

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 00:20:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618576.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_SRR618576 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618576_1.fastq.gz SRR618576_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 00:20:05 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618576.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	58,522,558
Mapped reads	56,620,456 / 96.75%
Unmapped reads	1,902,102 / 3.25%
Mapped paired reads	56,620,456 / 96.75%
Mapped reads, first in pair	28,546,883 / 48.78%
Mapped reads, second in pair	28,073,573 / 47.97%
Mapped reads, both in pair	55,584,654 / 94.98%
Mapped reads, singletons	1,035,802 / 1.77%
Secondary alignments	0
Supplementary alignments	61,632 / 0.11%
Read min/max/mean length	30 / 100 / 100.04
Duplicated reads (estimated)	13,246,873 / 22.64%
Duplication rate	20.92%
Clipped reads	8,895,537 / 15.2%

2.2. ACGT Content

Number/percentage of A's	1,459,314,749 / 26.81%
Number/percentage of C's	1,244,149,438 / 22.86%
Number/percentage of T's	1,460,508,303 / 26.83%
Number/percentage of G's	1,278,797,422 / 23.49%
Number/percentage of N's	226,364 / 0%

GC Percentage	46.35%
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2.3. Coverage

Mean	1.7594
Standard Deviation	7.176

2.4. Mapping Quality

Mean Mapping Quality	54.02
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2.5. Insert size

Mean	23,818.13
Standard Deviation	1,539,535.94
P25/Median/P75	180 / 210 / 250

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	68,980,651
Insertions	939,958
Mapped reads with at least one insertion	1.64%
Deletions	2,491,355
Mapped reads with at least one deletion	4.3%
Homopolymer indels	52.46%

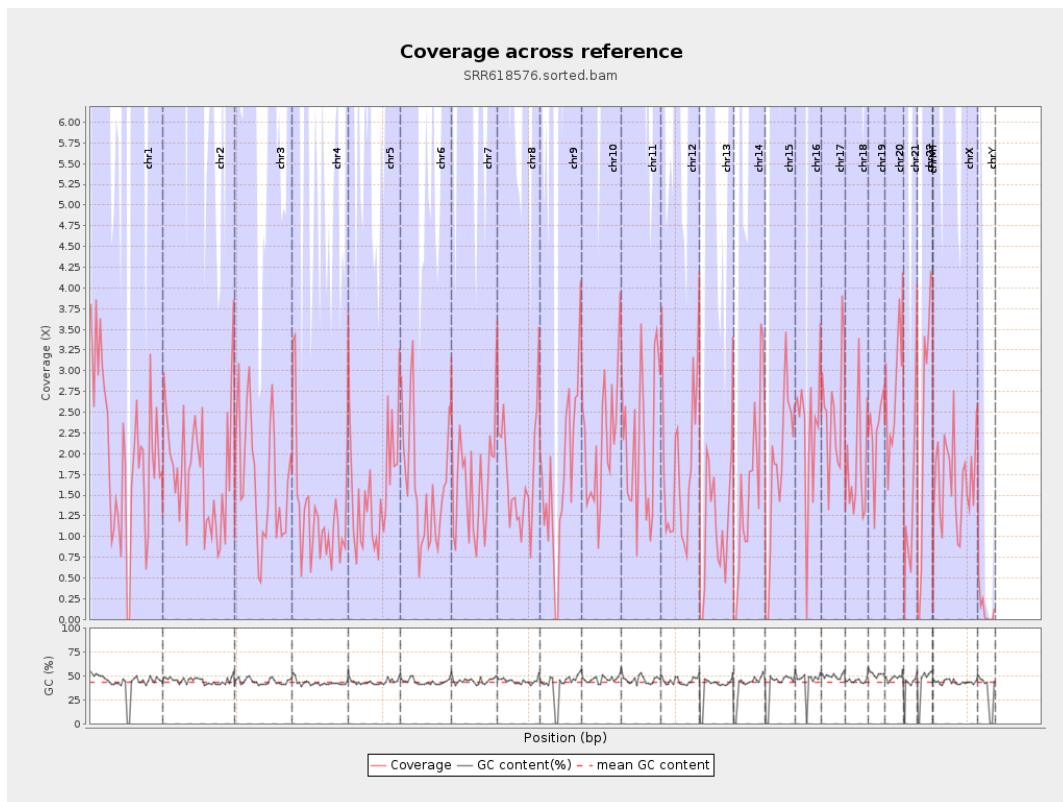
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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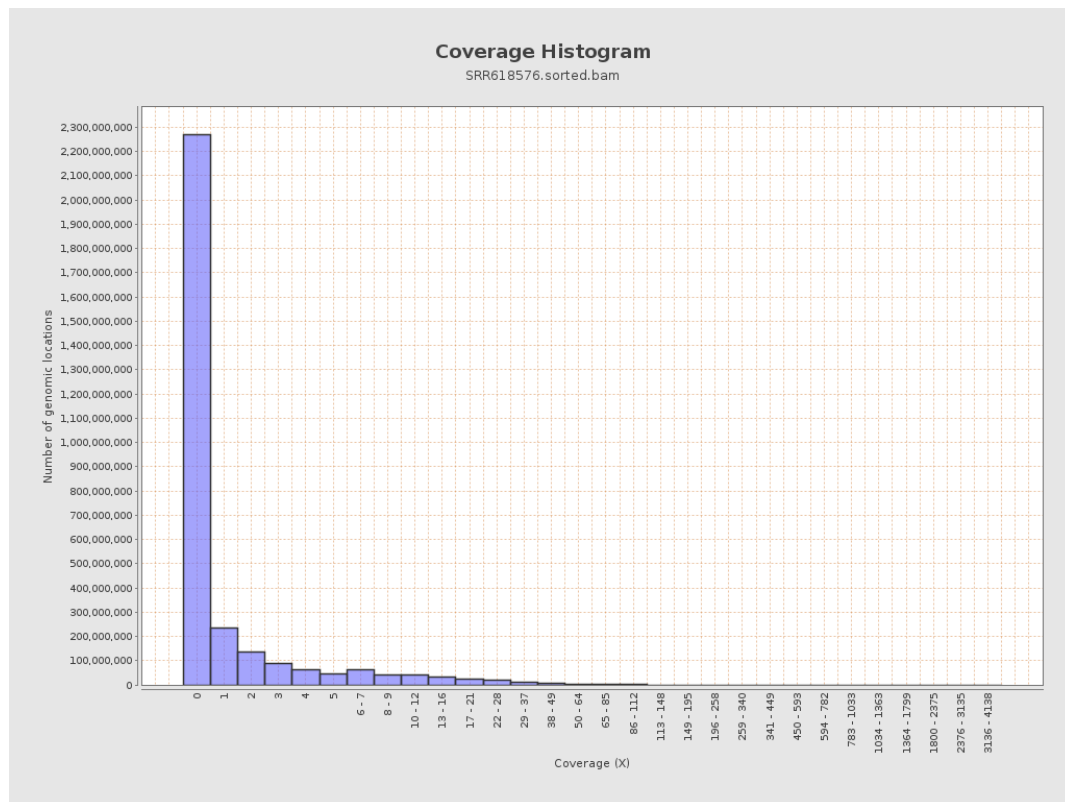
		bases	coverage	deviation
chr1	249250621	492689557	1.9767	8.1958
chr2	243199373	433854253	1.7839	7.2495
chr3	198022430	330828421	1.6707	6.0321
chr4	191154276	242905206	1.2707	6.0616
chr5	180915260	283917675	1.5693	5.7973
chr6	171115067	273639442	1.5992	5.9579
chr7	159138663	262753829	1.6511	6.1926
chr8	146364022	253364659	1.7311	6.275
chr9	141213431	244365521	1.7305	7.7433
chr10	135534747	285949215	2.1098	7.5489
chr11	135006516	285732093	2.1164	8.2373
chr12	133851895	246540304	1.8419	6.7086
chr13	115169878	132135540	1.1473	4.6915
chr14	107349540	171666995	1.5991	6.6859
chr15	102531392	187969966	1.8333	6.911
chr16	90354753	205533305	2.2747	10.176
chr17	81195210	201974186	2.4875	8.6907
chr18	78077248	138489091	1.7737	7.8352
chr19	59128983	133384595	2.2558	8.9444
chr20	63025520	173745557	2.7567	9.0666
chr21	48129895	71572249	1.4871	11.6034
chr22	51304566	122432161	2.3864	9.3707
chrMT	16571	1192	0.0719	0.4222
chrX	155270560	263964889	1.7	6.1501

chrY	59373566	7004231	0.118	2.9067
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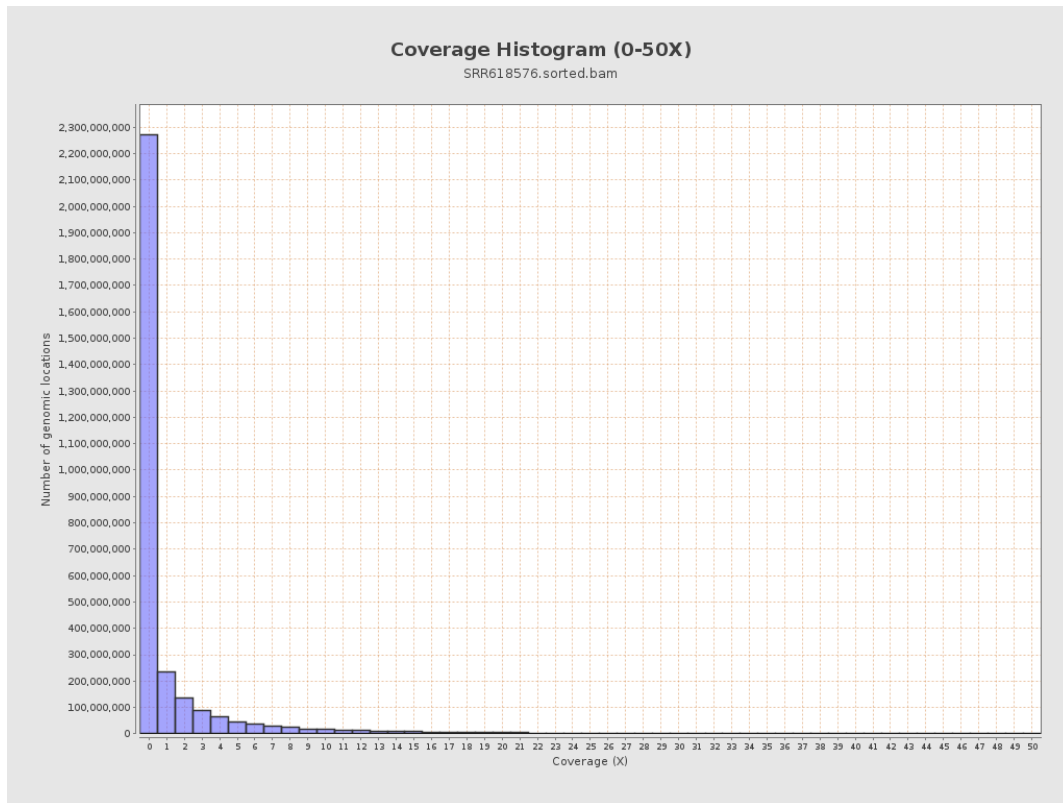
3. Results : Coverage across reference



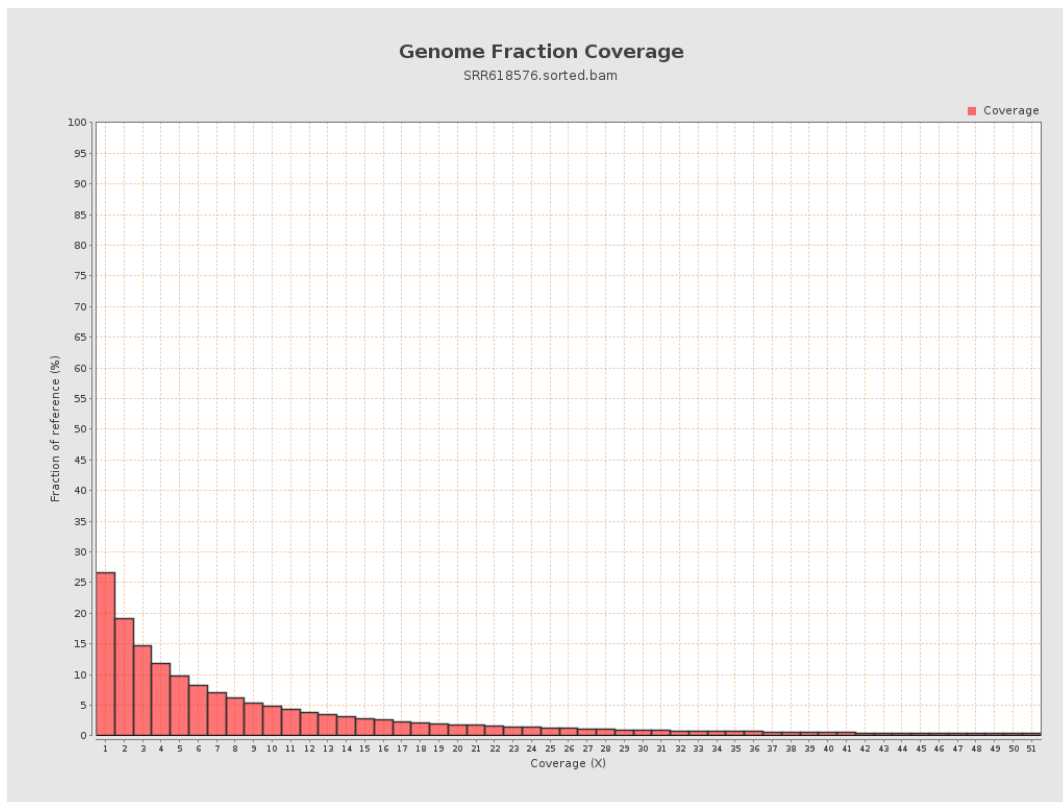
4. Results : Coverage Histogram



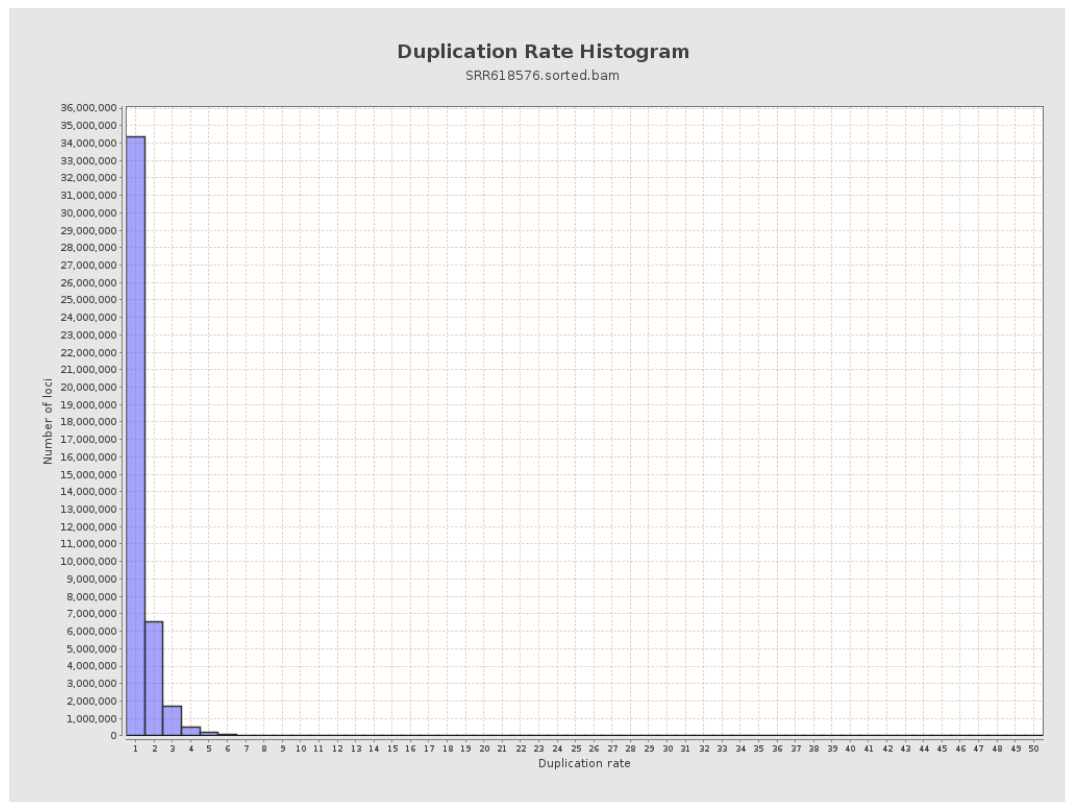
5. Results : Coverage Histogram (0-50X)



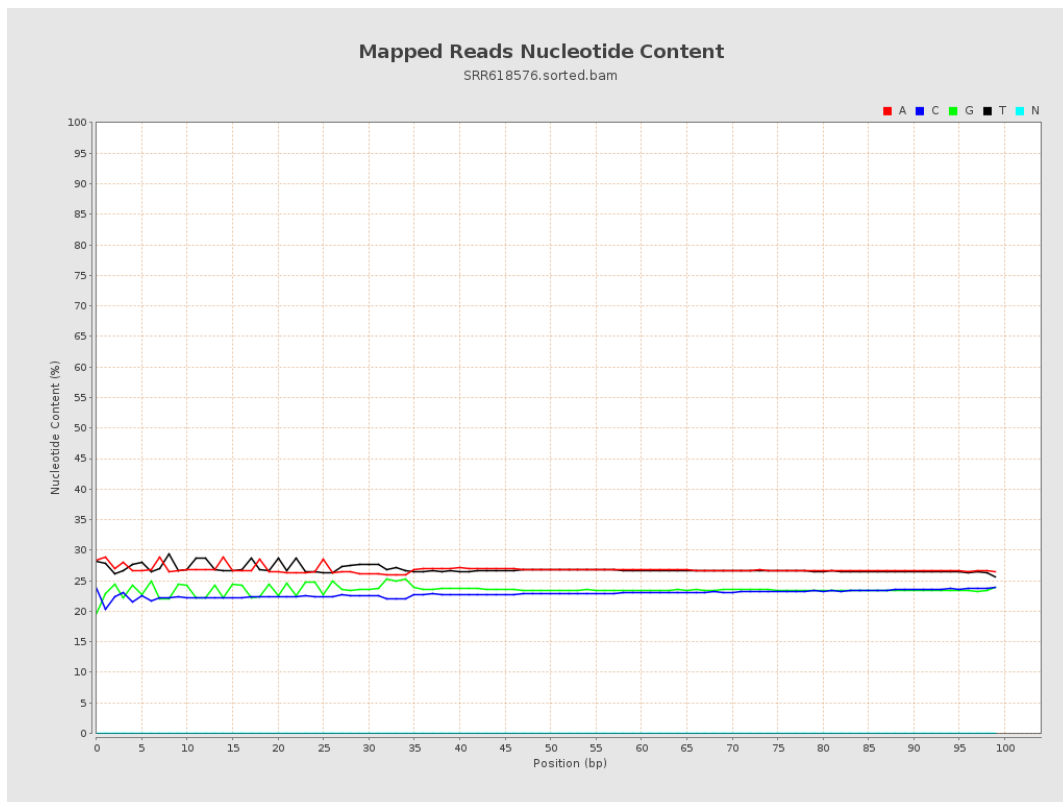
6. Results : Genome Fraction Coverage



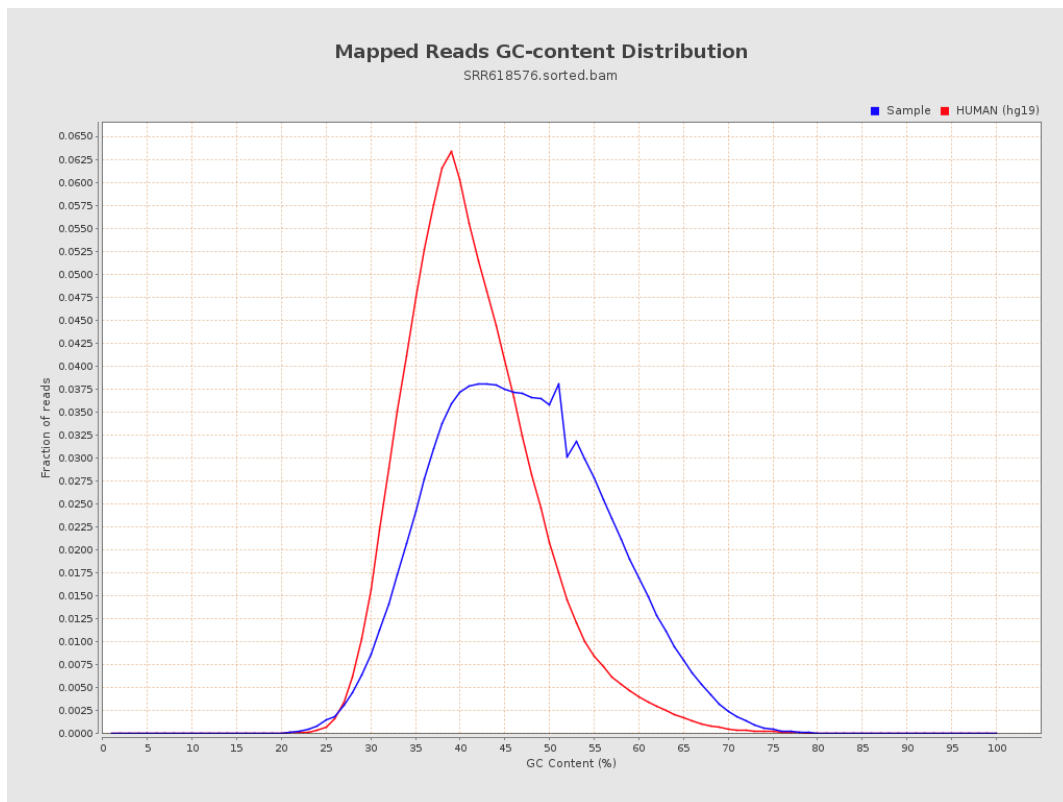
7. Results : Duplication Rate Histogram



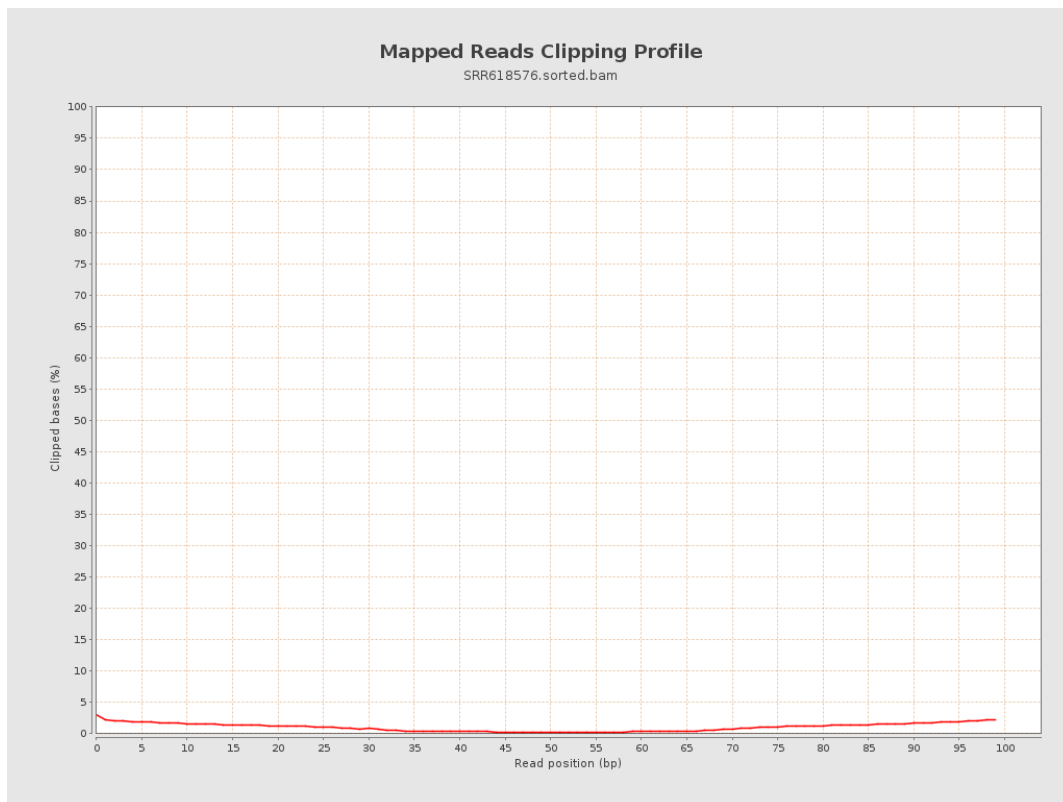
8. Results : Mapped Reads Nucleotide Content



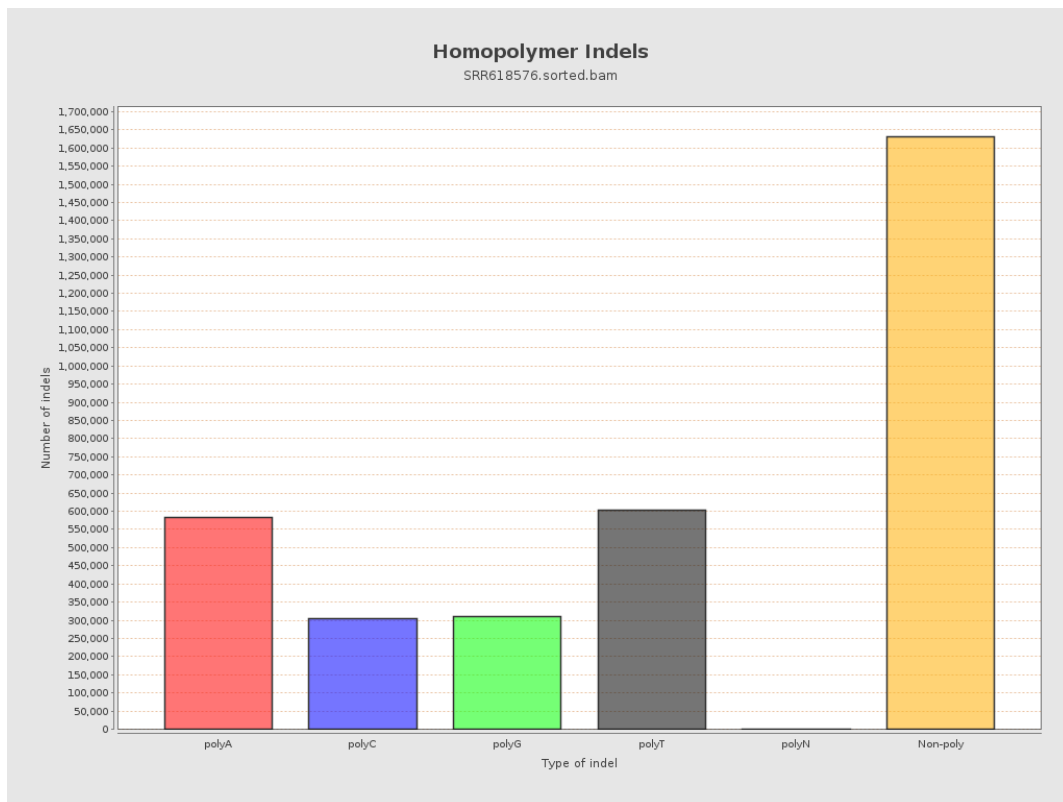
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



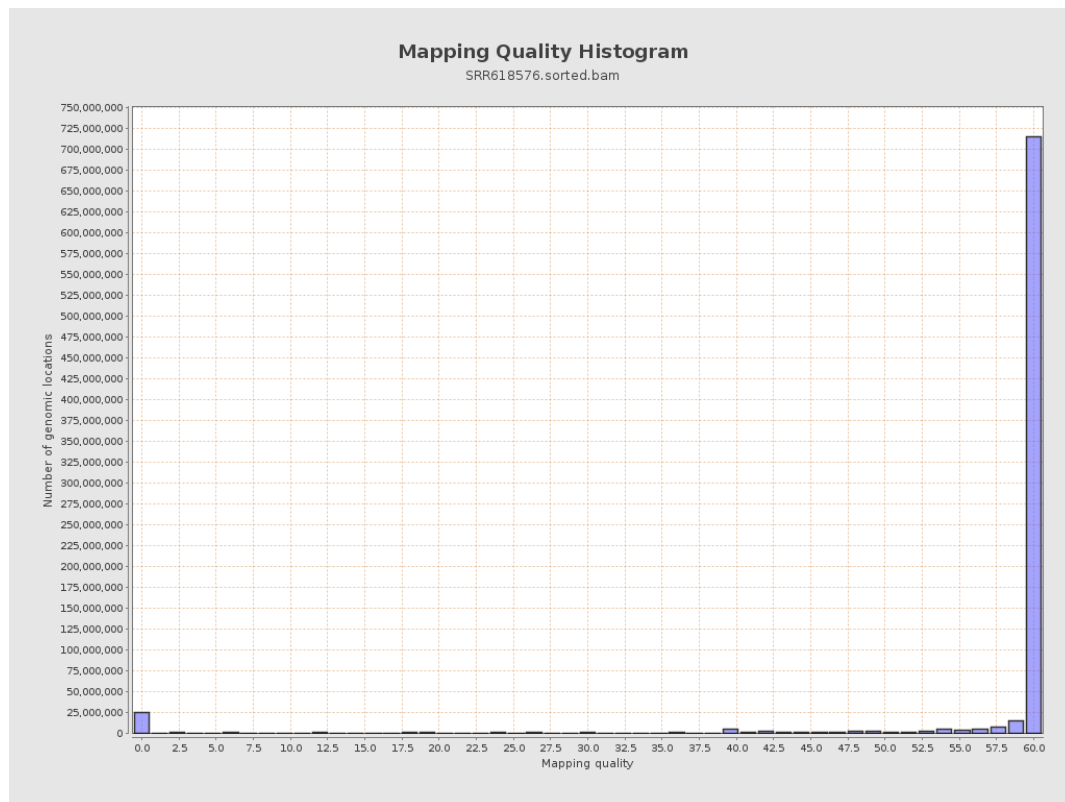
11. Results : Homopolymer Indels



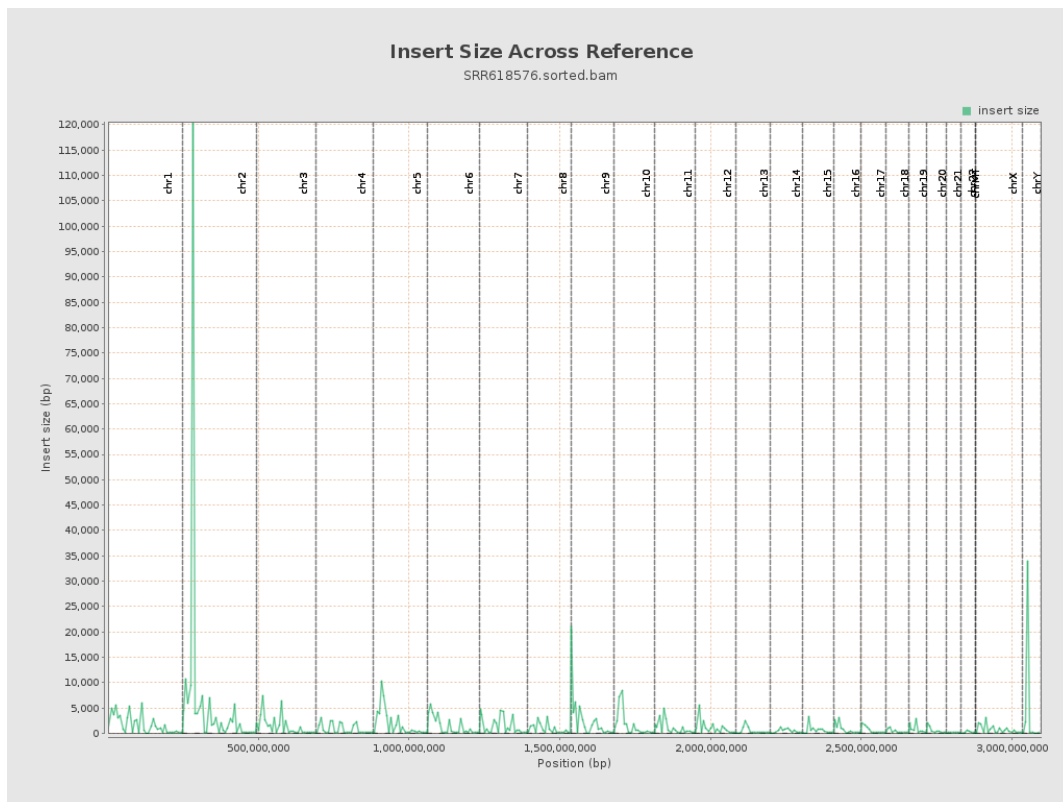
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

