

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 05:02:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618608.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_SRR618608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618608_1.fastq.gz SRR618608_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 05:02:25 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	54,416,916
Mapped reads	50,699,438 / 93.17%
Unmapped reads	3,717,478 / 6.83%
Mapped paired reads	50,699,438 / 93.17%
Mapped reads, first in pair	26,034,507 / 47.84%
Mapped reads, second in pair	24,664,931 / 45.33%
Mapped reads, both in pair	48,313,168 / 88.78%
Mapped reads, singletons	2,386,270 / 4.39%
Secondary alignments	0
Supplementary alignments	168,570 / 0.31%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	25,313,233 / 46.52%
Duplication rate	37.51%
Clipped reads	12,604,312 / 23.16%

2.2. ACGT Content

Number/percentage of A's	1,247,334,208 / 26.37%
Number/percentage of C's	1,080,310,310 / 22.84%
Number/percentage of T's	1,268,433,189 / 26.82%
Number/percentage of G's	1,130,036,225 / 23.89%
Number/percentage of N's	3,489,307 / 0.07%

GC Percentage	46.73%
---------------	--------

2.3. Coverage

Mean	1.5288
Standard Deviation	7.5903

2.4. Mapping Quality

Mean Mapping Quality	53.77
----------------------	-------

2.5. Insert size

Mean	98,981.64
Standard Deviation	3,168,655.43
P25/Median/P75	174 / 201 / 238

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	71,892,286
Insertions	876,542
Mapped reads with at least one insertion	1.7%
Deletions	2,296,861
Mapped reads with at least one deletion	4.42%
Homopolymer indels	51.93%

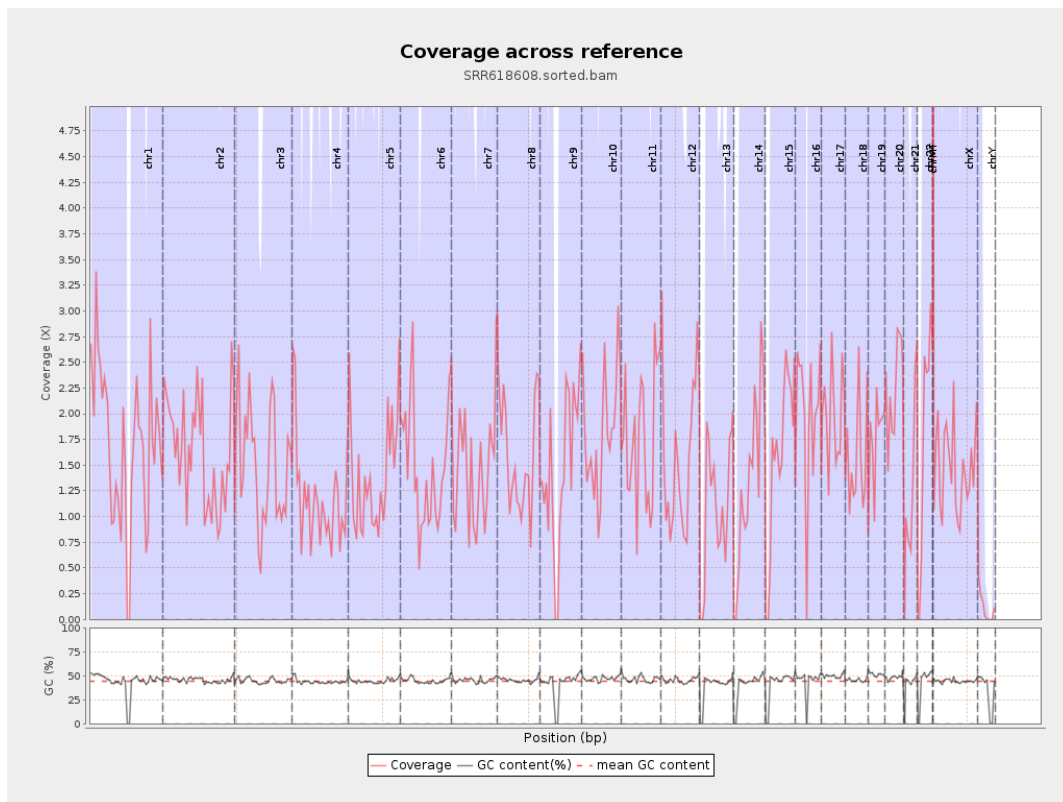
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

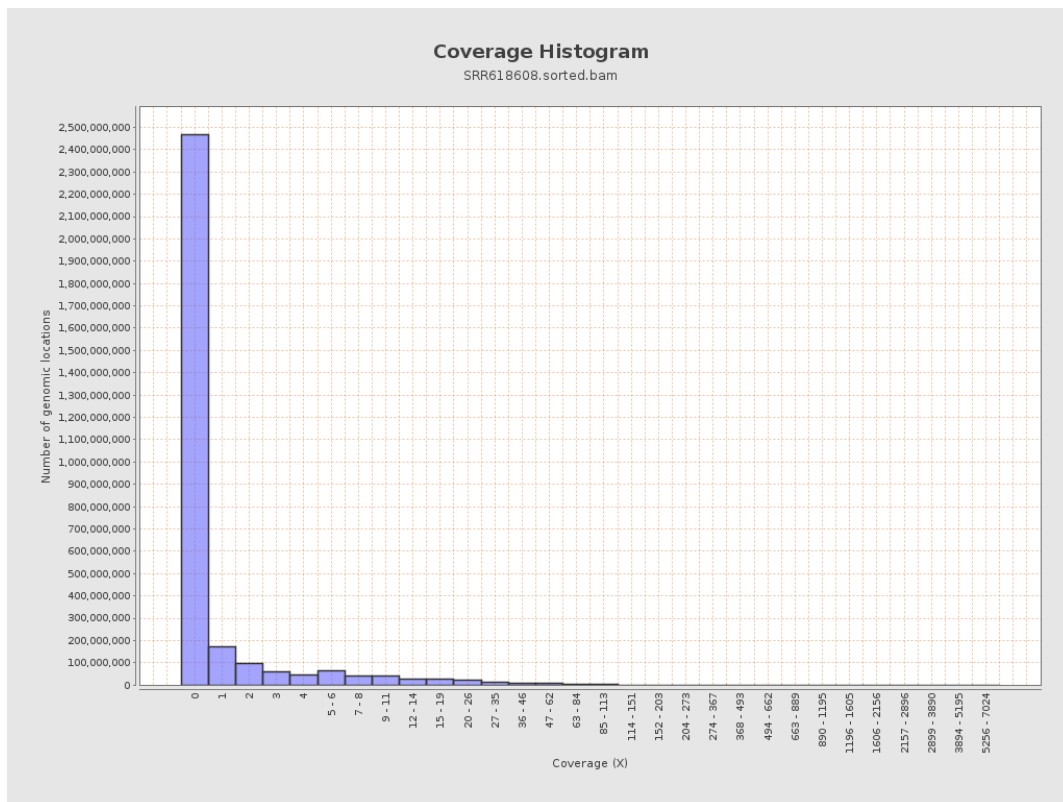
		bases	coverage	deviation
chr1	249250621	420489715	1.687	8.9339
chr2	243199373	396109584	1.6287	8.2763
chr3	198022430	295994554	1.4948	6.7285
chr4	191154276	223508472	1.1693	6.2893
chr5	180915260	256334256	1.4169	6.3478
chr6	171115067	251490481	1.4697	6.7742
chr7	159138663	234056287	1.4708	7.1034
chr8	146364022	231411448	1.5811	6.9102
chr9	141213431	206341494	1.4612	7.7472
chr10	135534747	245588935	1.812	8.037
chr11	135006516	236364802	1.7508	8.0452
chr12	133851895	211768735	1.5821	7.5547
chr13	115169878	124308725	1.0794	5.5009
chr14	107349540	145908437	1.3592	6.379
chr15	102531392	160907660	1.5694	7.8891
chr16	90354753	177282398	1.9621	12.7776
chr17	81195210	161246996	1.9859	8.1378
chr18	78077248	119329102	1.5283	6.4425
chr19	59128983	104631171	1.7695	8.207
chr20	63025520	142281842	2.2575	9.2613
chr21	48129895	62227482	1.2929	8.5006
chr22	51304566	90555425	1.7651	8.4086
chrMT	16571	188327	11.3649	42.1514
chrX	155270560	227993167	1.4684	6.3183

chrY	59373566	6404341	0.1079	3.8855
------	----------	---------	--------	--------

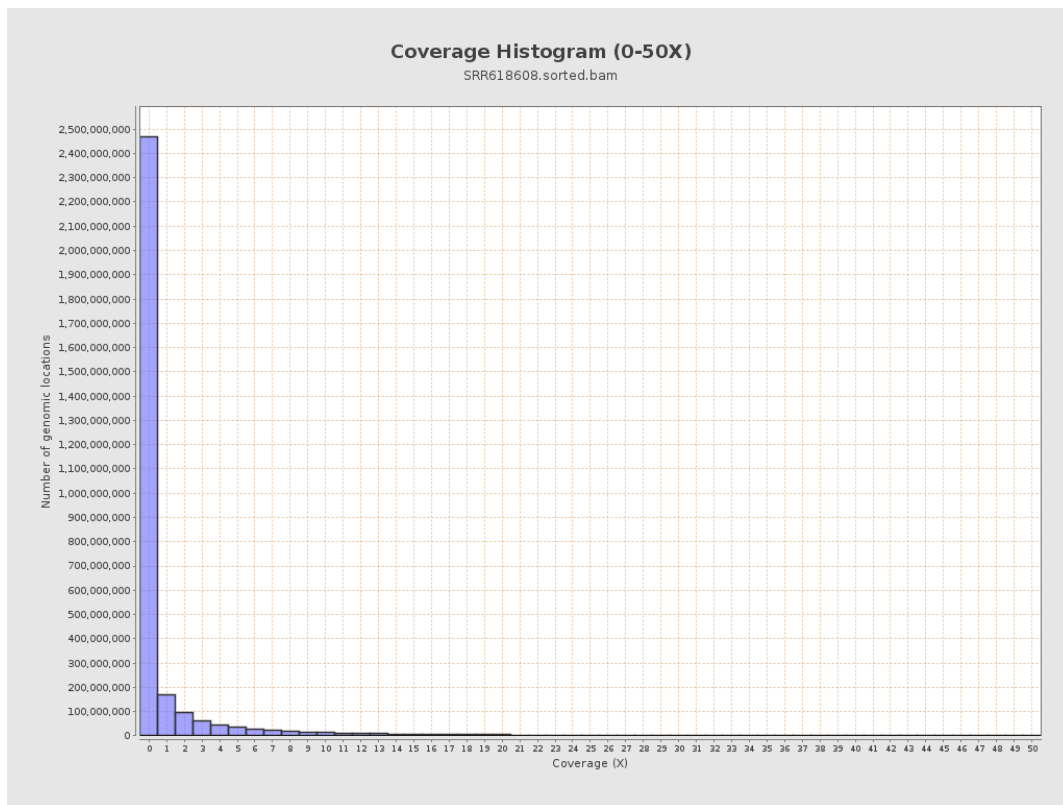
3. Results : Coverage across reference



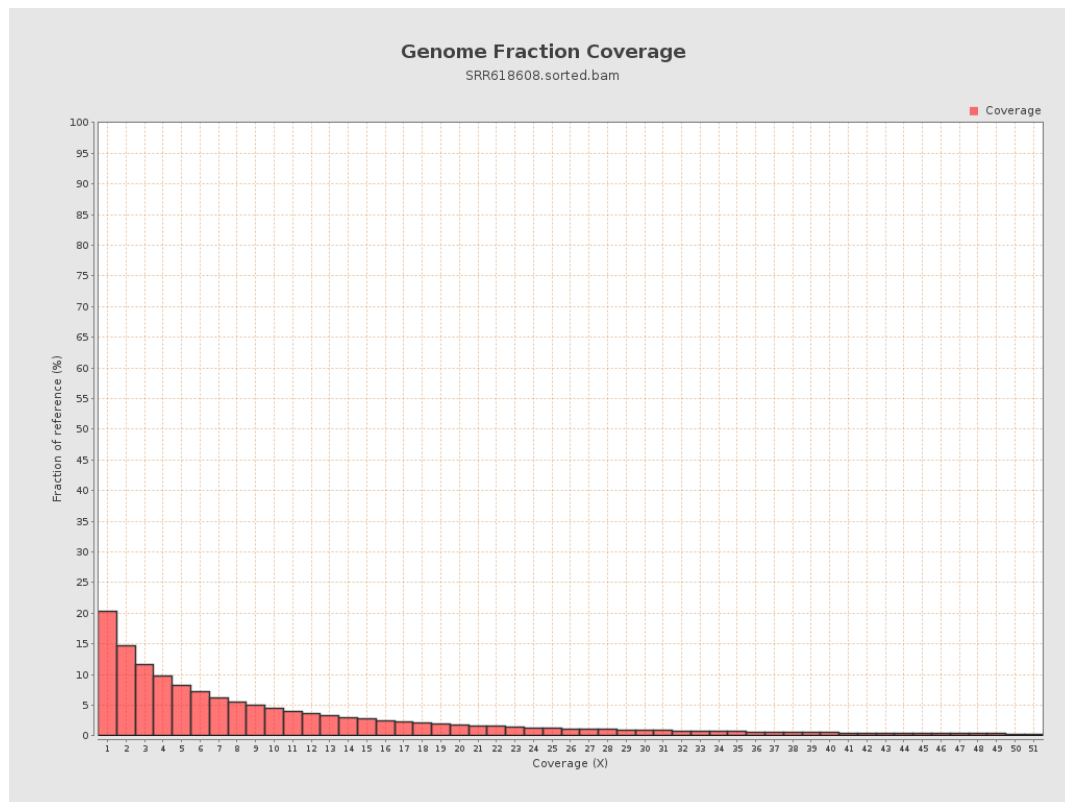
4. Results : Coverage Histogram



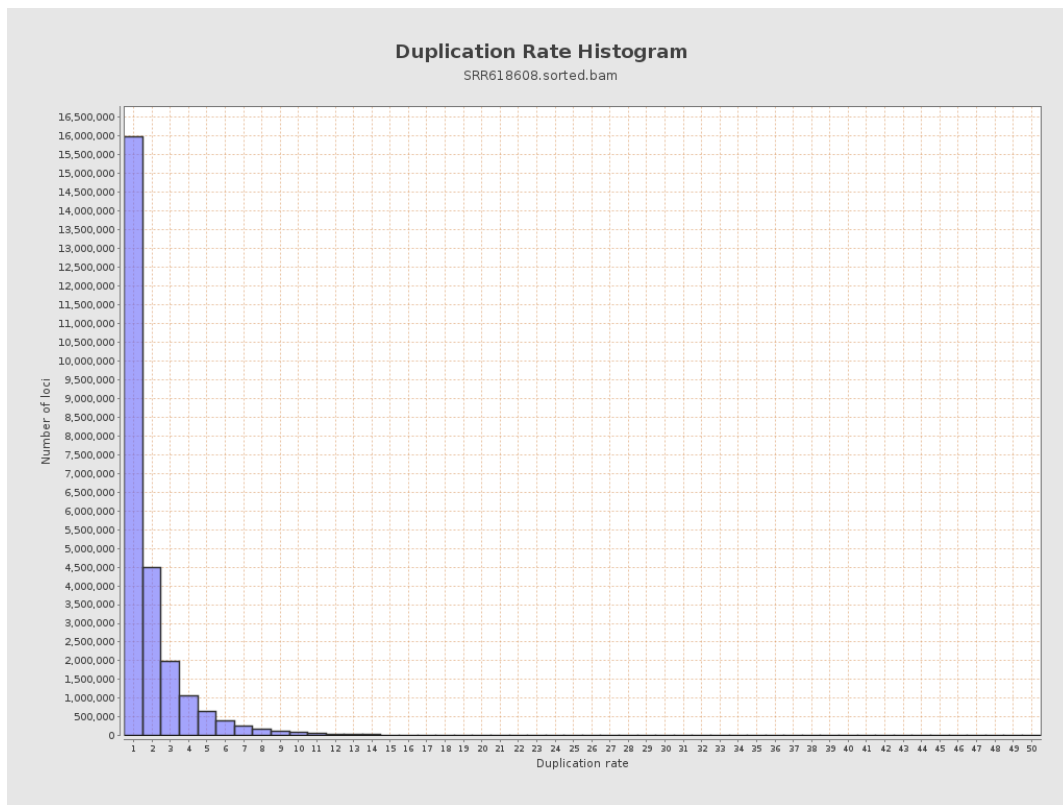
5. Results : Coverage Histogram (0-50X)



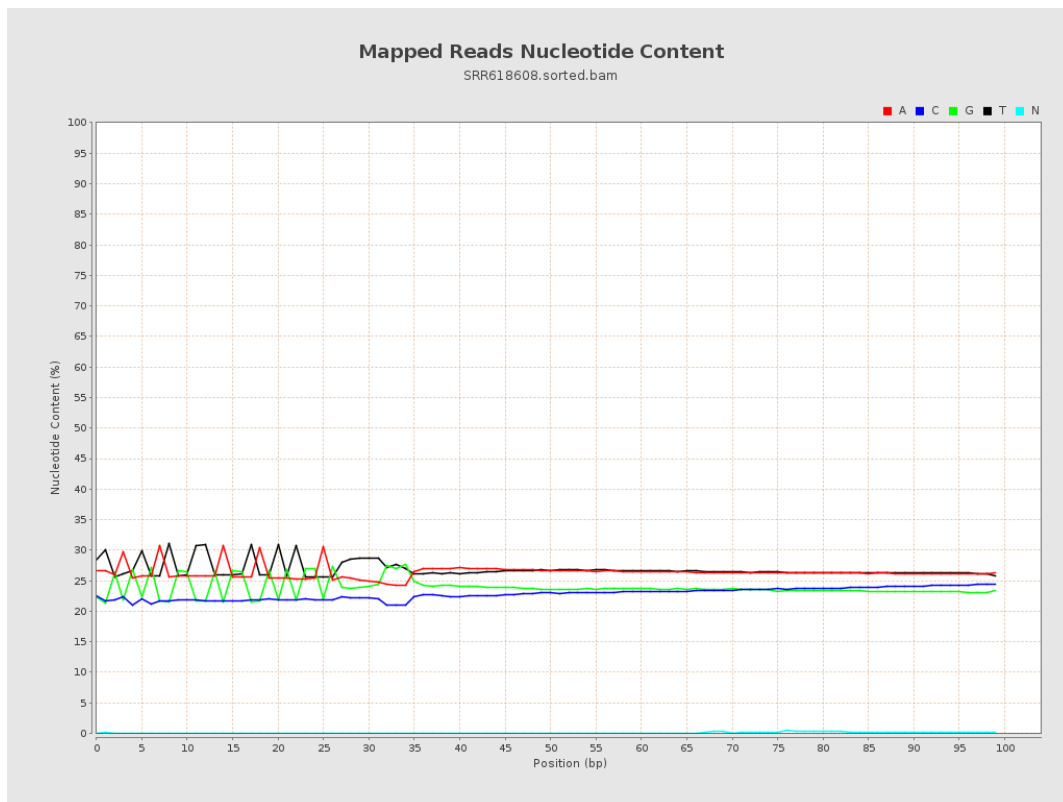
6. Results : Genome Fraction Coverage



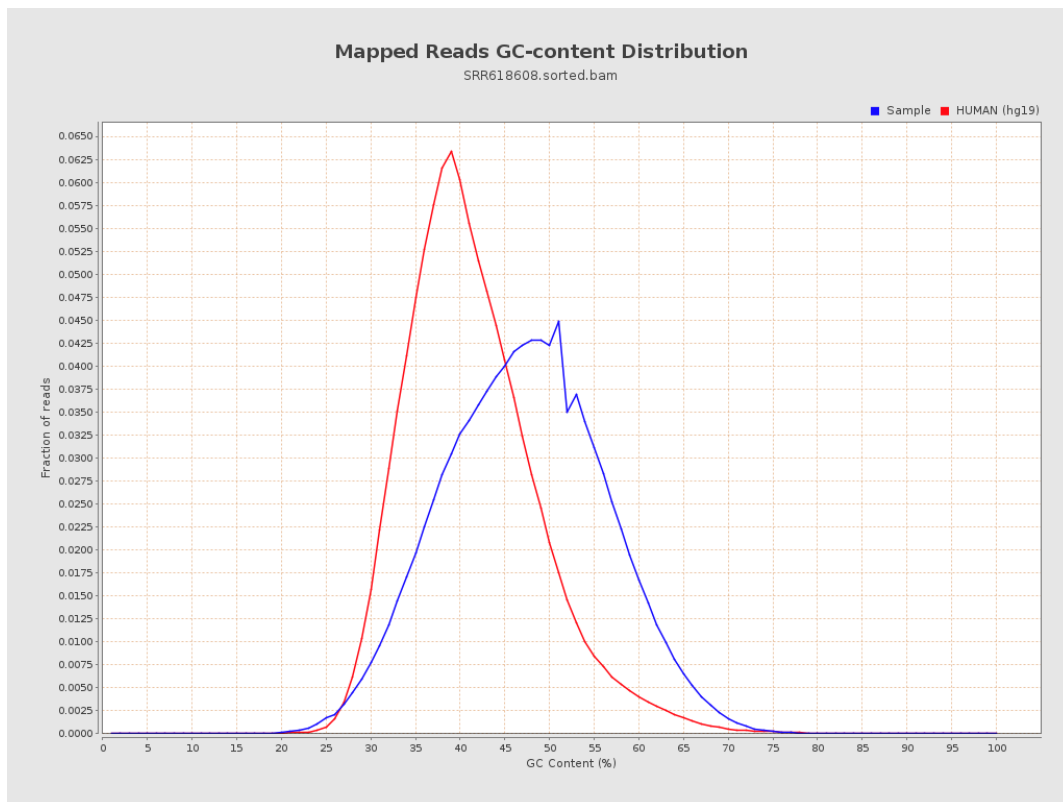
7. Results : Duplication Rate Histogram



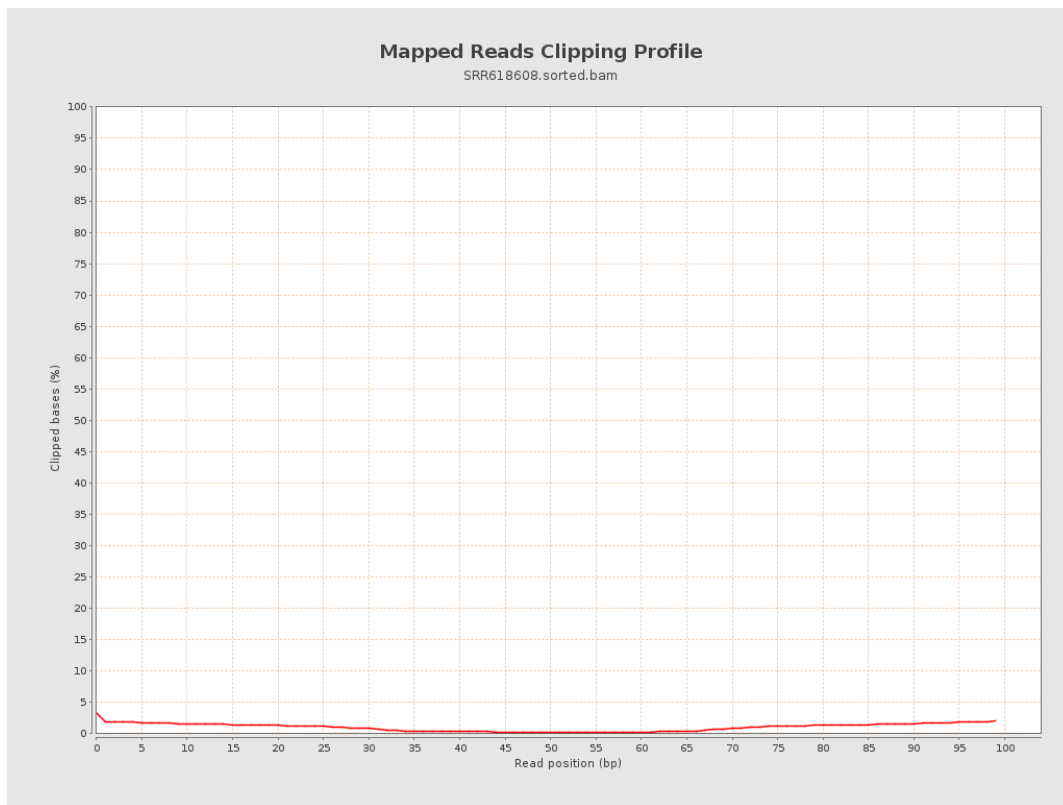
8. Results : Mapped Reads Nucleotide Content



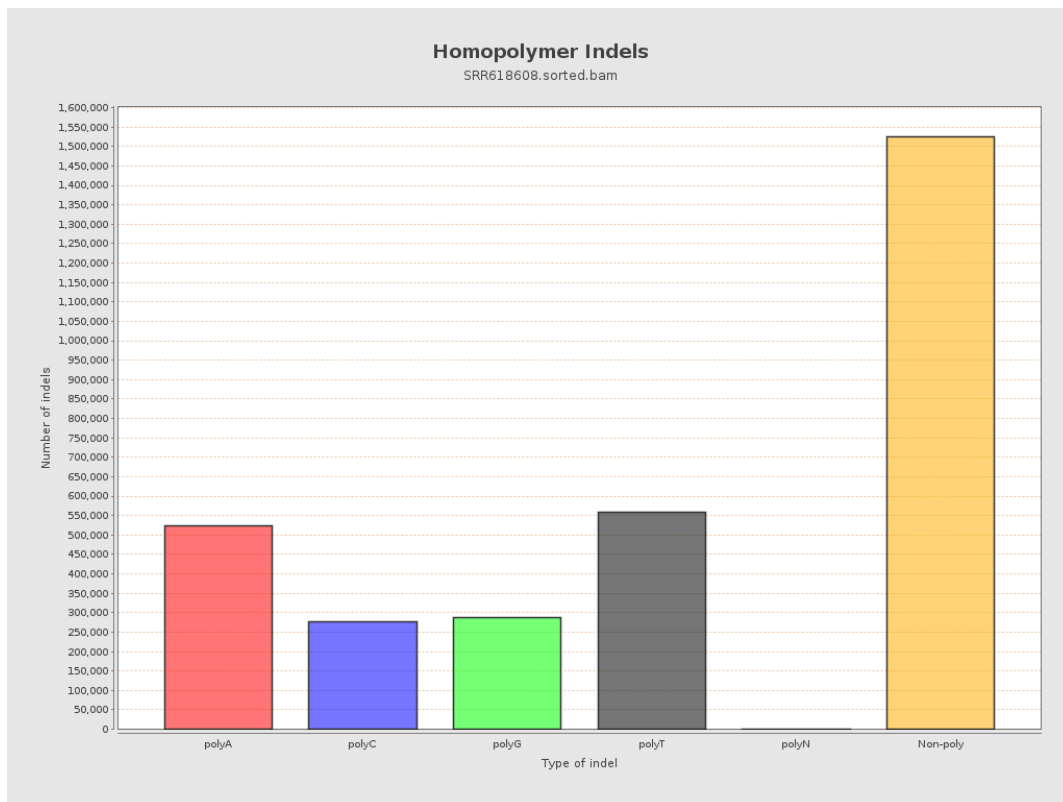
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



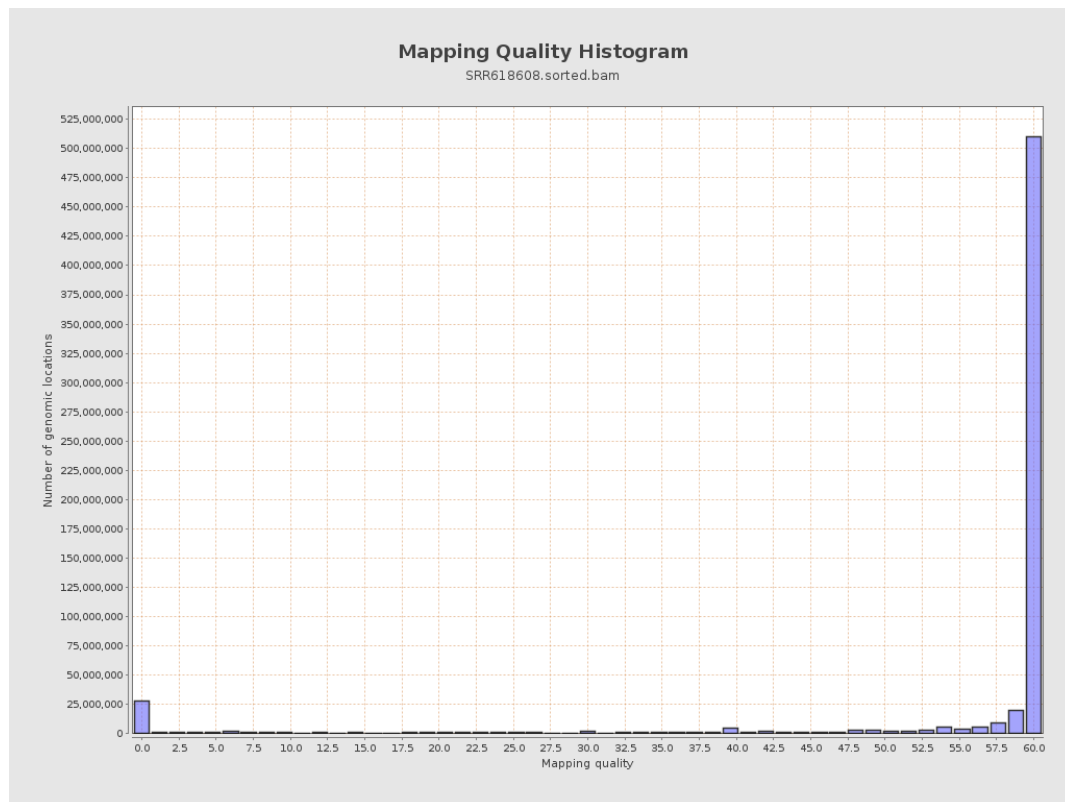
11. Results : Homopolymer Indels



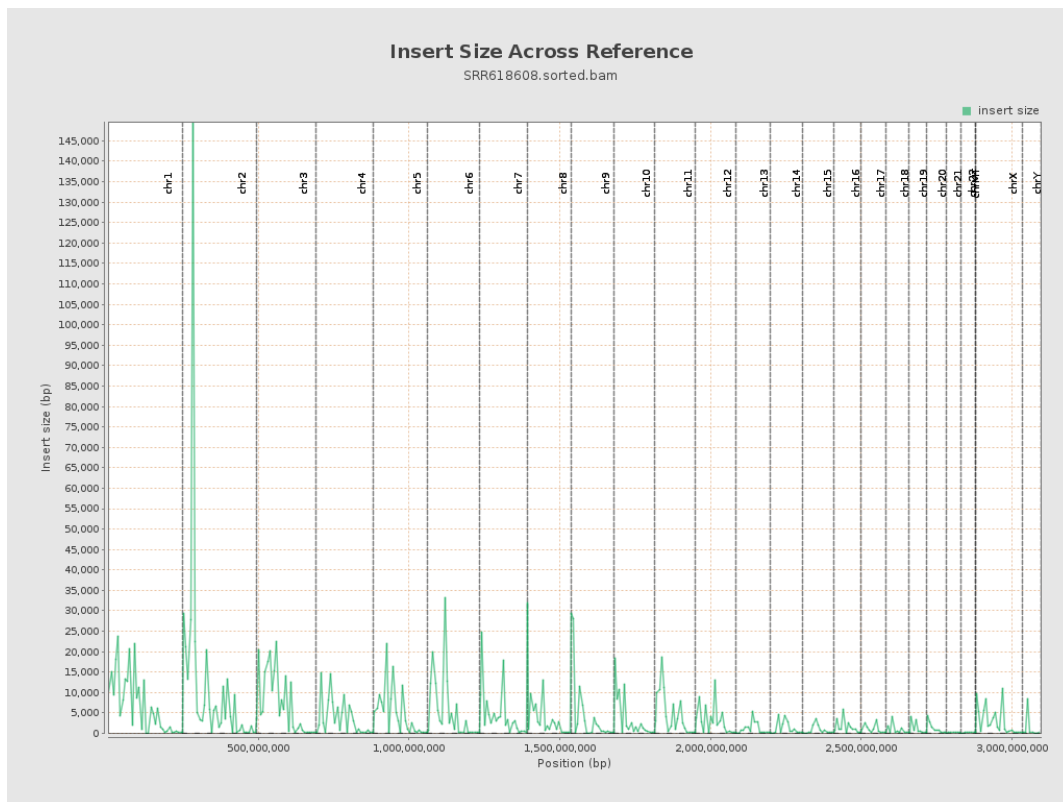
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

