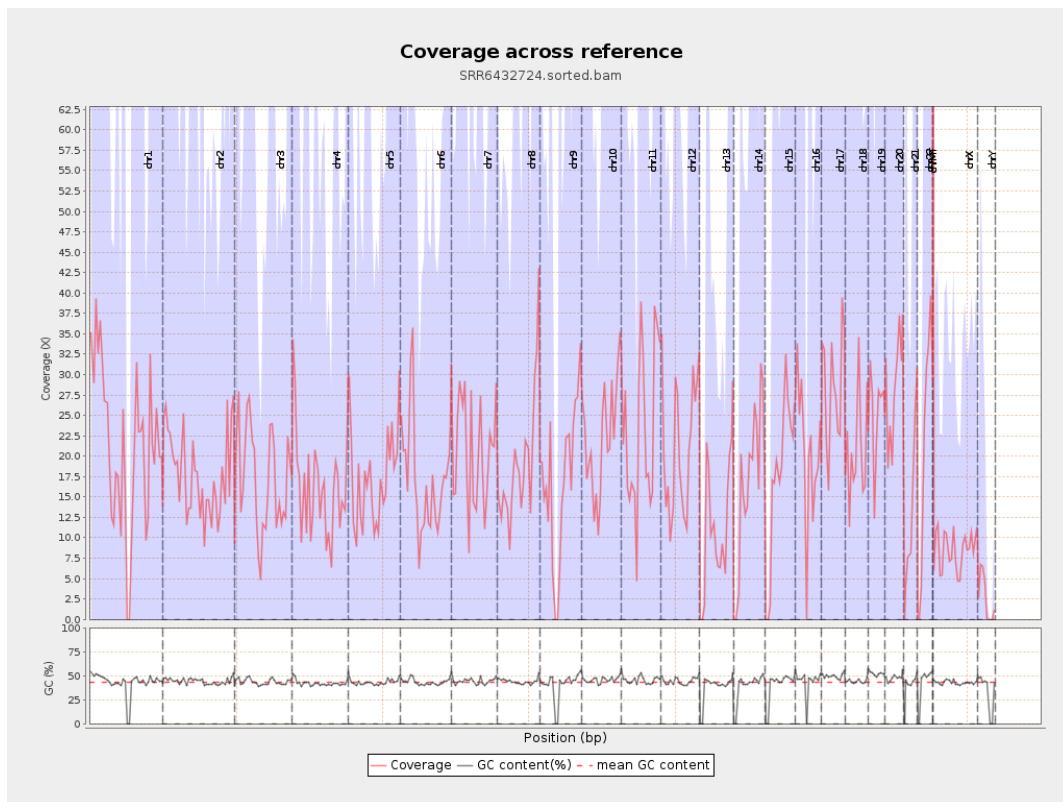
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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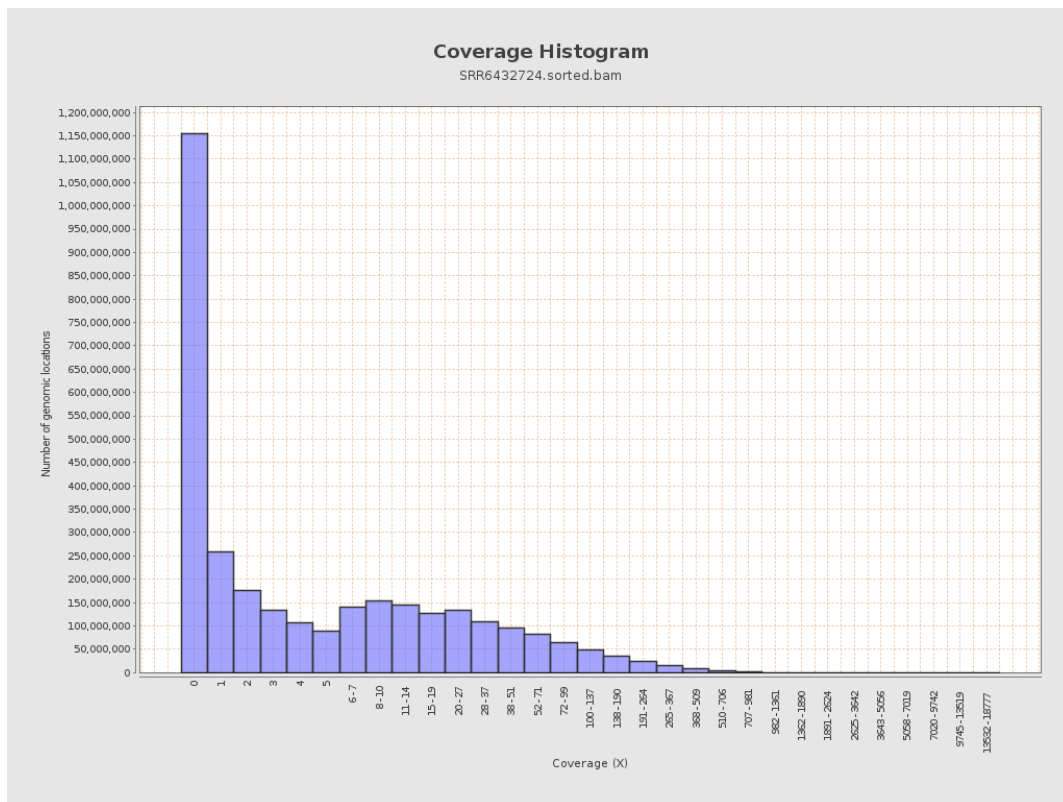
		bases	coverage	deviation
chr1	249250621	5294459605	21.2415	59.5359
chr2	243199373	4325166283	17.7844	55.0915
chr3	198022430	3381973486	17.0787	45.9758
chr4	191154276	3069220759	16.0562	46.4024
chr5	180915260	3159559426	17.4643	48.5368
chr6	171115067	2915459247	17.038	47.0313
chr7	159138663	3295653757	20.7093	55.3076
chr8	146364022	2798119719	19.1175	52.7971
chr9	141213431	2380146861	16.855	54.5984
chr10	135534747	2985026590	22.0241	56.9815
chr11	135006516	3149370329	23.3275	61.1153
chr12	133851895	2819979282	21.0679	56.0208
chr13	115169878	1281757961	11.1293	36.468
chr14	107349540	1813493710	16.8934	48.7751
chr15	102531392	1791132768	17.4691	50.4717
chr16	90354753	1855360874	20.5342	62.8833
chr17	81195210	2299834627	28.3248	71.4569
chr18	78077248	1588396576	20.3439	57.2693
chr19	59128983	1489230495	25.1861	67.3551
chr20	63025520	1770125436	28.0859	68.6535
chr21	48129895	633906638	13.1707	51.4855
chr22	51304566	1085770230	21.1632	61.6633
chrMT	16571	6662458	402.0553	734.6067
chrX	155270560	1325386594	8.536	25.3716

chrY	59373566	162724883	2.7407	22.9709
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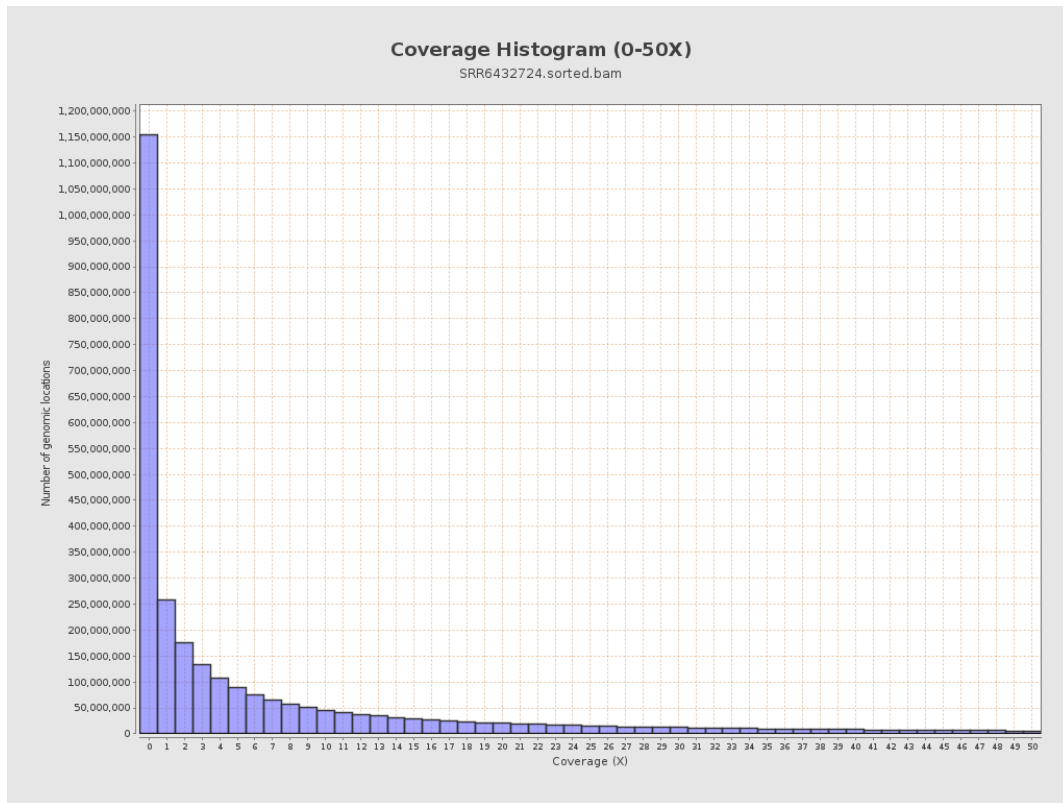
3. Results : Coverage across reference



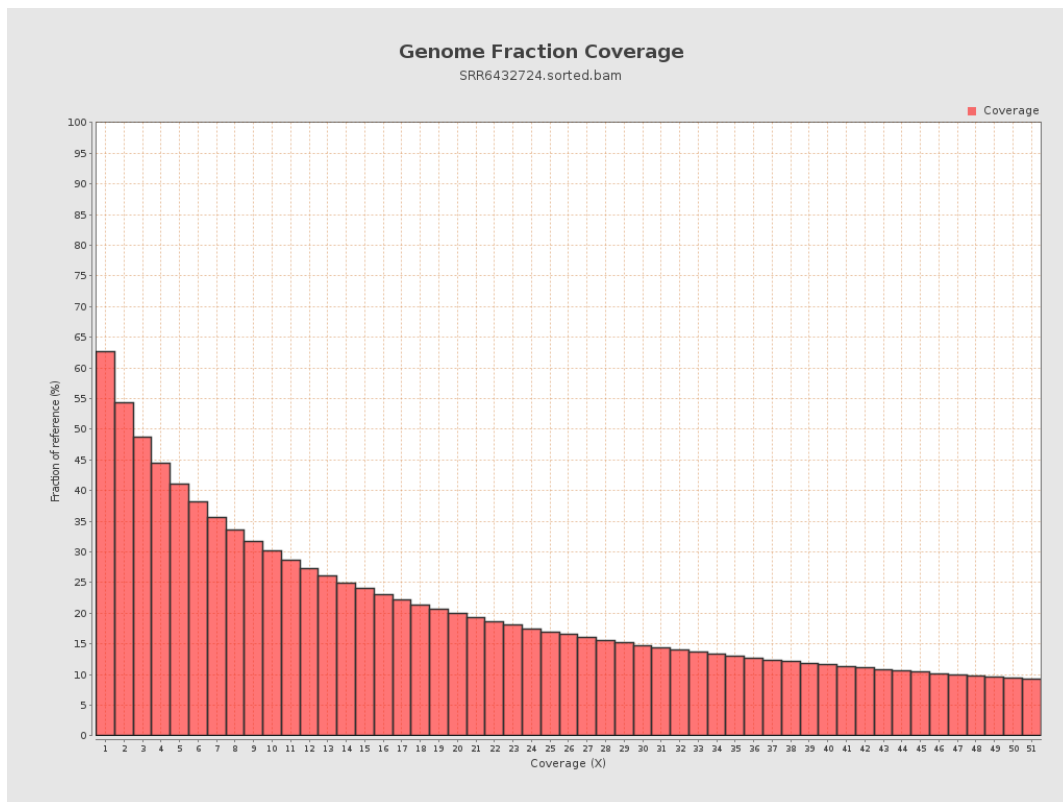
4. Results : Coverage Histogram



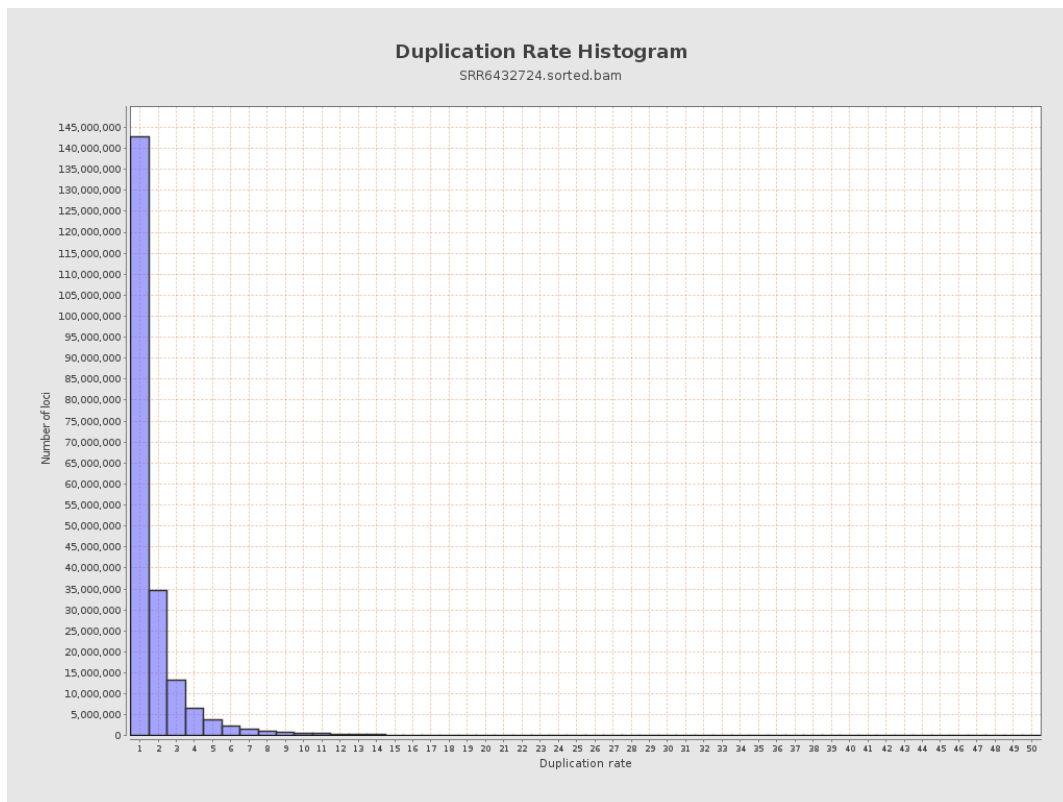
5. Results : Coverage Histogram (0-50X)



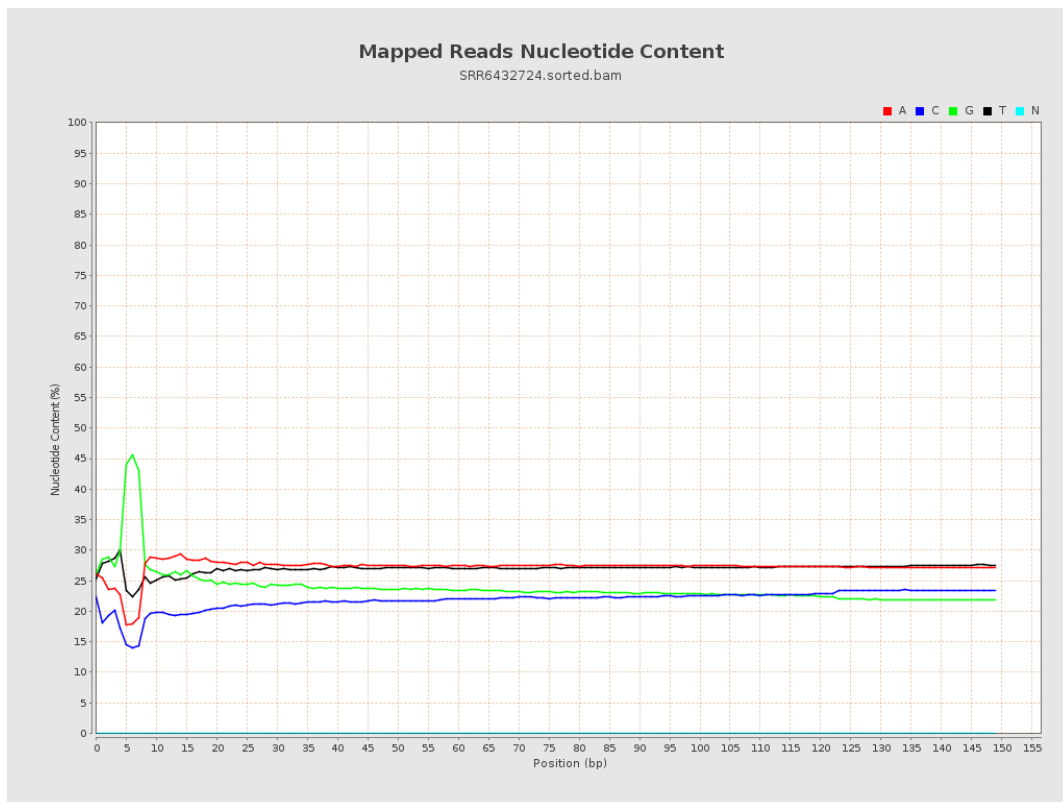
6. Results : Genome Fraction Coverage



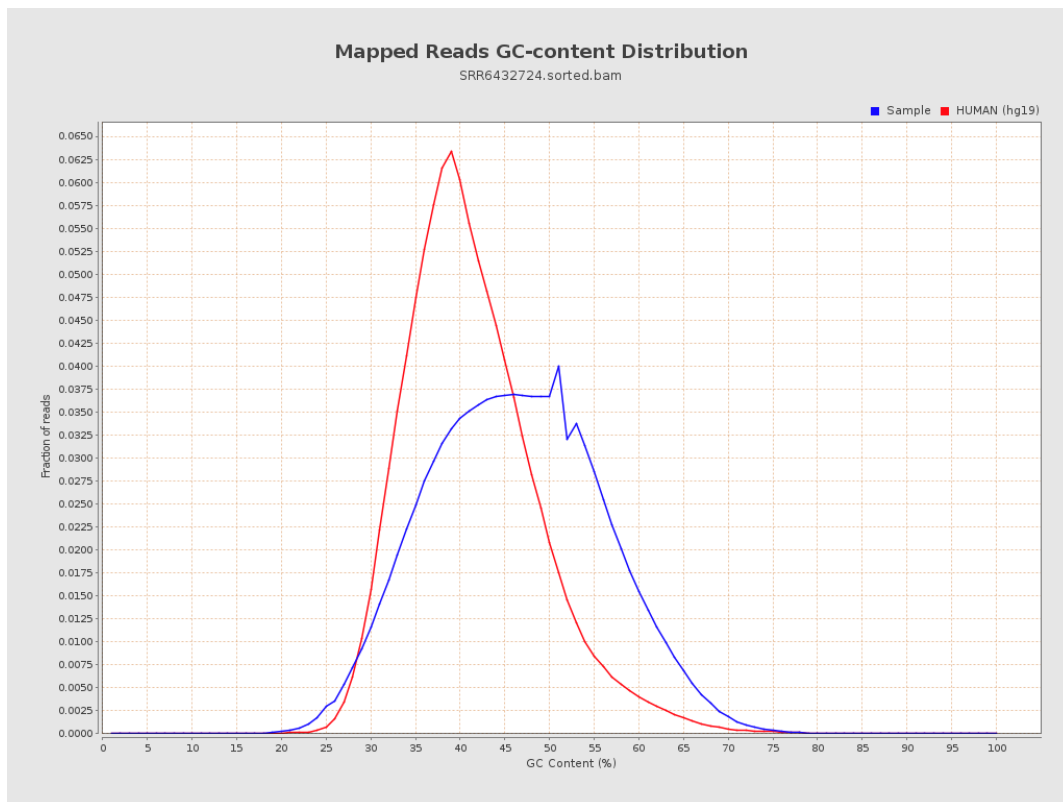
7. Results : Duplication Rate Histogram



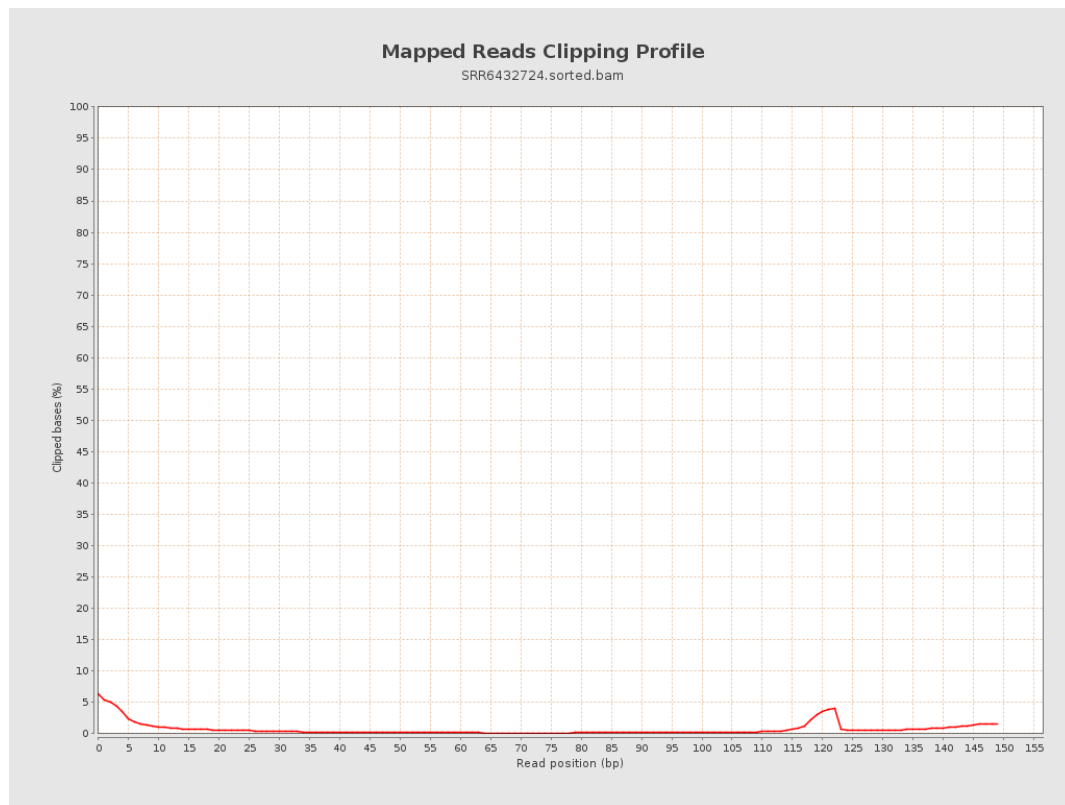
8. Results : Mapped Reads Nucleotide Content



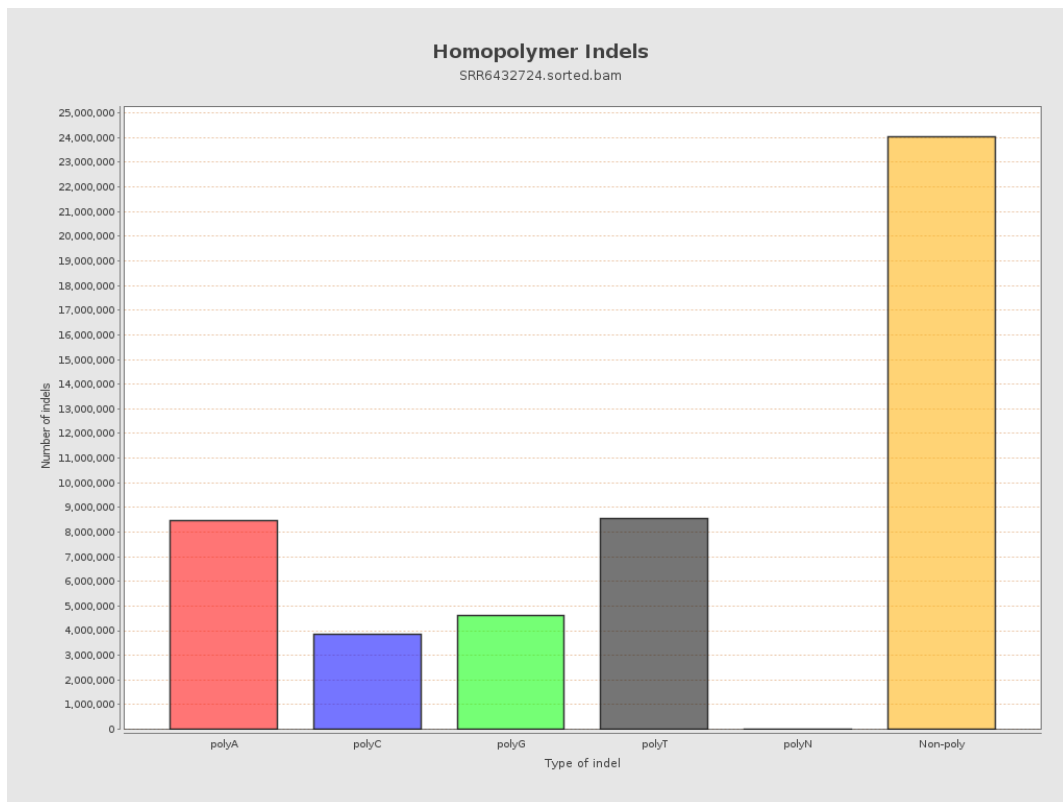
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



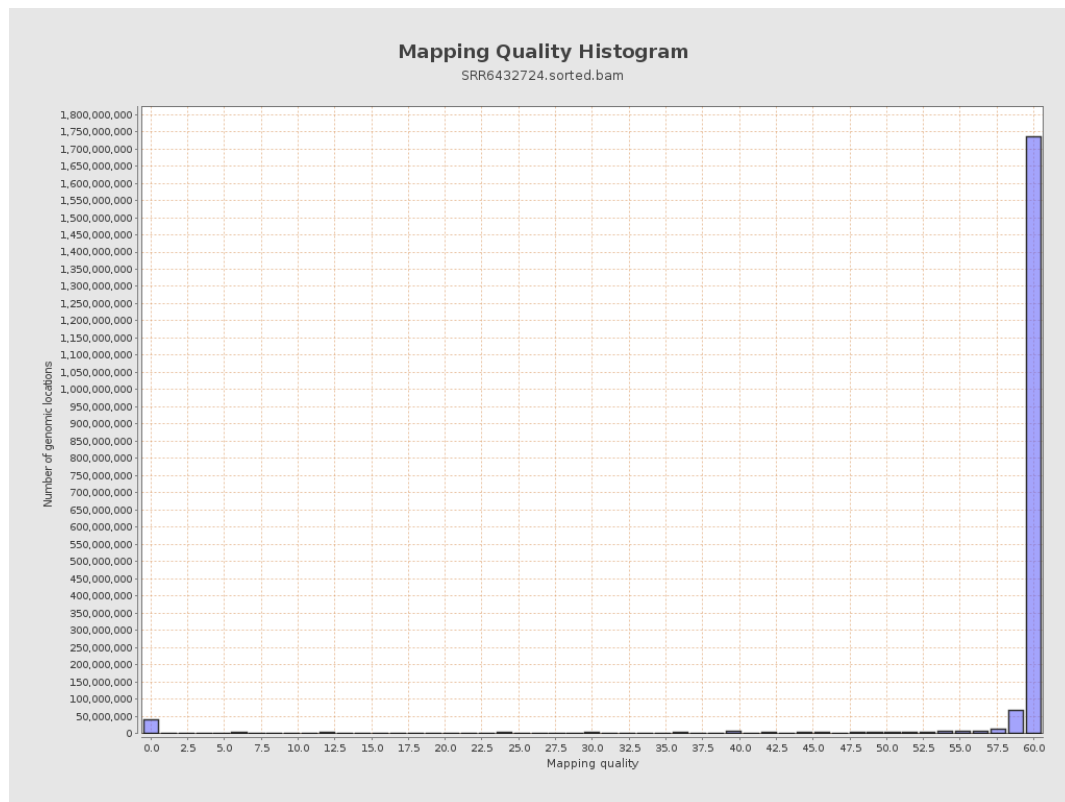
11. Results : Homopolymer Indels



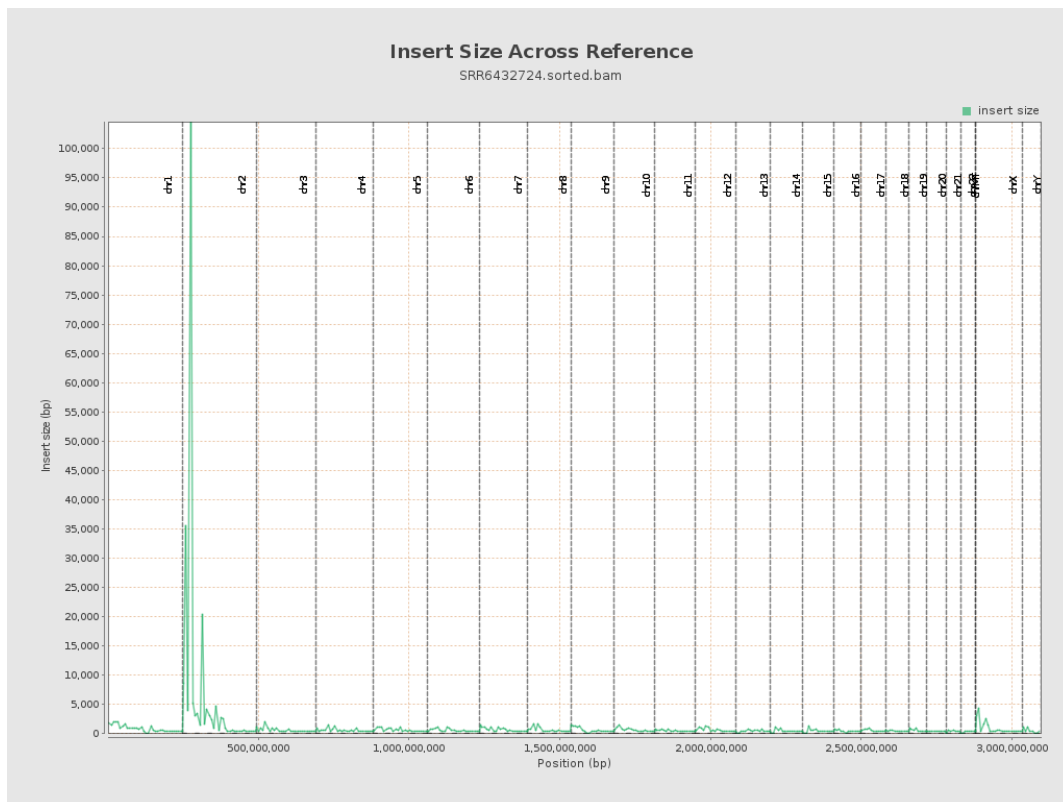
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

