

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 04:16:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618607.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_SRR618607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618607_1.fastq.gz SRR618607_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 04:16:41 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618607.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,481,152
Mapped reads	36,183,650 / 94.03%
Unmapped reads	2,297,502 / 5.97%
Mapped paired reads	36,183,650 / 94.03%
Mapped reads, first in pair	18,280,415 / 47.5%
Mapped reads, second in pair	17,903,235 / 46.52%
Mapped reads, both in pair	35,386,692 / 91.96%
Mapped reads, singletons	796,958 / 2.07%
Secondary alignments	0
Supplementary alignments	54,593 / 0.14%
Read min/max/mean length	30 / 100 / 100.06
Duplicated reads (estimated)	5,267,611 / 13.69%
Duplication rate	12.94%
Clipped reads	6,659,941 / 17.31%

2.2. ACGT Content

Number/percentage of A's	929,881,931 / 26.97%
Number/percentage of C's	775,223,621 / 22.49%
Number/percentage of T's	935,543,148 / 27.14%
Number/percentage of G's	806,410,130 / 23.39%
Number/percentage of N's	152,534 / 0%

GC Percentage	45.88%
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2.3. Coverage

Mean	1.1143
Standard Deviation	4.718

2.4. Mapping Quality

Mean Mapping Quality	52.53
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2.5. Insert size

Mean	29,361.96
Standard Deviation	1,703,703.65
P25/Median/P75	180 / 210 / 249

2.6. Mismatches and indels

General error rate	1.33%
Mismatches	44,823,838
Insertions	628,583
Mapped reads with at least one insertion	1.71%
Deletions	1,681,010
Mapped reads with at least one deletion	4.53%
Homopolymer indels	52.26%

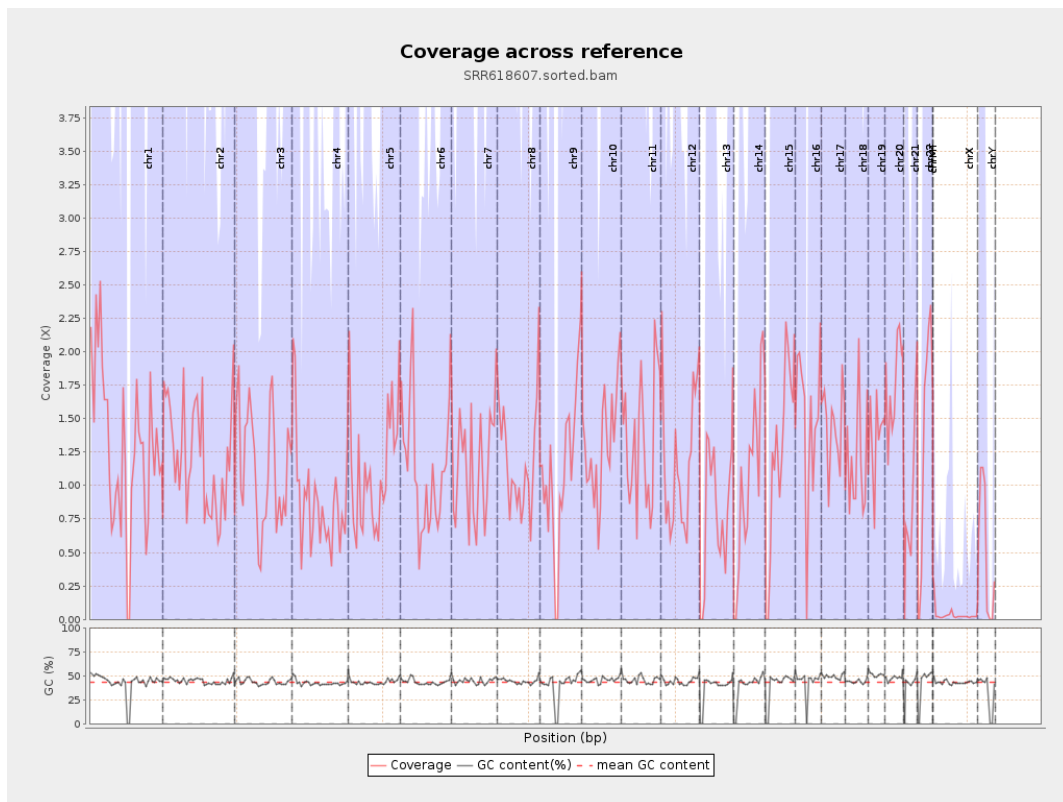
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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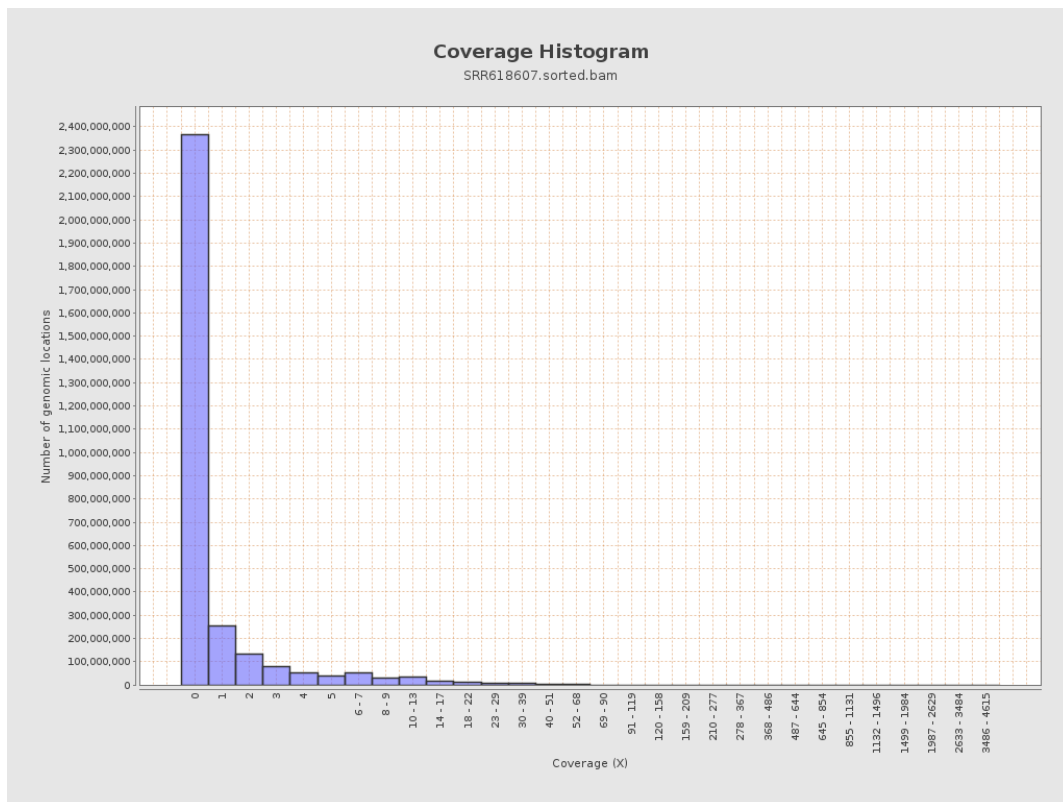
		bases	coverage	deviation
chr1	249250621	318186260	1.2766	5.0949
chr2	243199373	296140146	1.2177	5.5458
chr3	198022430	223162035	1.127	3.9408
chr4	191154276	168464352	0.8813	3.7654
chr5	180915260	204022869	1.1277	3.9164
chr6	171115067	191172751	1.1172	4.1585
chr7	159138663	186054009	1.1691	4.109
chr8	146364022	172344700	1.1775	4.1263
chr9	141213431	156521719	1.1084	5.2816
chr10	135534747	177108019	1.3067	4.6883
chr11	135006516	181723666	1.346	4.9372
chr12	133851895	158419172	1.1835	4.3307
chr13	115169878	91907276	0.798	3.0595
chr14	107349540	113733343	1.0595	4.227
chr15	102531392	126422224	1.233	4.5243
chr16	90354753	134054681	1.4836	9.5339
chr17	81195210	117470478	1.4468	5.0509
chr18	78077248	90722613	1.162	4.9656
chr19	59128983	79967420	1.3524	5.1749
chr20	63025520	111121956	1.7631	5.775
chr21	48129895	44942252	0.9338	5.9053
chr22	51304566	69173625	1.3483	5.3615
chrMT	16571	5330	0.3216	0.9657
chrX	155270560	5269676	0.0339	0.8739

chrY	59373566	31419254	0.5292	4.0558
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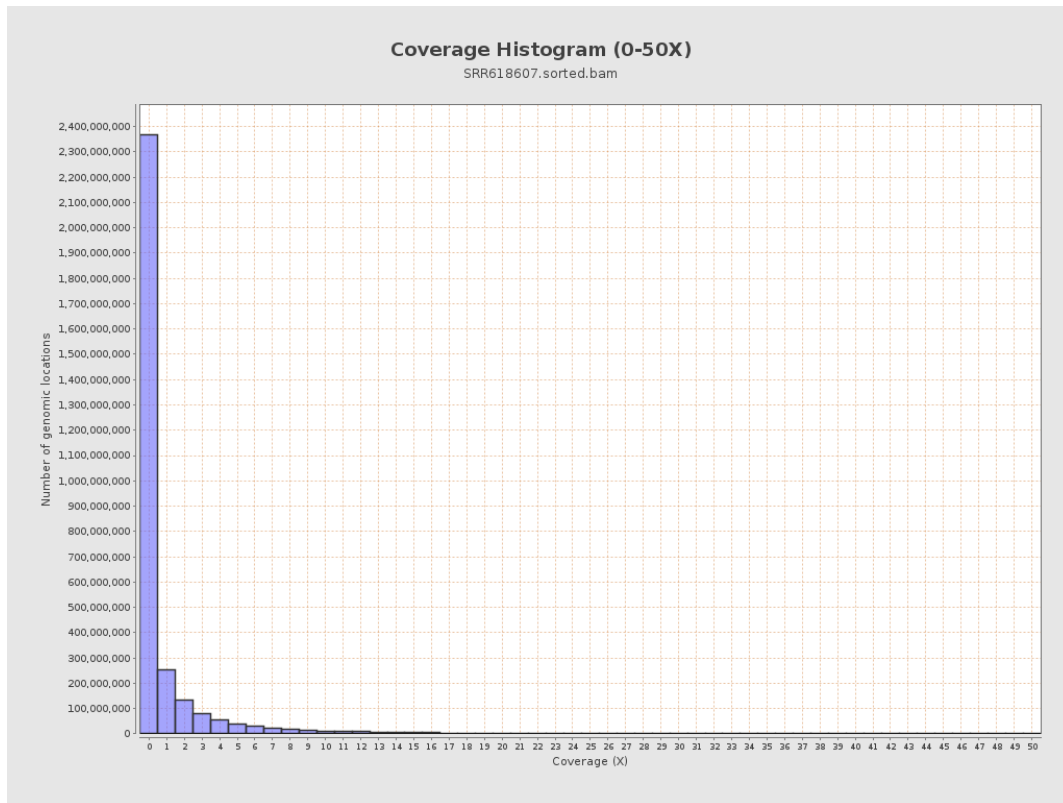
3. Results : Coverage across reference



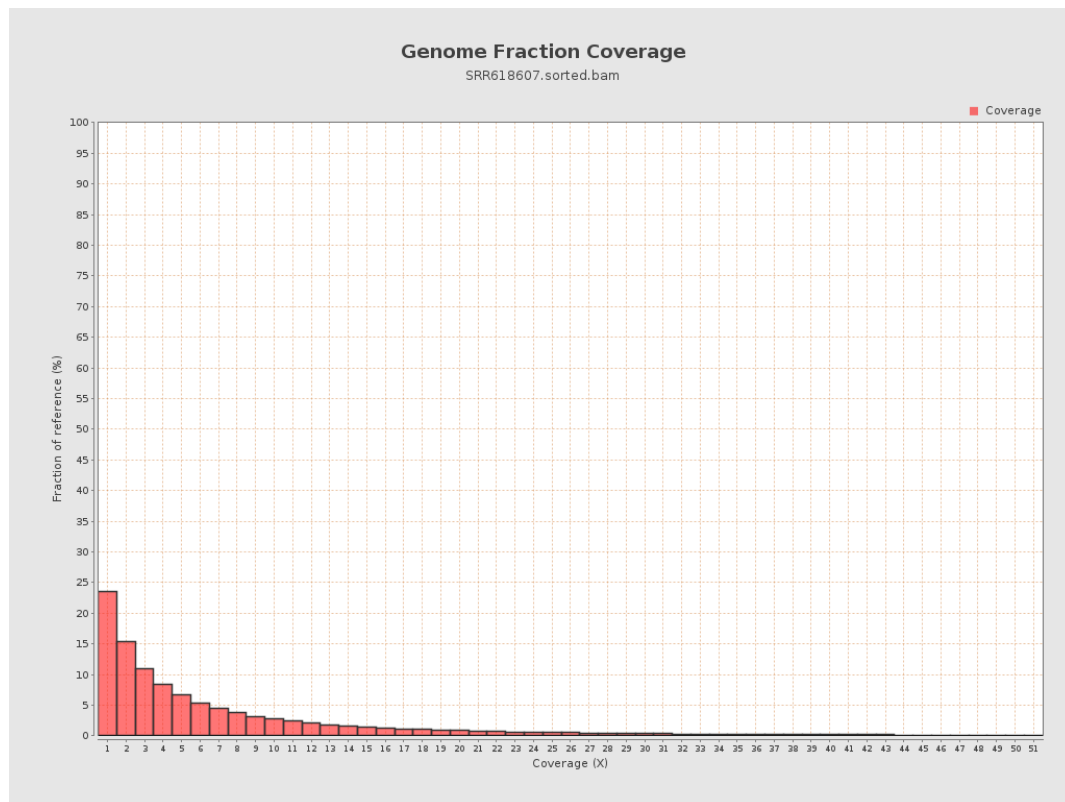
4. Results : Coverage Histogram



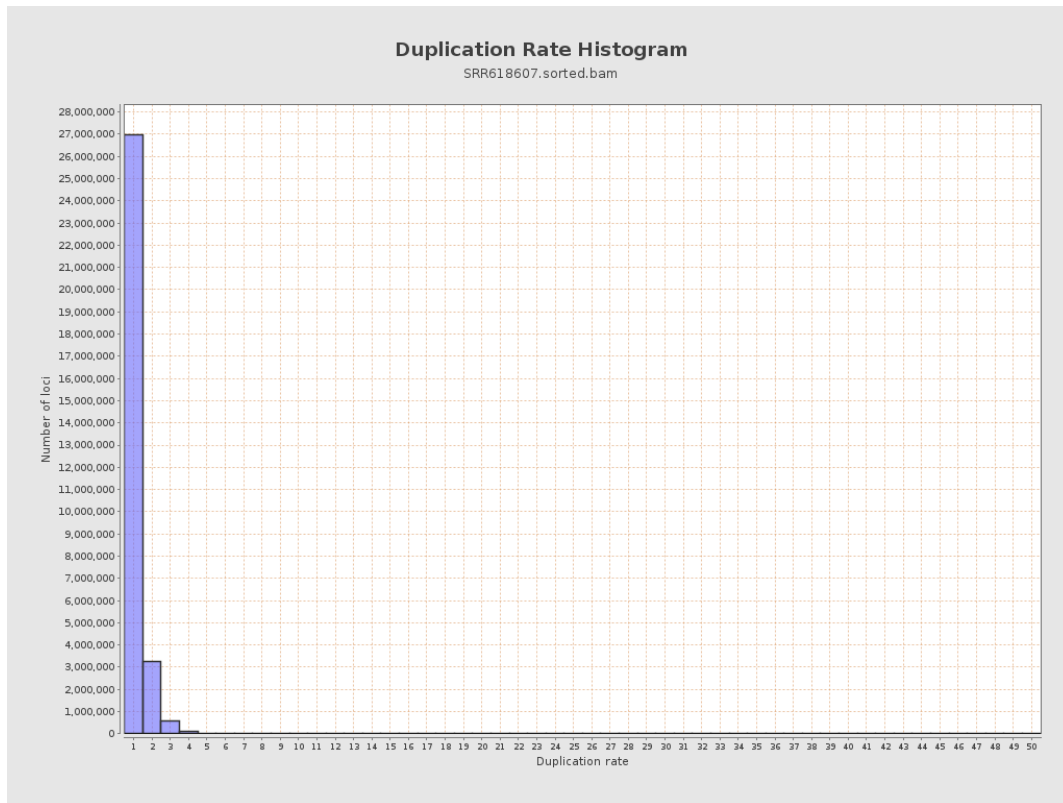
5. Results : Coverage Histogram (0-50X)



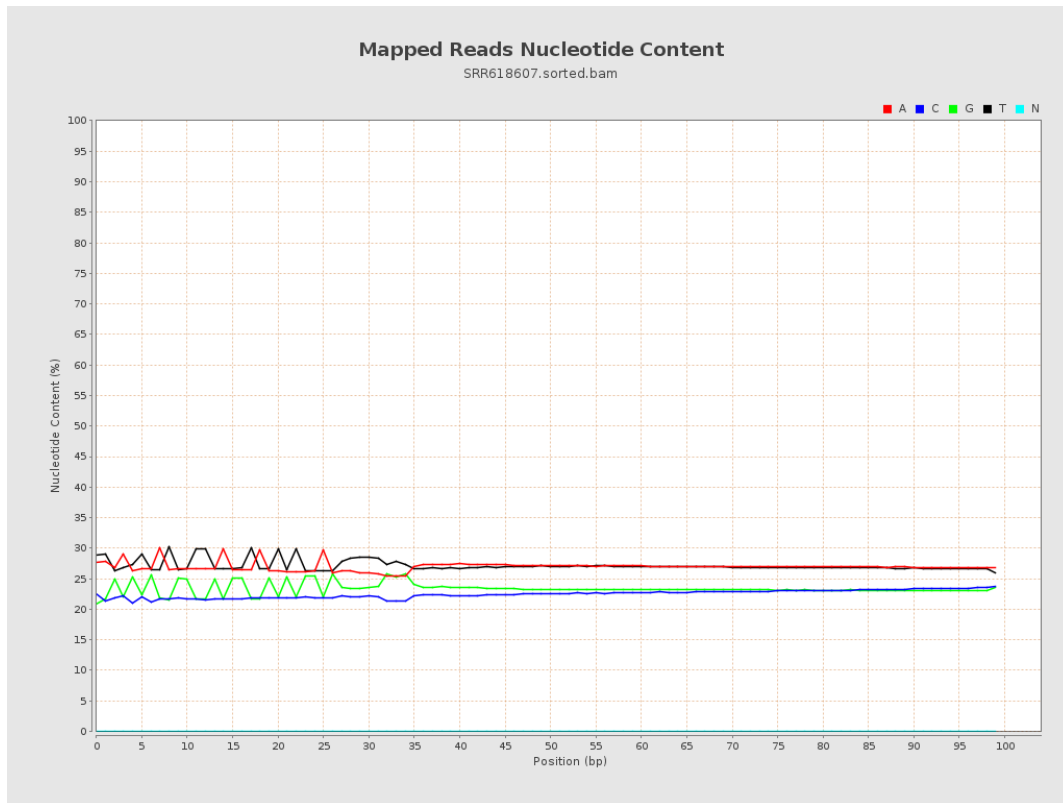
6. Results : Genome Fraction Coverage



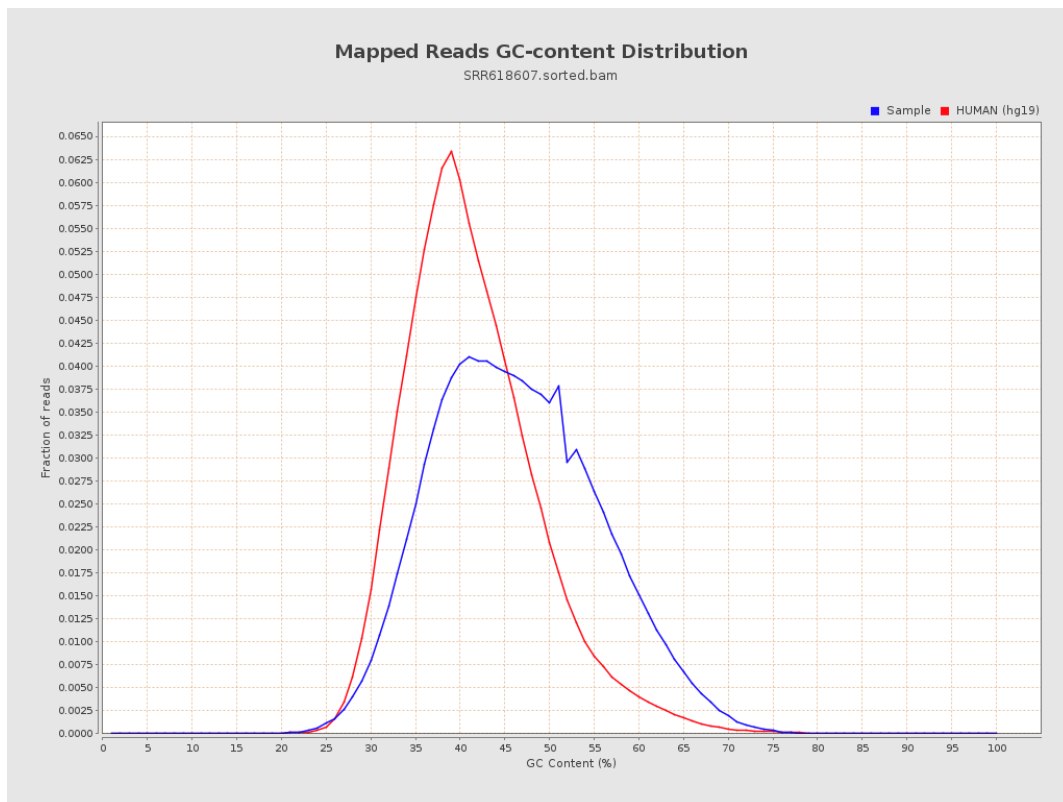
7. Results : Duplication Rate Histogram



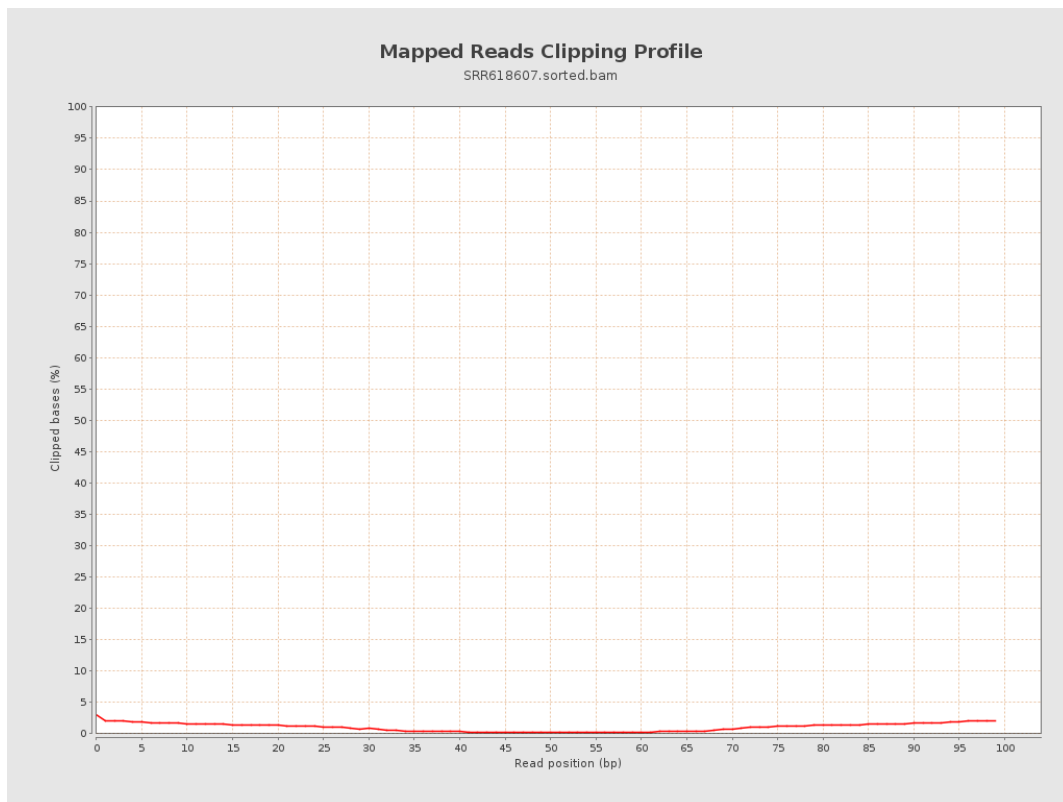
8. Results : Mapped Reads Nucleotide Content



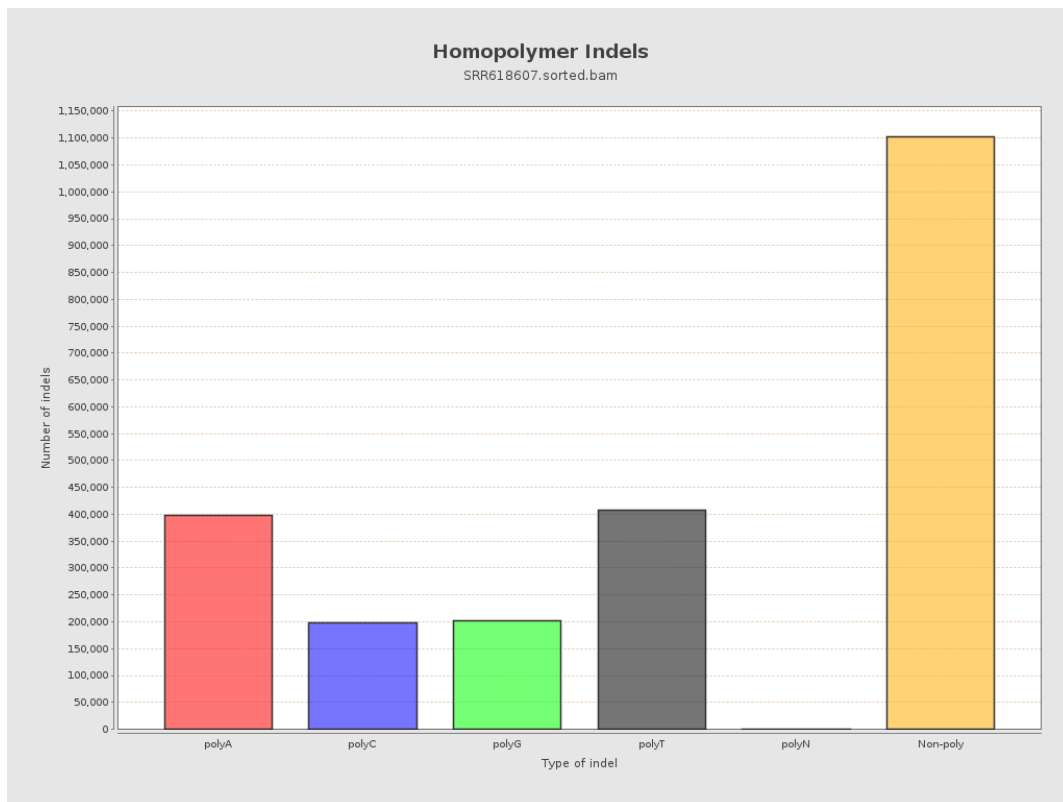
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



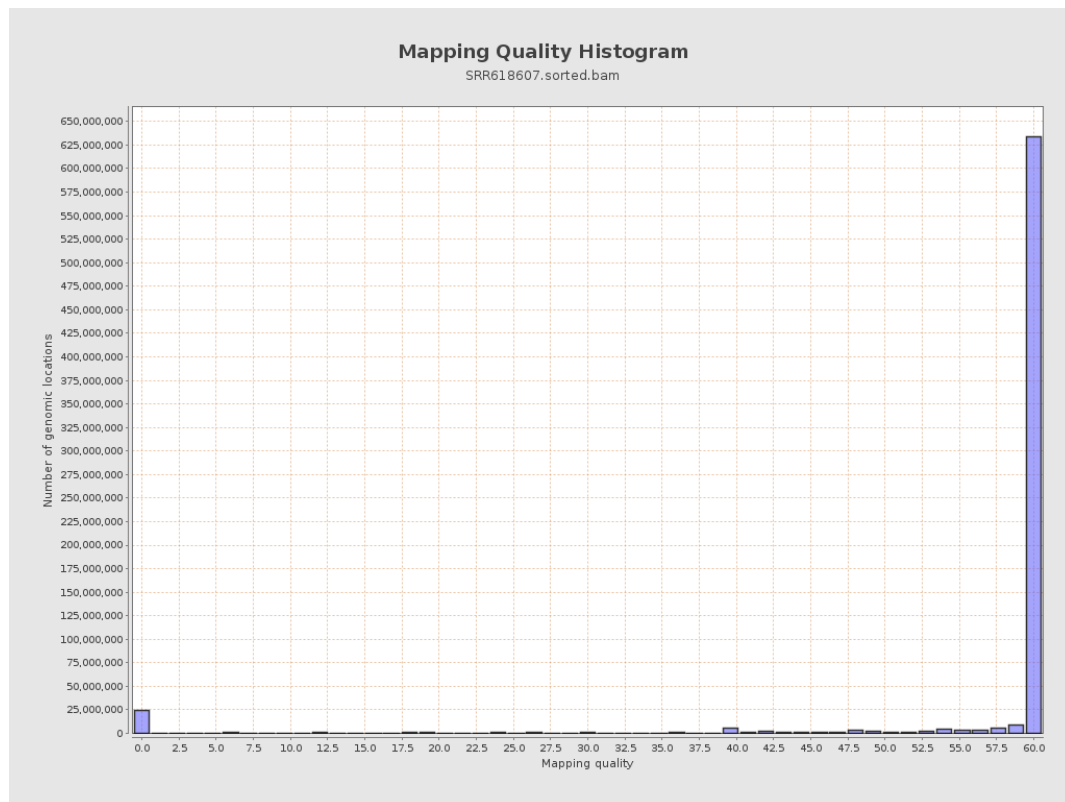
11. Results : Homopolymer Indels



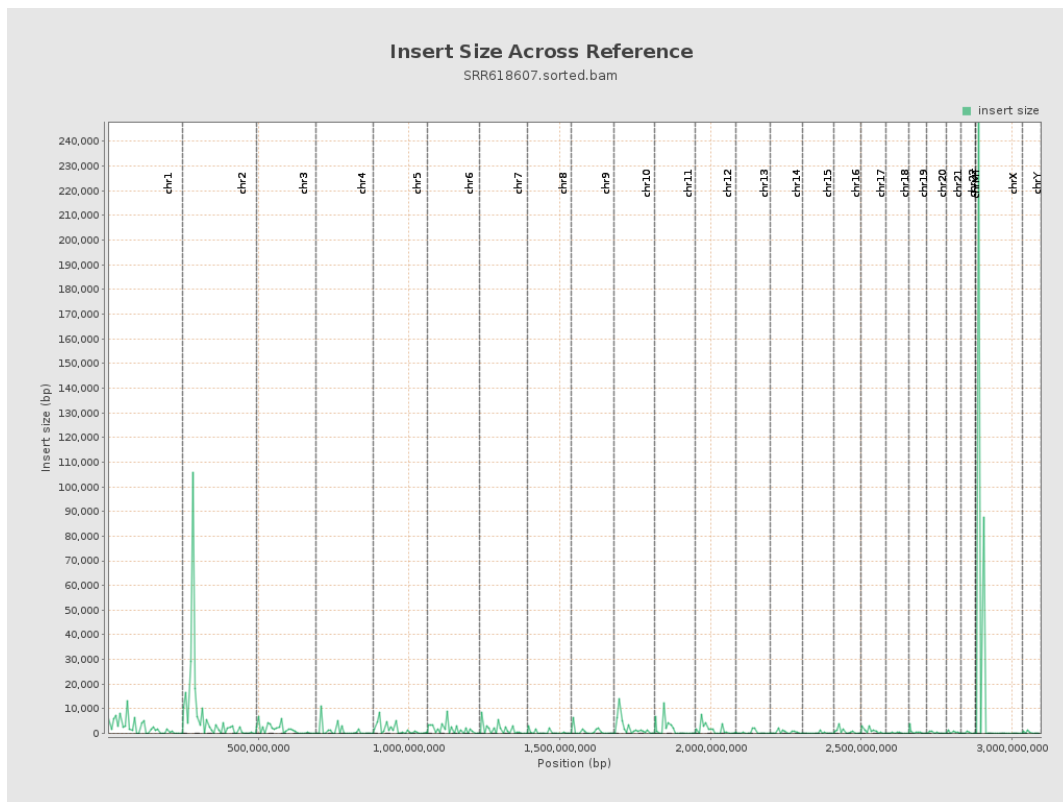
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

