

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 10:11:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618616.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_SRR618616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618616_1.fastq.gz SRR618616_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 10:11:51 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,972,054
Mapped reads	30,325,080 / 84.3%
Unmapped reads	5,646,974 / 15.7%
Mapped paired reads	30,325,080 / 84.3%
Mapped reads, first in pair	15,354,130 / 42.68%
Mapped reads, second in pair	14,970,950 / 41.62%
Mapped reads, both in pair	29,324,382 / 81.52%
Mapped reads, singletons	1,000,698 / 2.78%
Secondary alignments	0
Supplementary alignments	52,172 / 0.15%
Read min/max/mean length	30 / 100 / 100.06
Duplicated reads (estimated)	7,355,081 / 20.45%
Duplication rate	21.27%
Clipped reads	5,252,382 / 14.6%

2.2. ACGT Content

Number/percentage of A's	773,961,904 / 26.74%
Number/percentage of C's	655,291,347 / 22.64%
Number/percentage of T's	778,404,415 / 26.89%
Number/percentage of G's	686,851,764 / 23.73%
Number/percentage of N's	160,420 / 0.01%

GC Percentage	46.37%
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2.3. Coverage

Mean	0.9357
Standard Deviation	4.2049

2.4. Mapping Quality

Mean Mapping Quality	52.53
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2.5. Insert size

Mean	37,036
Standard Deviation	1,916,011.18
P25/Median/P75	188 / 216 / 253

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	33,541,294
Insertions	503,754
Mapped reads with at least one insertion	1.63%
Deletions	1,318,724
Mapped reads with at least one deletion	4.25%
Homopolymer indels	52.44%

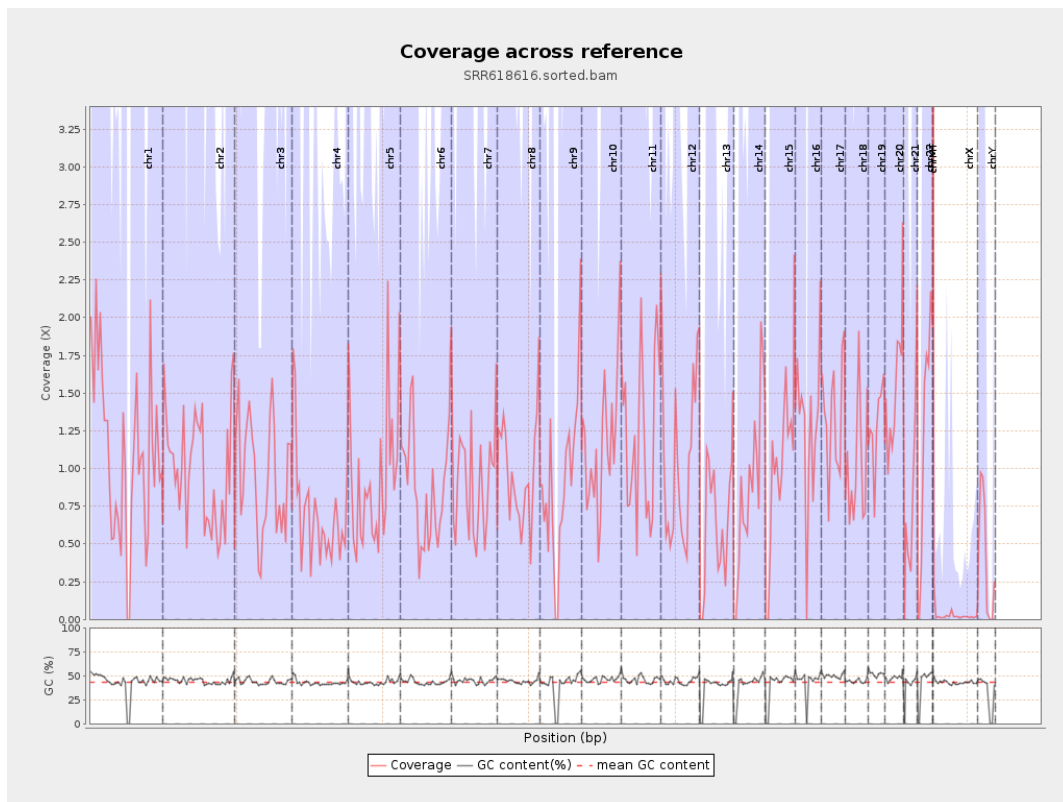
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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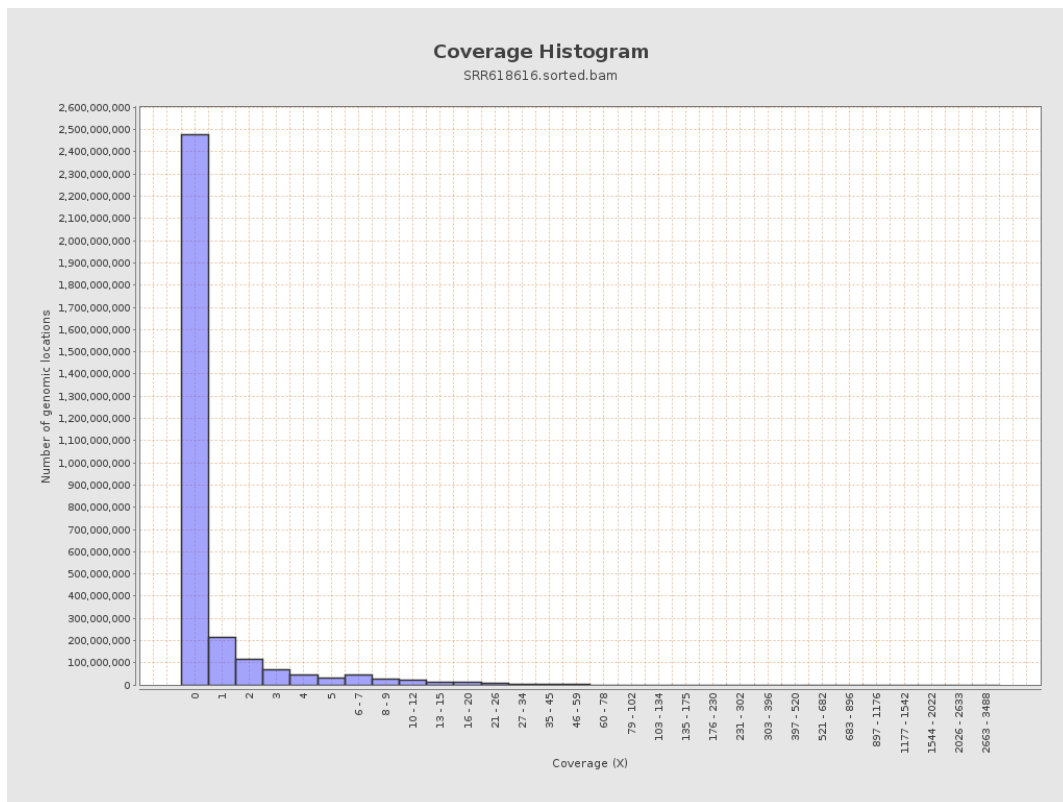
		bases	coverage	deviation
chr1	249250621	271686077	1.09	4.9401
chr2	243199373	241305825	0.9922	4.7426
chr3	198022430	187048314	0.9446	3.6583
chr4	191154276	132582938	0.6936	3.3415
chr5	180915260	170846570	0.9443	3.6946
chr6	171115067	149186921	0.8719	3.5208
chr7	159138663	147201004	0.925	3.6259
chr8	146364022	141273481	0.9652	3.7238
chr9	141213431	128213805	0.9079	4.1885
chr10	135534747	156009771	1.1511	4.3529
chr11	135006516	163489172	1.211	4.7589
chr12	133851895	139176708	1.0398	4.0924
chr13	115169878	72031258	0.6254	2.7126
chr14	107349540	93791585	0.8737	3.7423
chr15	102531392	100731608	0.9824	4.0522
chr16	90354753	116066407	1.2846	7.2429
chr17	81195210	107519390	1.3242	5.0545
chr18	78077248	77177033	0.9885	4.1655
chr19	59128983	75203264	1.2719	5.0949
chr20	63025520	94583374	1.5007	4.9763
chr21	48129895	39104576	0.8125	6.0466
chr22	51304566	62327983	1.2149	4.9759
chrMT	16571	174038	10.5026	31.4353
chrX	155270560	4354932	0.028	0.8528

chrY	59373566	25416318	0.4281	3.2681
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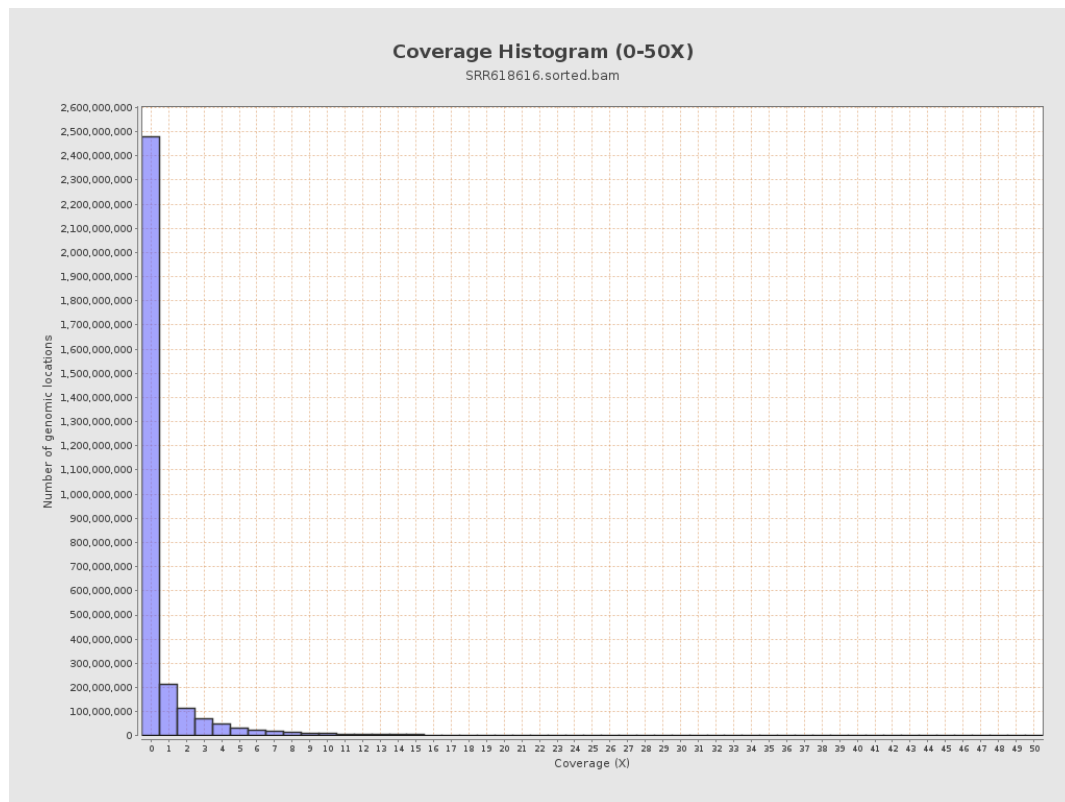
3. Results : Coverage across reference



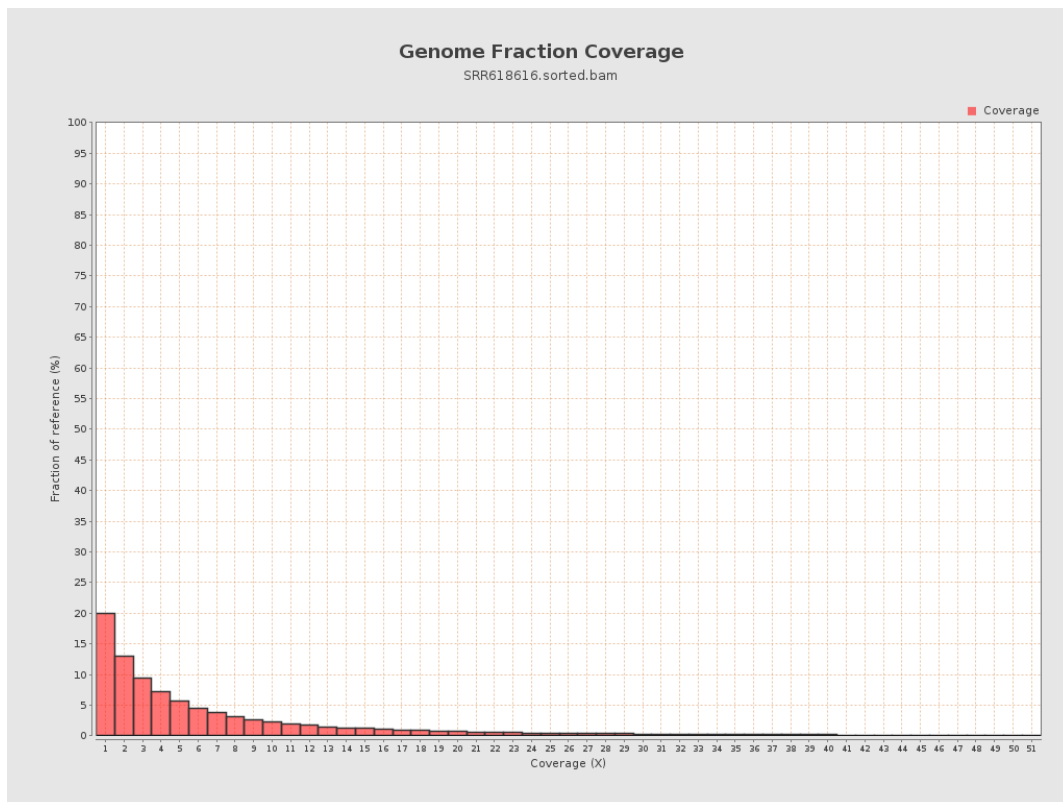
4. Results : Coverage Histogram



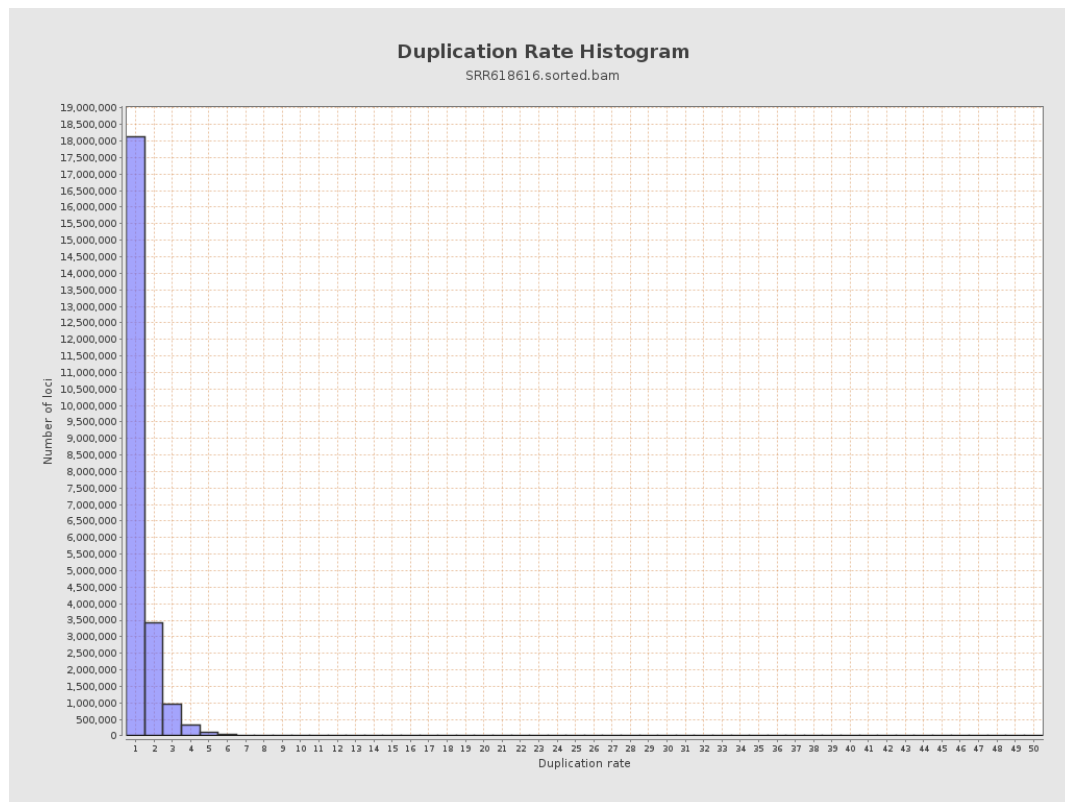
5. Results : Coverage Histogram (0-50X)



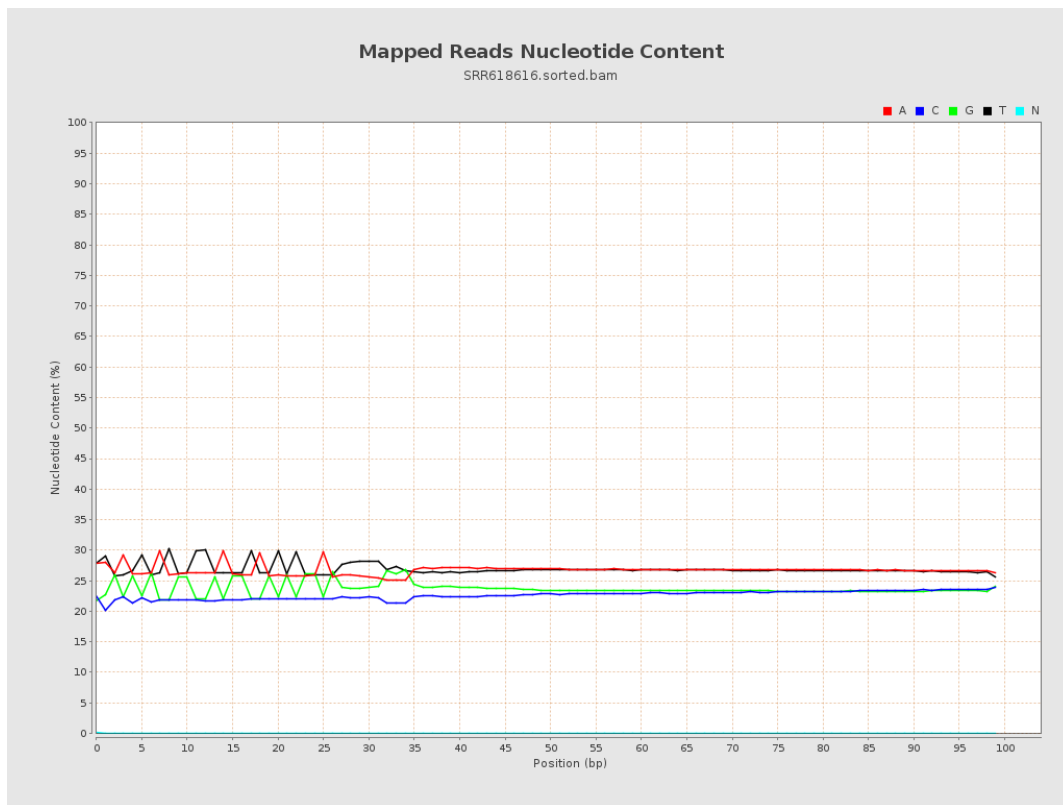
6. Results : Genome Fraction Coverage



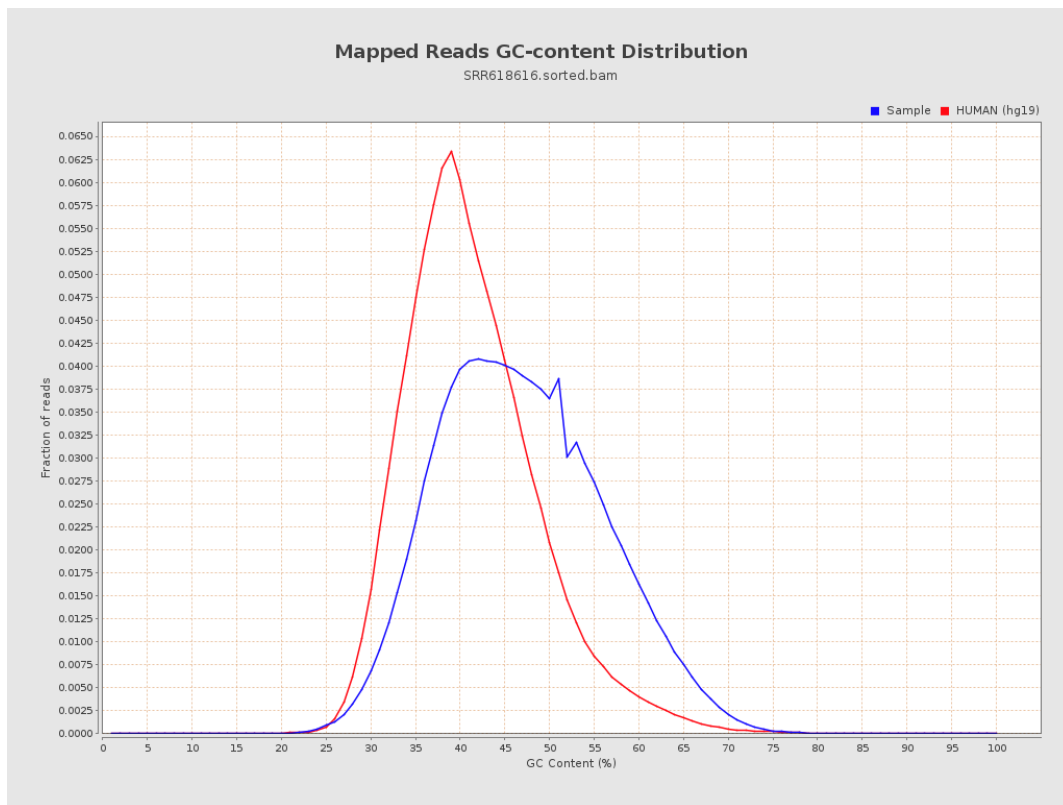
7. Results : Duplication Rate Histogram



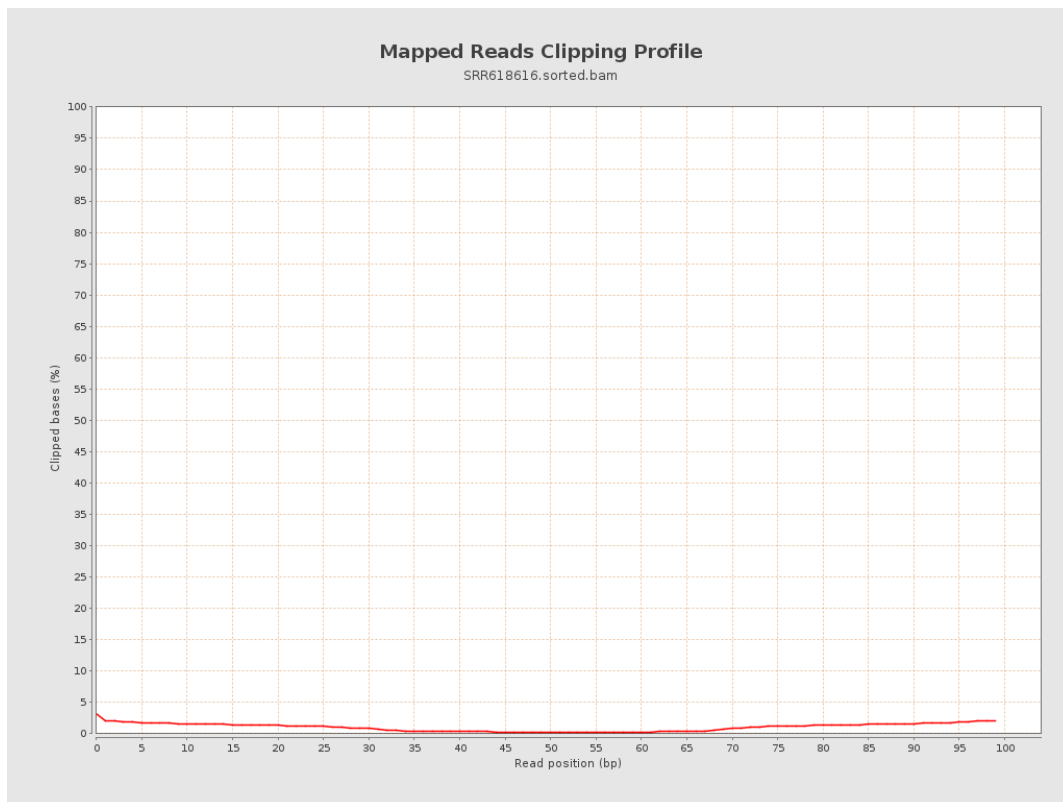
8. Results : Mapped Reads Nucleotide Content



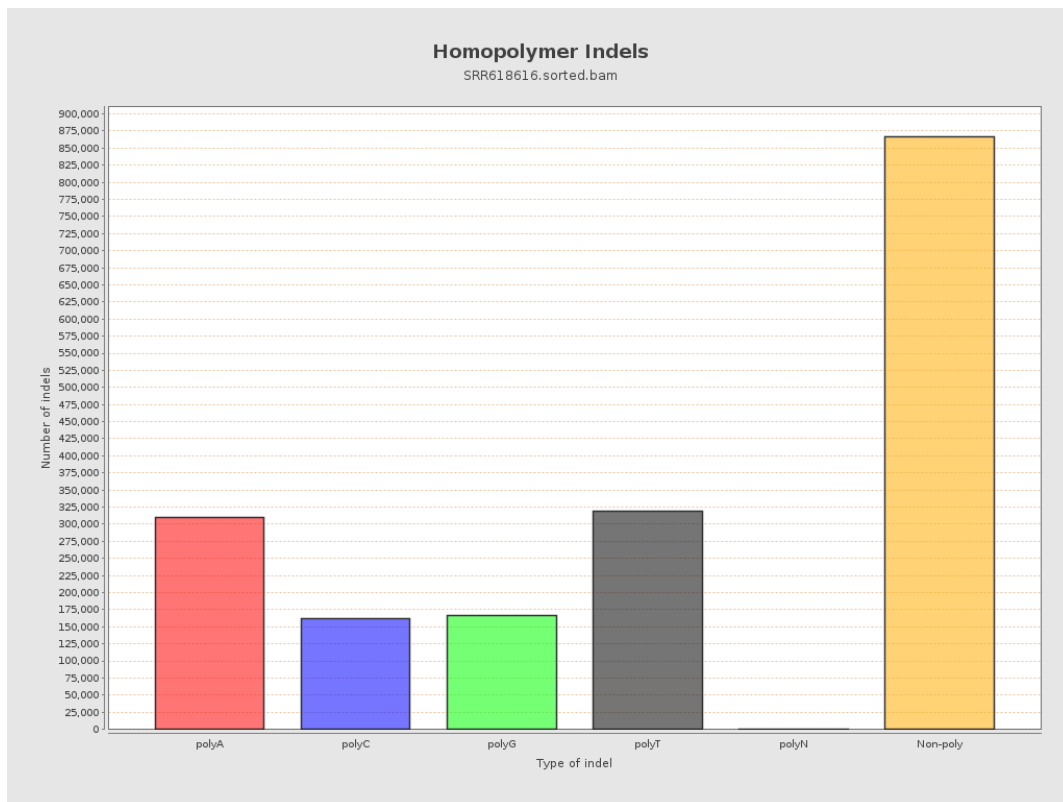
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



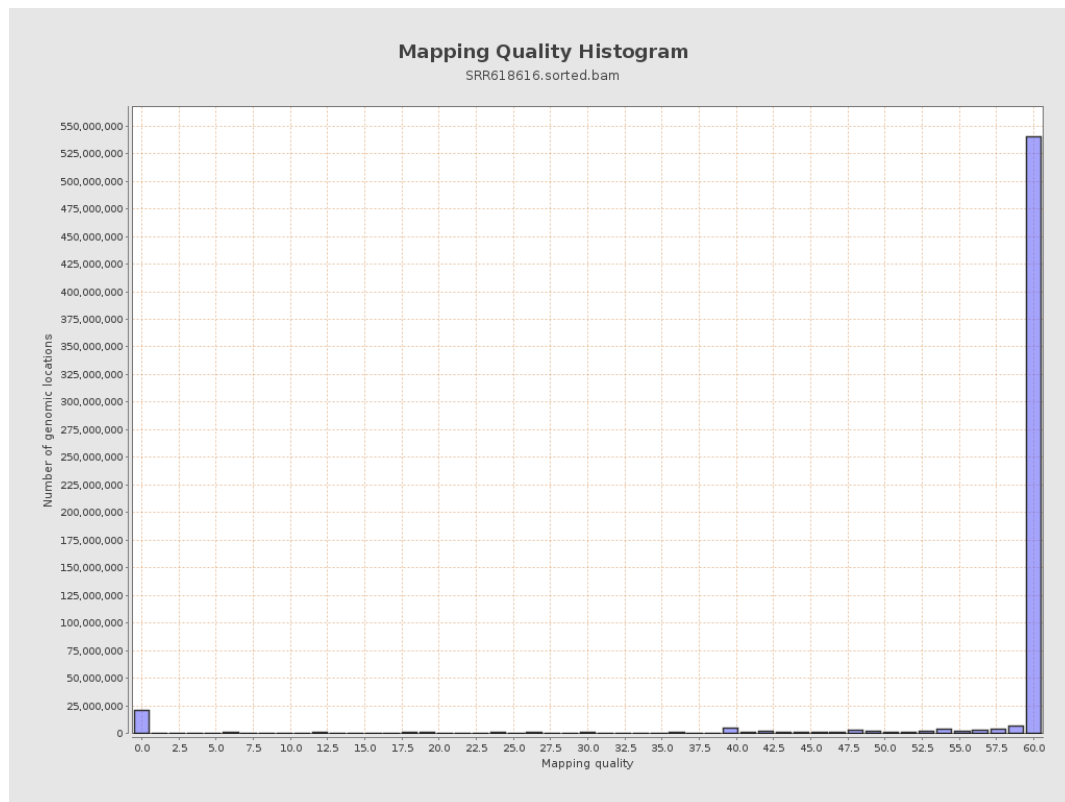
11. Results : Homopolymer Indels



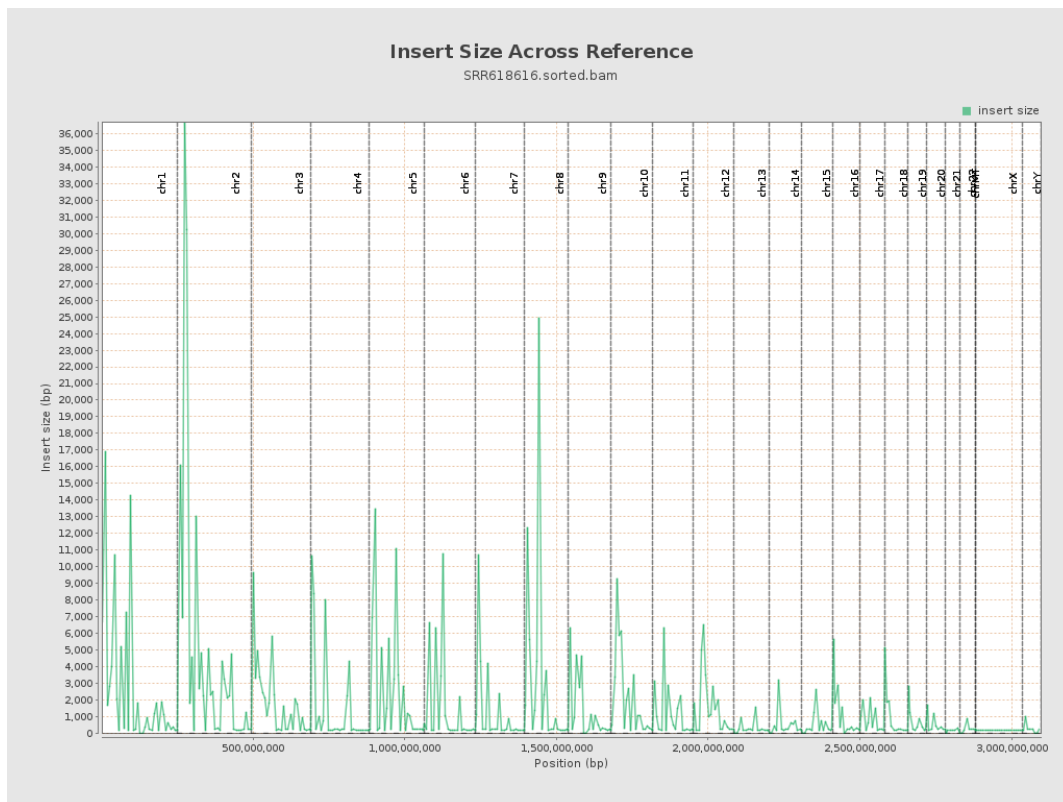
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

