

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 09:41:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618585.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_SRR618585 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618585_1.fastq.gz SRR618585_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 09:41:40 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618585.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	63,657,516
Mapped reads	54,407,376 / 85.47%
Unmapped reads	9,250,140 / 14.53%
Mapped paired reads	54,407,376 / 85.47%
Mapped reads, first in pair	27,483,657 / 43.17%
Mapped reads, second in pair	26,923,719 / 42.29%
Mapped reads, both in pair	53,316,754 / 83.76%
Mapped reads, singletons	1,090,622 / 1.71%
Secondary alignments	0
Supplementary alignments	157,454 / 0.25%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	9,920,537 / 15.58%
Duplication rate	15.71%
Clipped reads	11,913,145 / 18.71%

2.2. ACGT Content

Number/percentage of A's	1,394,633,398 / 27.21%
Number/percentage of C's	1,123,013,256 / 21.91%
Number/percentage of T's	1,414,109,926 / 27.59%
Number/percentage of G's	1,193,106,004 / 23.28%
Number/percentage of N's	248,857 / 0%

GC Percentage	45.19%
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2.3. Coverage

Mean	1.6567
Standard Deviation	6.1583

2.4. Mapping Quality

Mean Mapping Quality	53.58
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2.5. Insert size

Mean	57,206
Standard Deviation	2,371,643.51
P25/Median/P75	161 / 188 / 226

2.6. Mismatches and indels

General error rate	1.28%
Mismatches	64,139,138
Insertions	910,656
Mapped reads with at least one insertion	1.65%
Deletions	2,563,005
Mapped reads with at least one deletion	4.59%
Homopolymer indels	52.81%

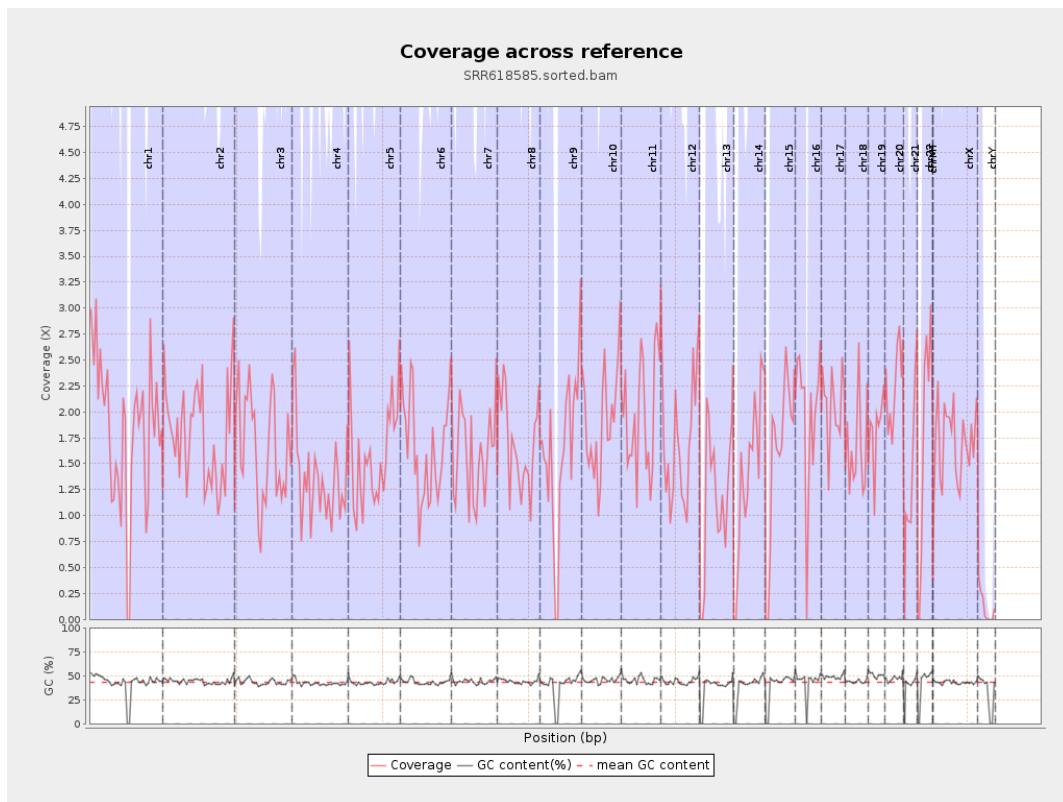
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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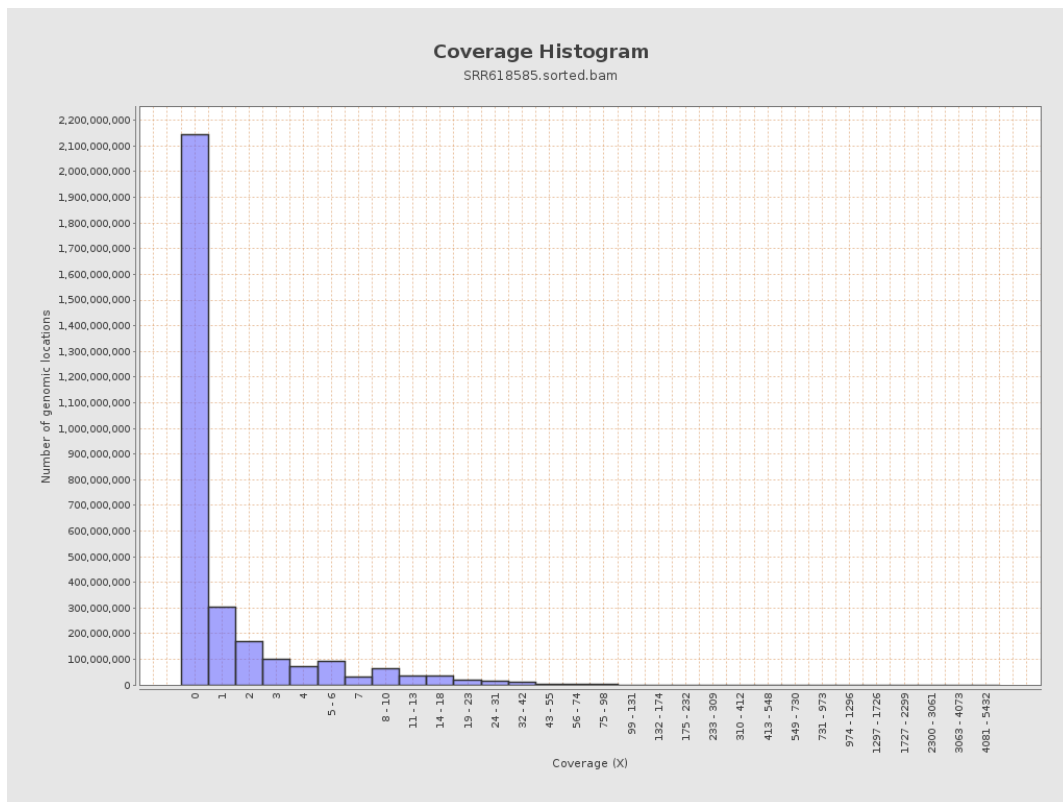
		bases	coverage	deviation
chr1	249250621	451410766	1.8111	7.3659
chr2	243199373	434218781	1.7854	6.9691
chr3	198022430	324184982	1.6371	5.0554
chr4	191154276	259468587	1.3574	4.7985
chr5	180915260	290725021	1.607	5.0092
chr6	171115067	279406845	1.6329	5.3193
chr7	159138663	255313519	1.6043	5.0836
chr8	146364022	247628093	1.6919	5.295
chr9	141213431	228607309	1.6189	7.4947
chr10	135534747	257873814	1.9026	5.8674
chr11	135006516	264988469	1.9628	7.4908
chr12	133851895	230026836	1.7185	5.374
chr13	115169878	135755583	1.1787	4.0619
chr14	107349540	152815920	1.4235	4.8212
chr15	102531392	164208771	1.6015	5.3397
chr16	90354753	177325523	1.9625	10.936
chr17	81195210	167986181	2.0689	6.8288
chr18	78077248	126919668	1.6256	7.1227
chr19	59128983	107720482	1.8218	6.6242
chr20	63025520	141258375	2.2413	6.4653
chr21	48129895	67964642	1.4121	7.1989
chr22	51304566	89580065	1.746	6.2281
chrMT	16571	6051	0.3652	1.2178
chrX	155270560	266235617	1.7147	5.2508

chrY	59373566	6955699	0.1172	3.736
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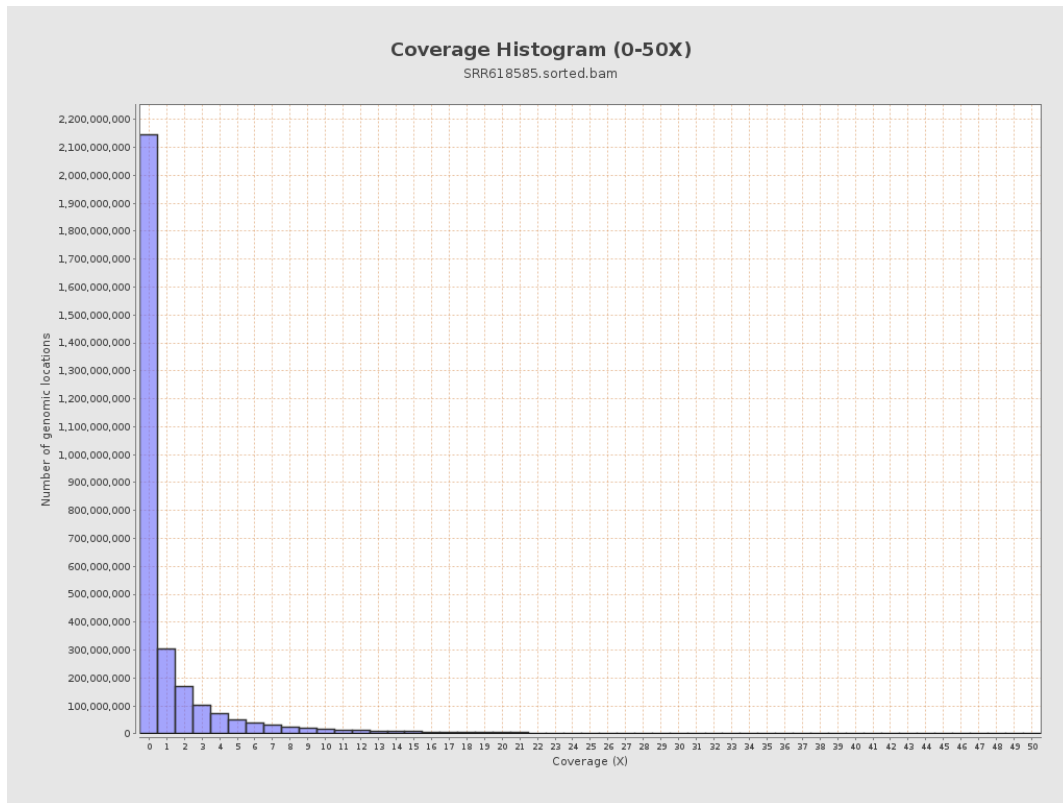
3. Results : Coverage across reference



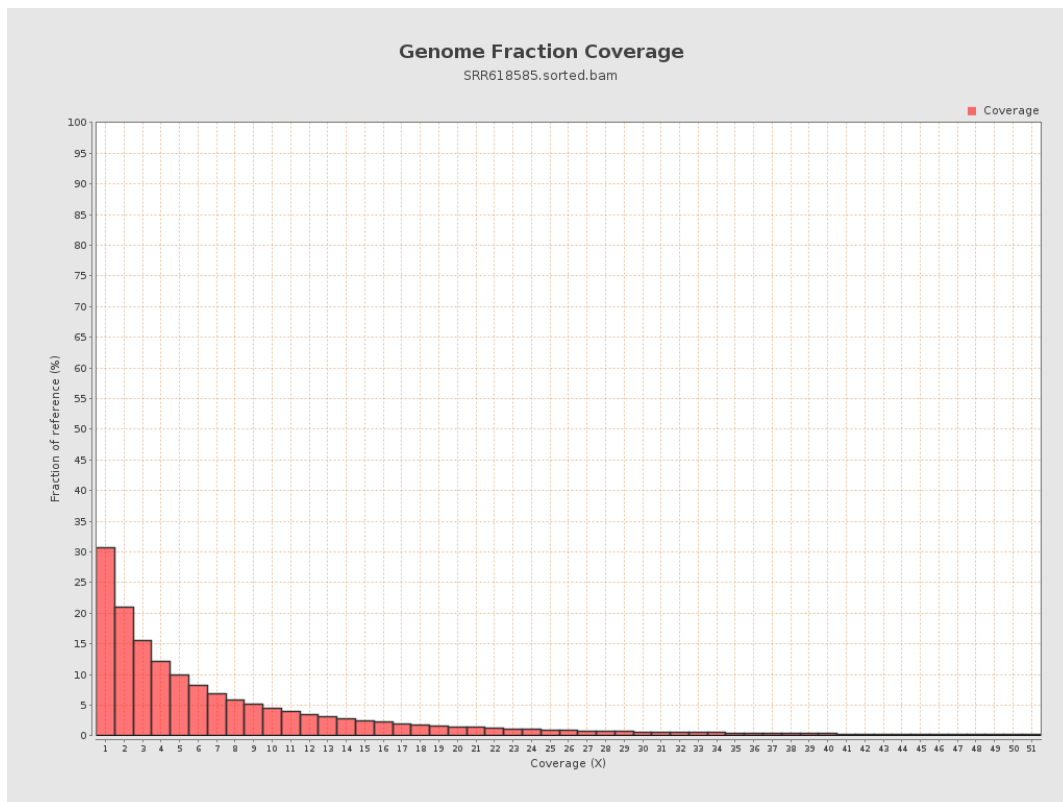
4. Results : Coverage Histogram



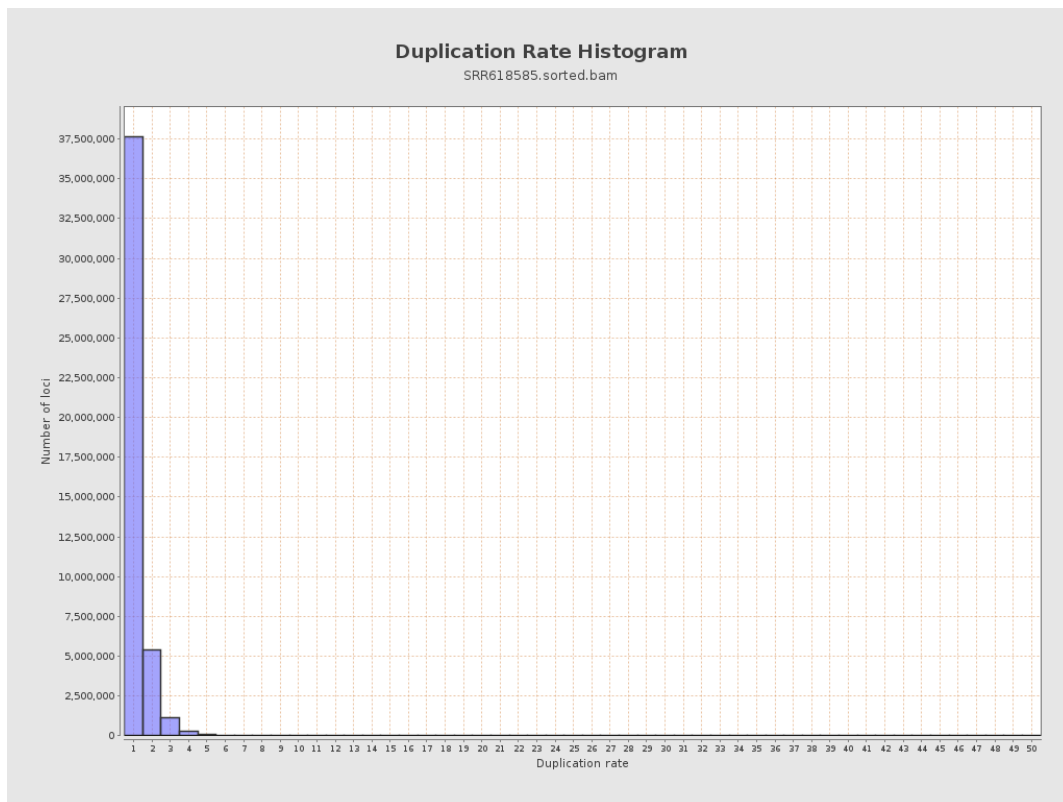
5. Results : Coverage Histogram (0-50X)



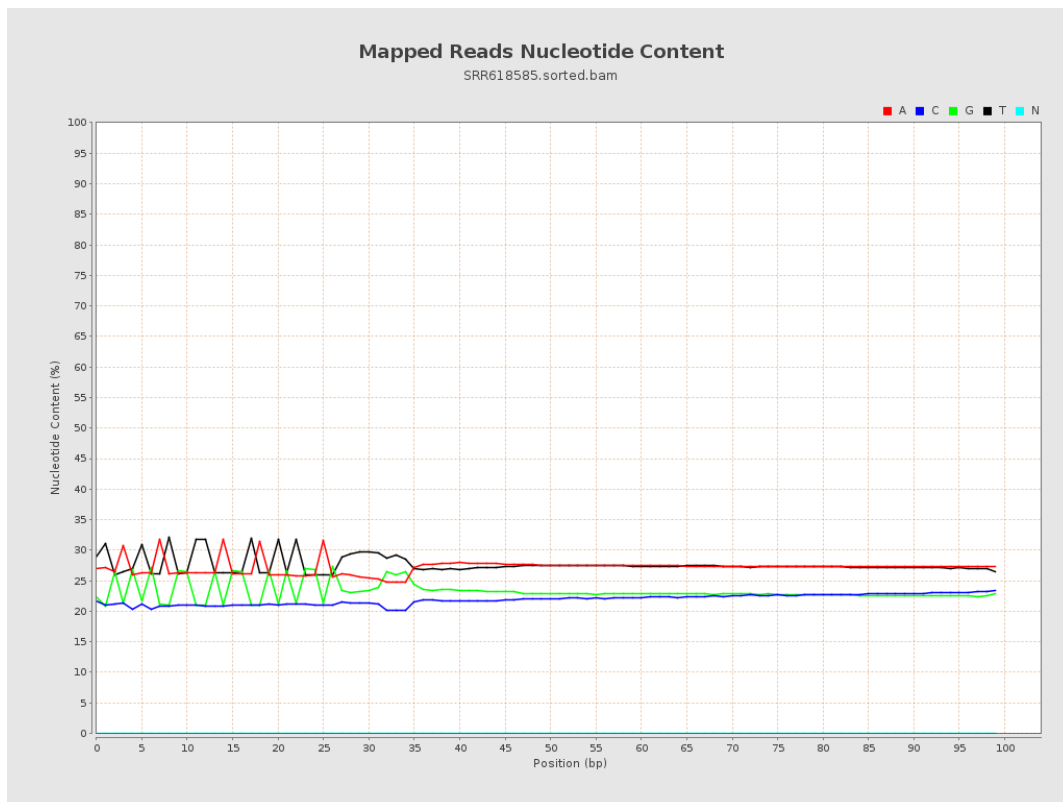
6. Results : Genome Fraction Coverage



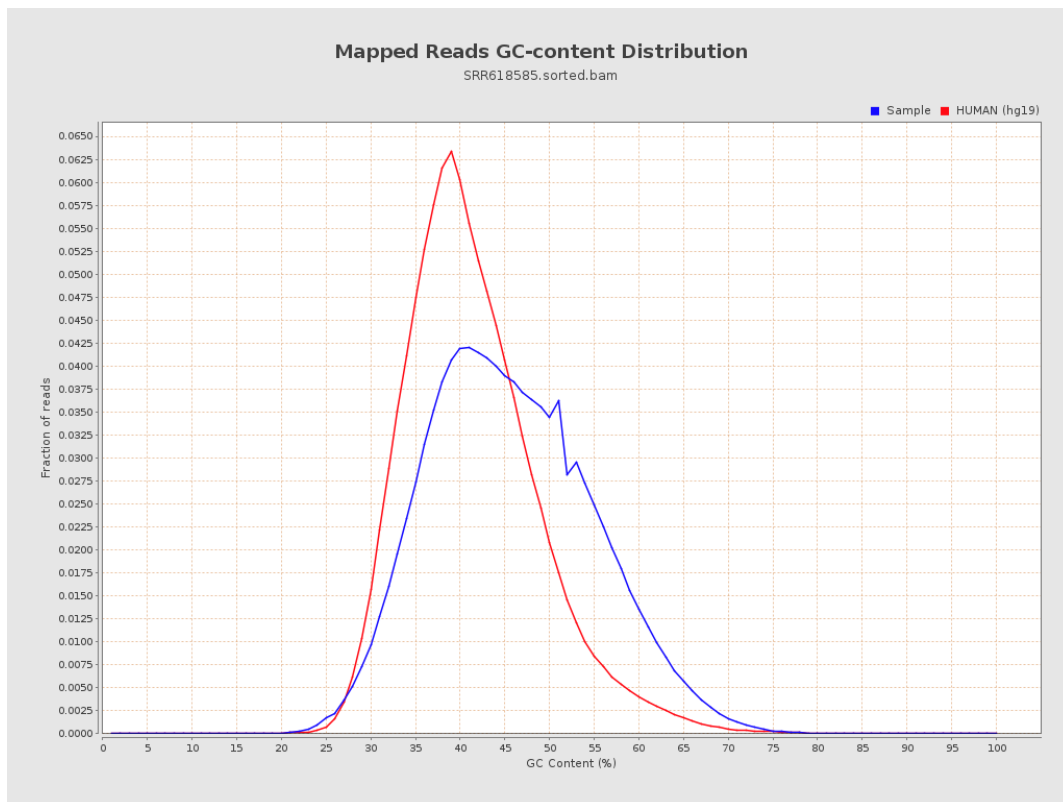
7. Results : Duplication Rate Histogram



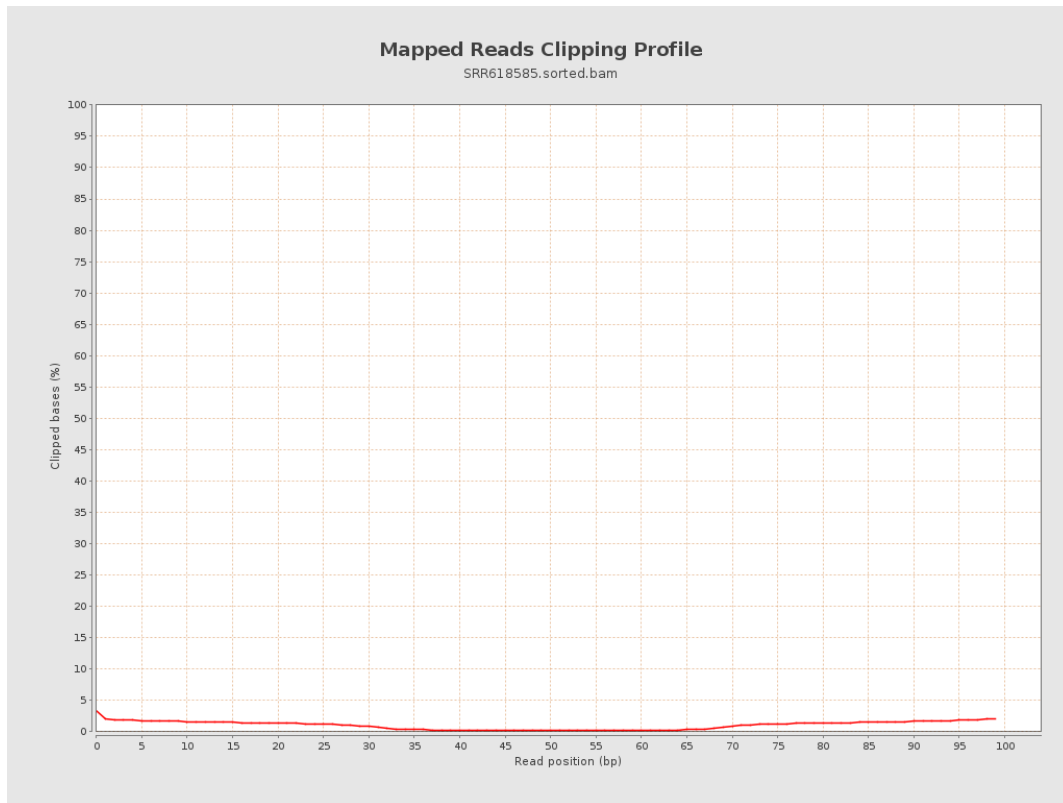
8. Results : Mapped Reads Nucleotide Content



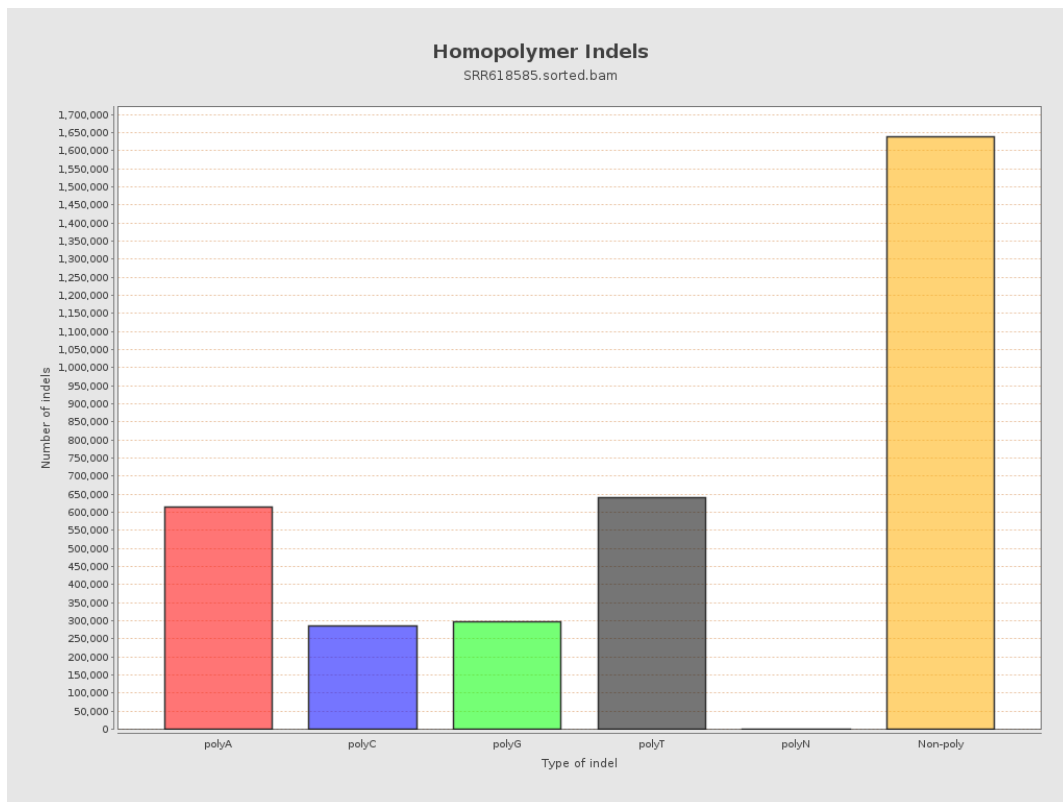
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



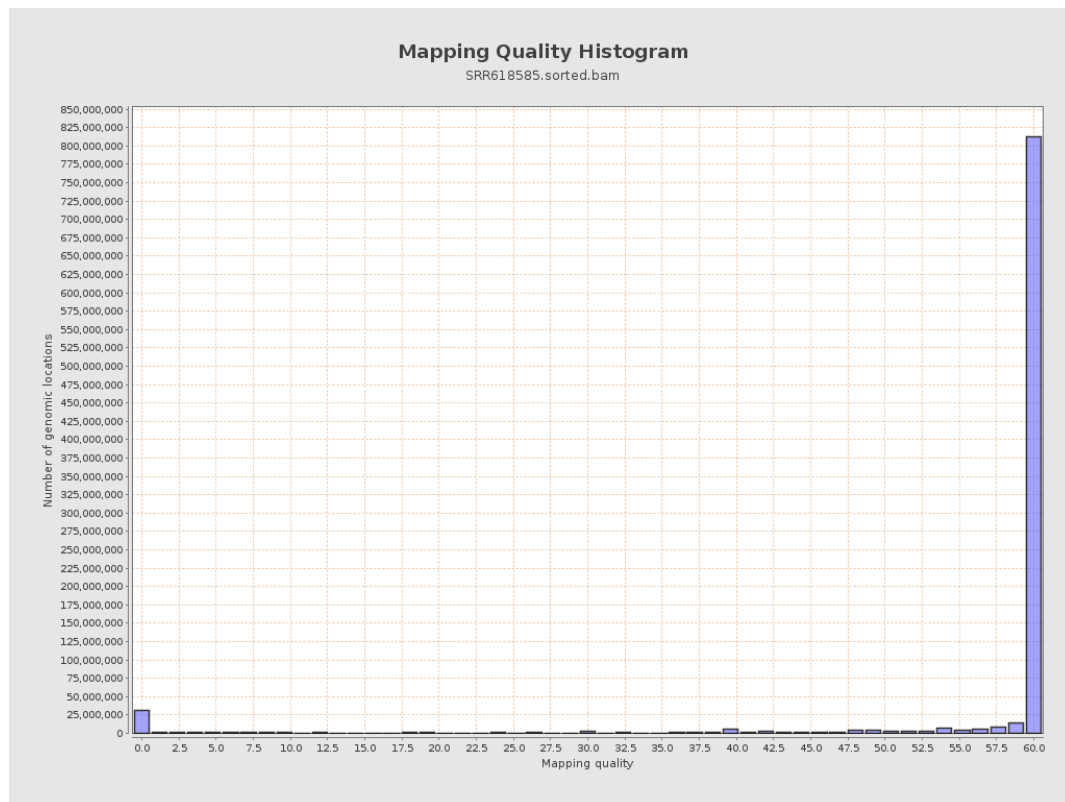
11. Results : Homopolymer Indels



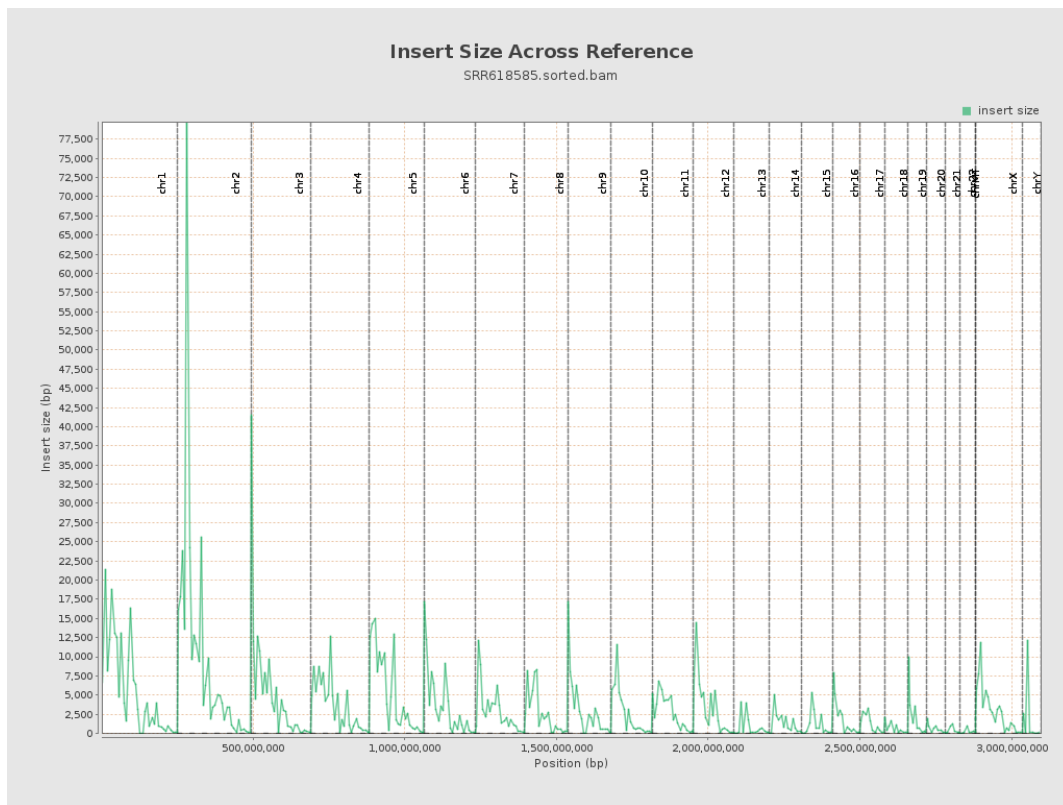
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

