

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 08:36:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618584.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_SRR618584 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618584_1.fastq.gz SRR618584_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 08:36:48 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618584.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	65,423,242
Mapped reads	63,040,982 / 96.36%
Unmapped reads	2,382,260 / 3.64%
Mapped paired reads	63,040,982 / 96.36%
Mapped reads, first in pair	31,861,399 / 48.7%
Mapped reads, second in pair	31,179,583 / 47.66%
Mapped reads, both in pair	61,736,660 / 94.37%
Mapped reads, singletons	1,304,322 / 1.99%
Secondary alignments	0
Supplementary alignments	266,349 / 0.41%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	20,167,883 / 30.83%
Duplication rate	26.37%
Clipped reads	14,878,580 / 22.74%

2.2. ACGT Content

Number/percentage of A's	1,623,946,573 / 27.48%
Number/percentage of C's	1,271,738,384 / 21.52%
Number/percentage of T's	1,646,768,282 / 27.87%
Number/percentage of G's	1,366,442,323 / 23.12%
Number/percentage of N's	259,816 / 0%

GC Percentage	44.65%
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2.3. Coverage

Mean	1.9101
Standard Deviation	7.6049

2.4. Mapping Quality

Mean Mapping Quality	53.58
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2.5. Insert size

Mean	71,418.62
Standard Deviation	2,642,298.41
P25/Median/P75	167 / 196 / 233

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	74,684,708
Insertions	1,081,485
Mapped reads with at least one insertion	1.69%
Deletions	2,966,687
Mapped reads with at least one deletion	4.59%
Homopolymer indels	52.58%

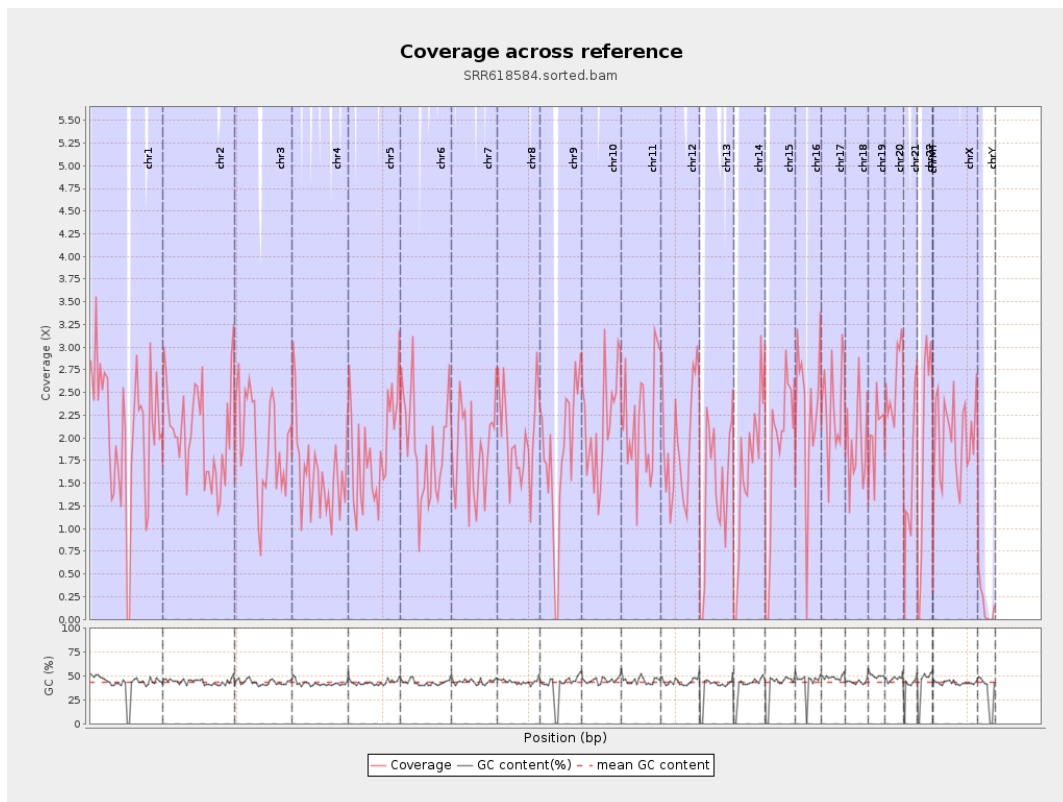
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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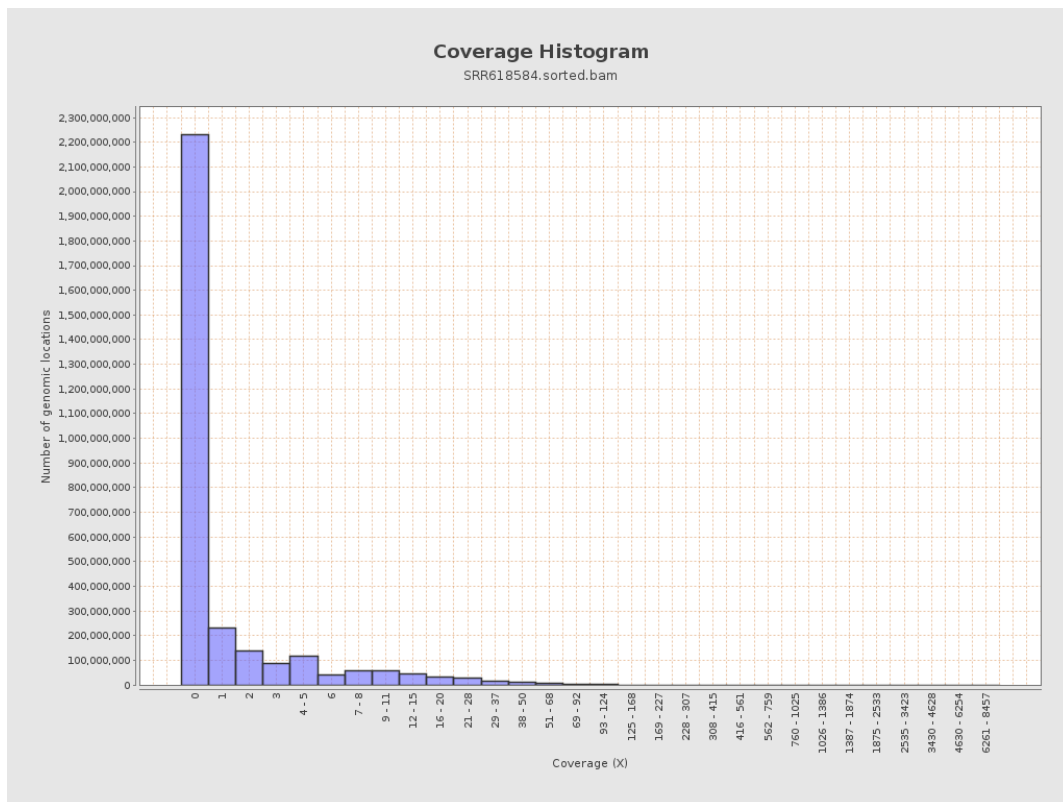
		bases	coverage	deviation
chr1	249250621	513695719	2.061	9.2088
chr2	243199373	498149142	2.0483	9.1081
chr3	198022430	383048851	1.9344	6.1007
chr4	191154276	308414135	1.6134	6.0353
chr5	180915260	338748213	1.8724	6.1515
chr6	171115067	324928098	1.8989	6.4346
chr7	159138663	294445596	1.8502	6.1248
chr8	146364022	292093828	1.9957	7.1199
chr9	141213431	255072124	1.8063	7.282
chr10	135534747	289969064	2.1394	7.0033
chr11	135006516	294645233	2.1825	7.6934
chr12	133851895	262616811	1.962	6.7207
chr13	115169878	163783772	1.4221	5.4159
chr14	107349540	176419715	1.6434	5.9878
chr15	102531392	189504843	1.8483	6.9412
chr16	90354753	205160885	2.2706	16.0698
chr17	81195210	189581482	2.3349	8.0606
chr18	78077248	149145394	1.9102	7.0486
chr19	59128983	120911775	2.0449	8.2064
chr20	63025520	165725270	2.6295	8.1291
chr21	48129895	75201594	1.5625	8.5897
chr22	51304566	100562964	1.9601	7.5811
chrMT	16571	4673	0.282	2.5147
chrX	155270560	312379146	2.0118	6.3863

chrY	59373566	9019429	0.1519	5.7063
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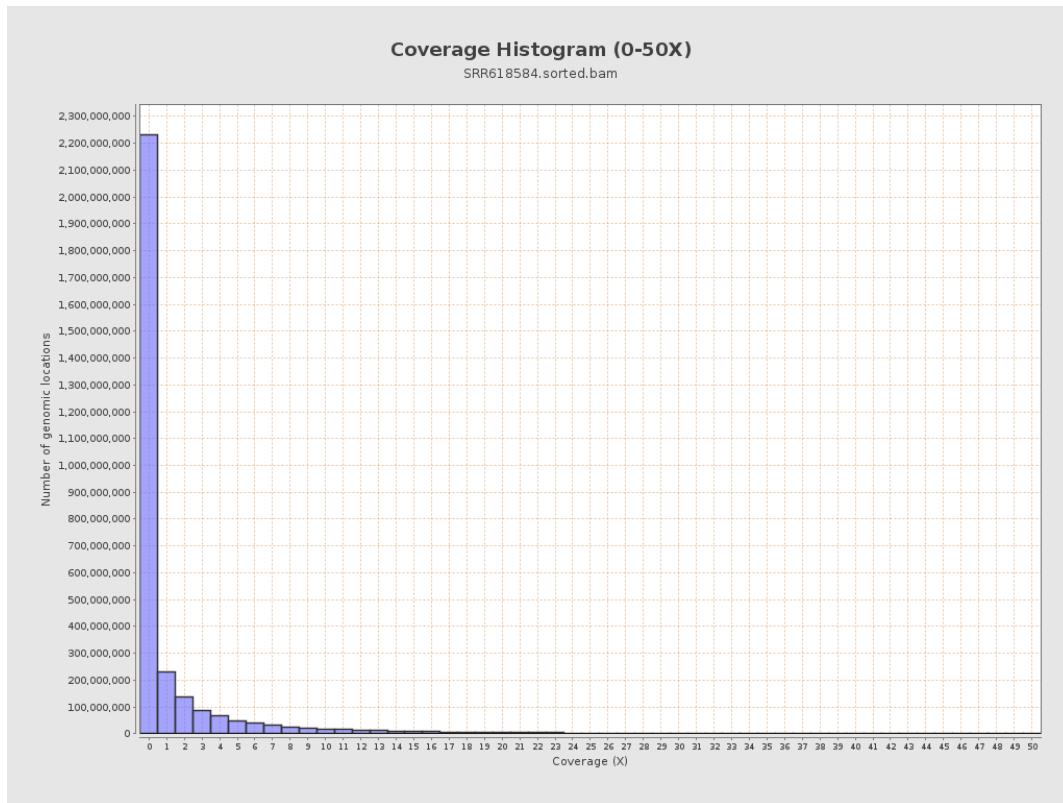
3. Results : Coverage across reference



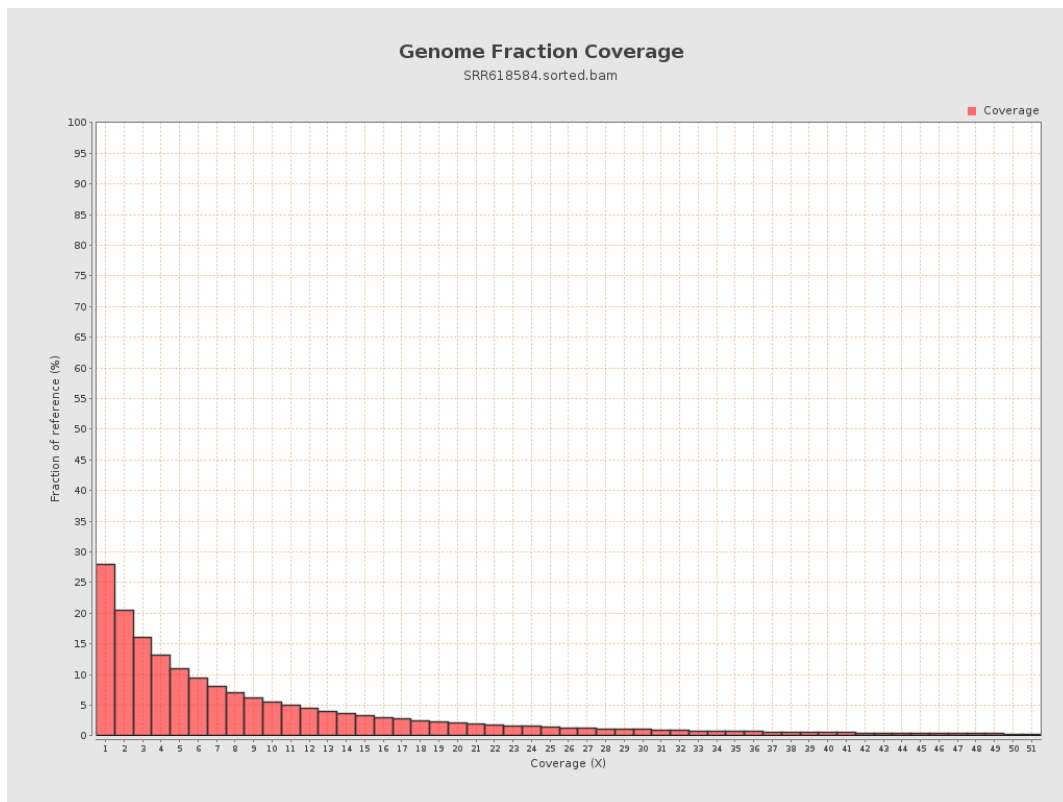
4. Results : Coverage Histogram



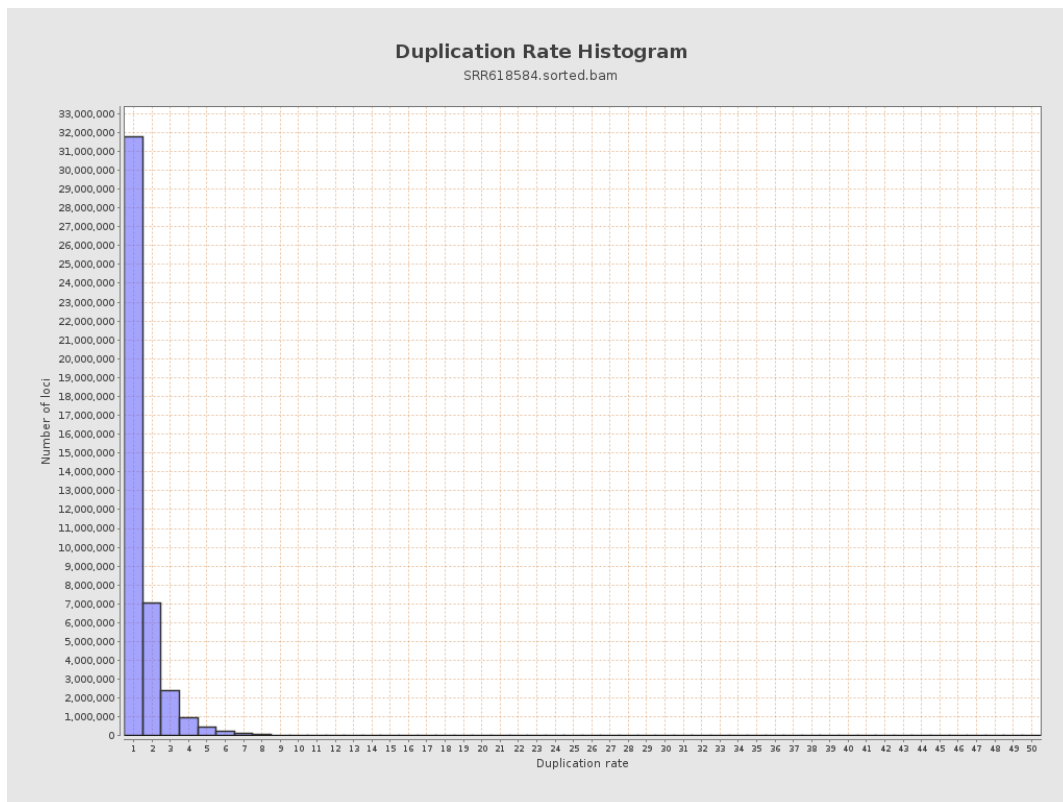
5. Results : Coverage Histogram (0-50X)



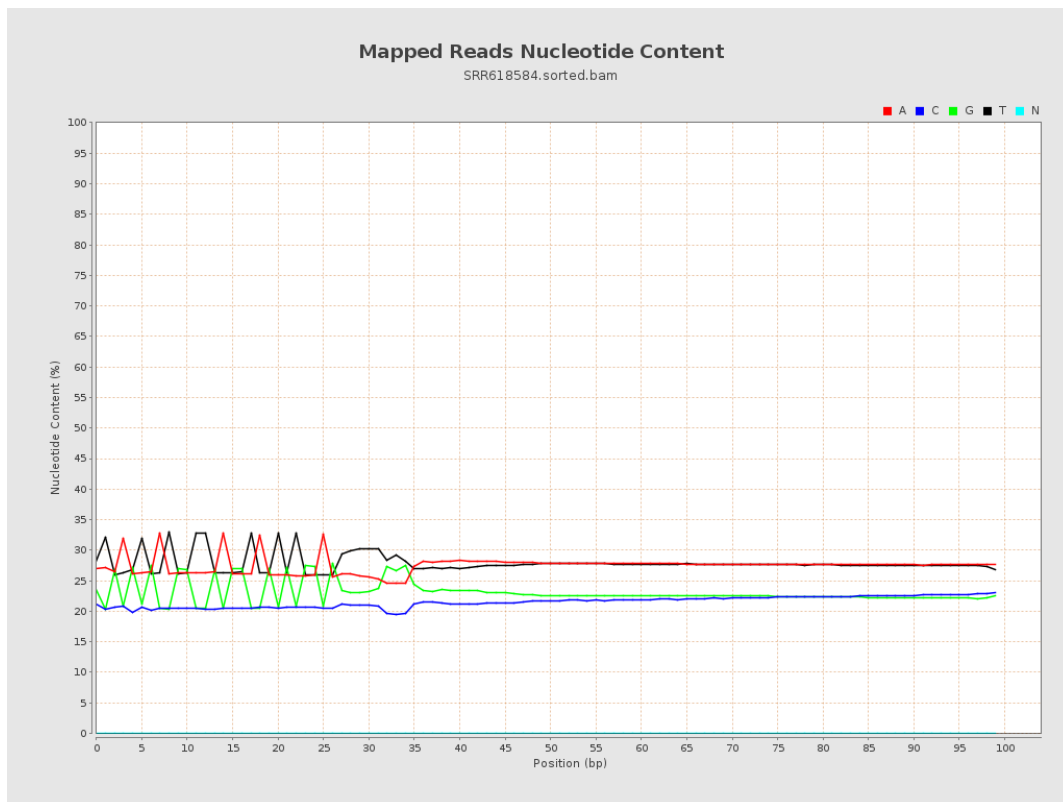
6. Results : Genome Fraction Coverage



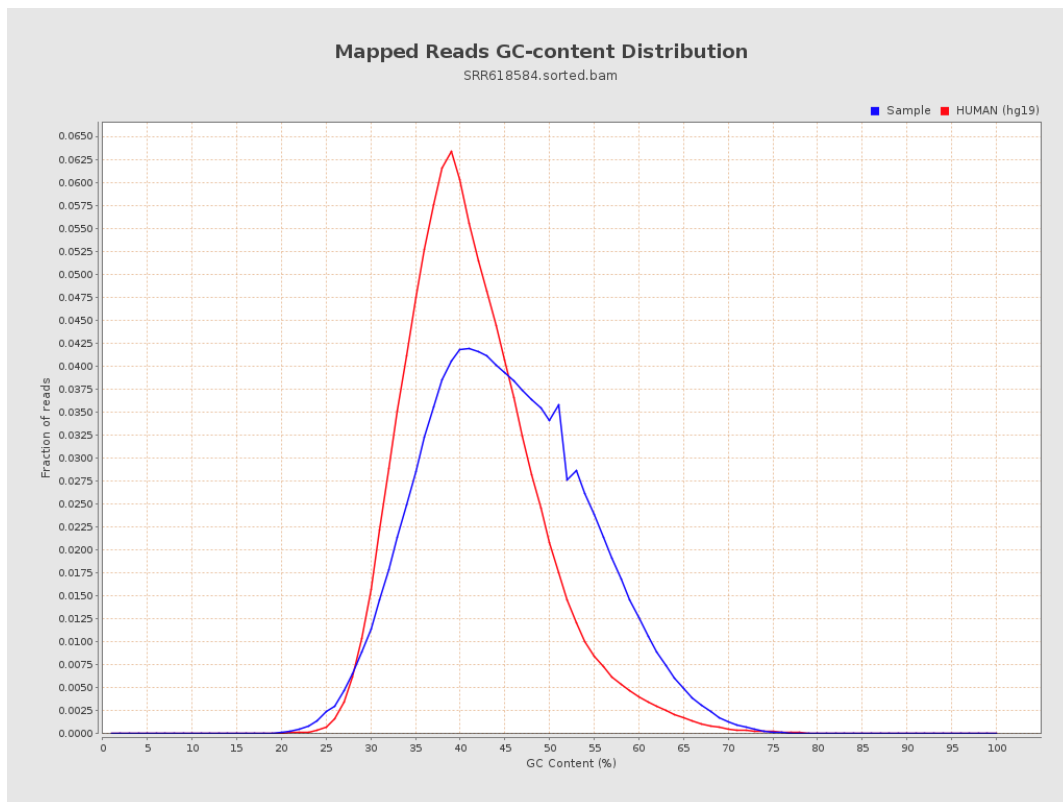
7. Results : Duplication Rate Histogram



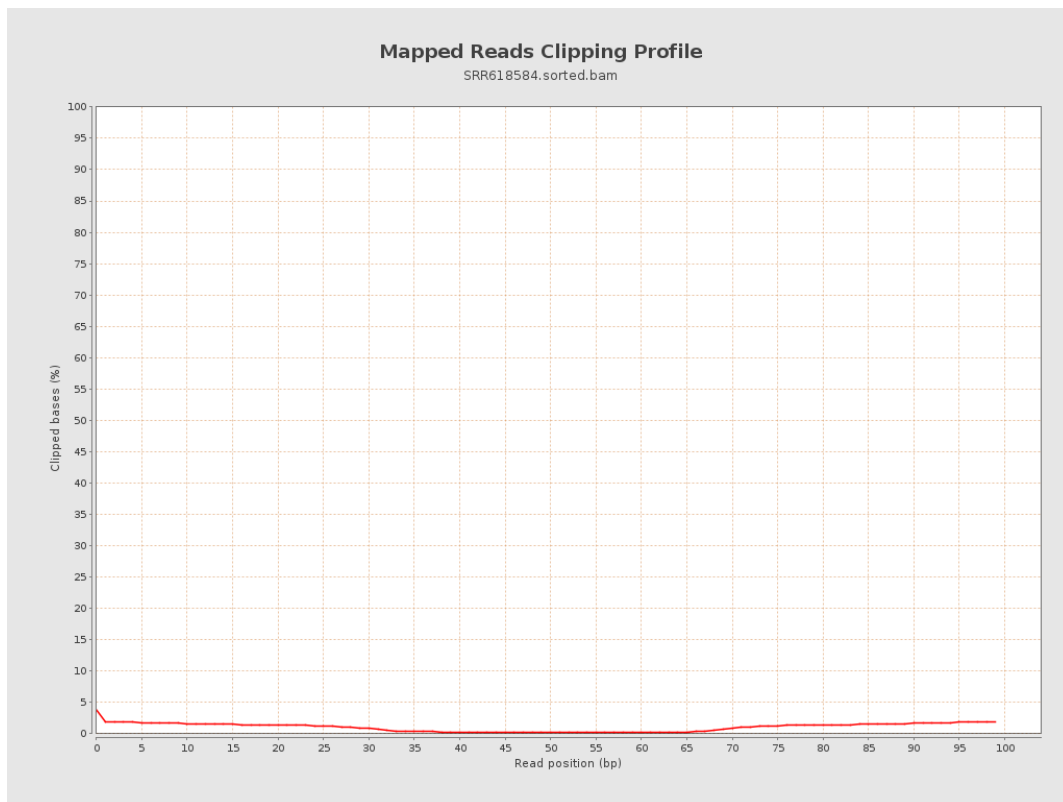
8. Results : Mapped Reads Nucleotide Content



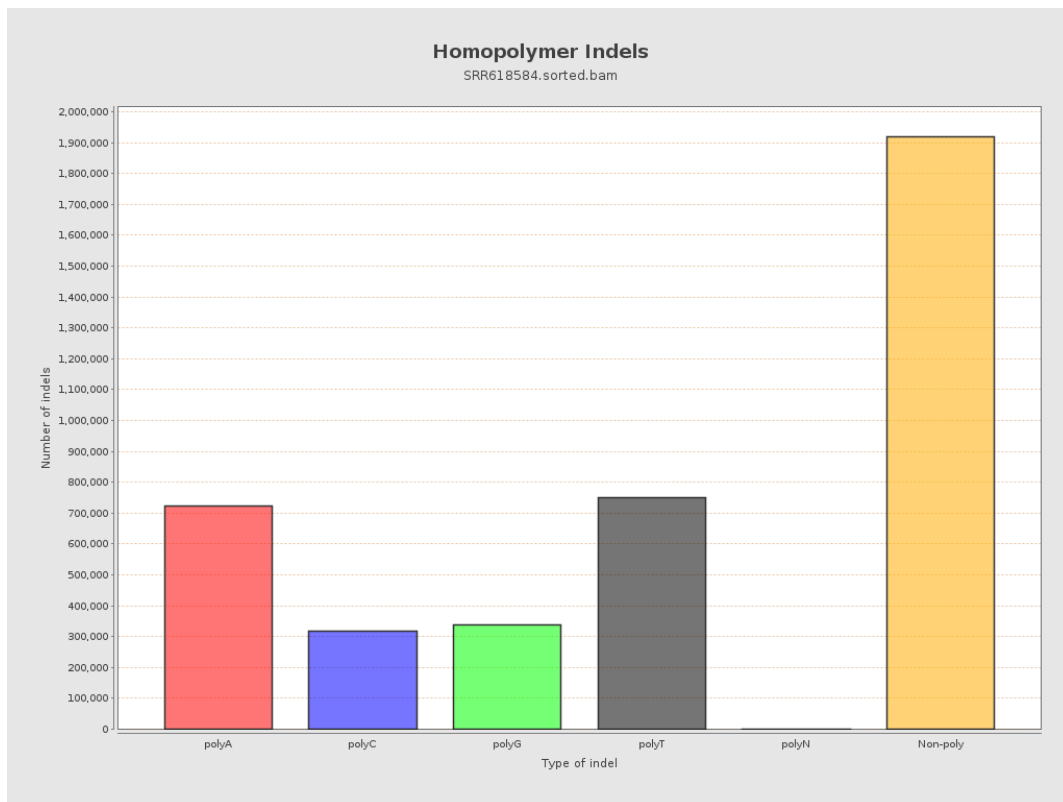
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



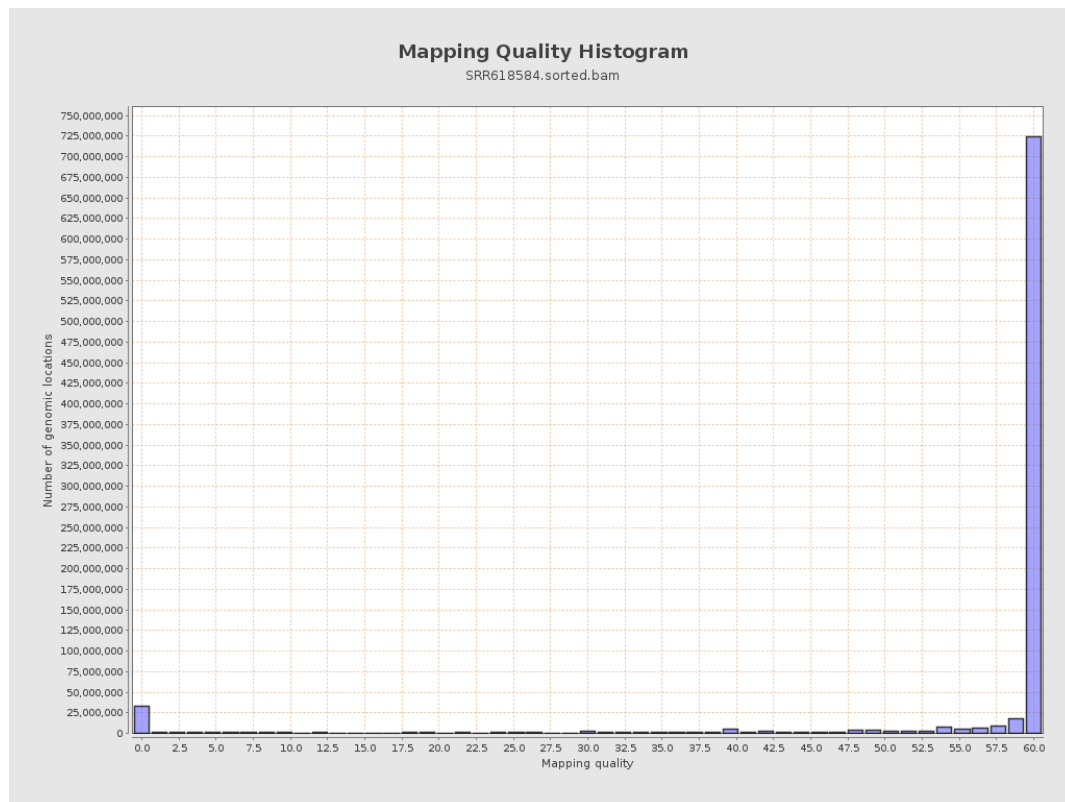
11. Results : Homopolymer Indels



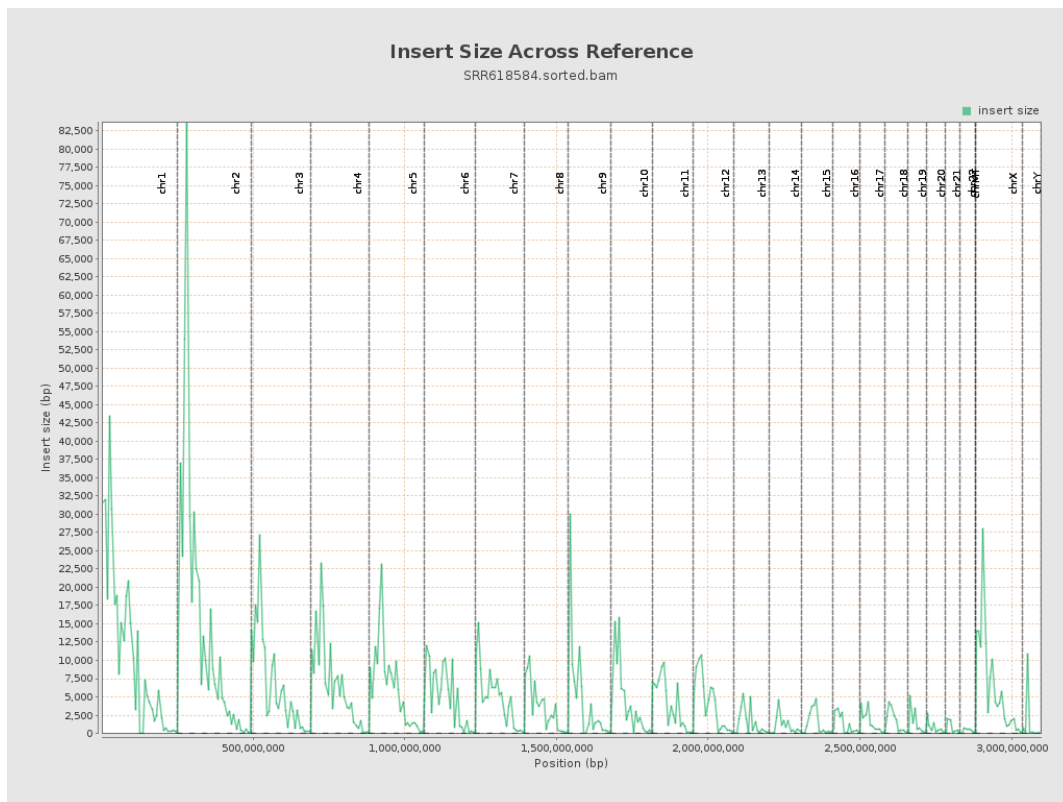
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

