

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 16:04:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618661.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_SRR618661 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618661.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 16:04:48 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618661.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,377,386
Mapped reads	27,568,285 / 93.84%
Unmapped reads	1,809,101 / 6.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,212 / 0.13%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	7,534,076 / 25.65%
Duplication rate	24.59%
Clipped reads	2,493,582 / 8.49%

2.2. ACGT Content

Number/percentage of A's	740,795,145 / 27.44%
Number/percentage of C's	591,568,177 / 21.91%
Number/percentage of T's	753,157,237 / 27.9%
Number/percentage of G's	587,503,050 / 21.76%
Number/percentage of N's	26,947,797 / 1%
GC Percentage	43.67%

2.3. Coverage

Mean	0.8728

Standard Deviation	3.8621
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	50.94
----------------------	-------

2.5. Mismatches and indels

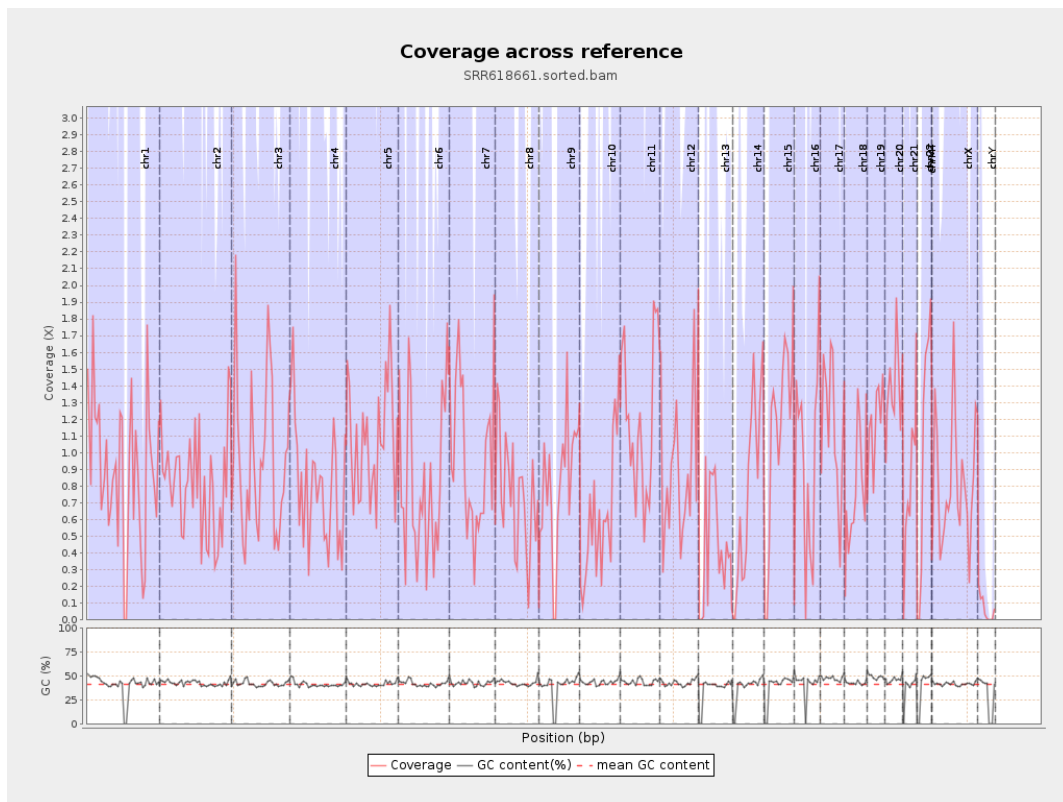
General error rate	1.98%
Mismatches	52,771,198
Insertions	492,032
Mapped reads with at least one insertion	1.76%
Deletions	1,365,552
Mapped reads with at least one deletion	4.83%
Homopolymer indels	53.48%

2.6. Chromosome stats

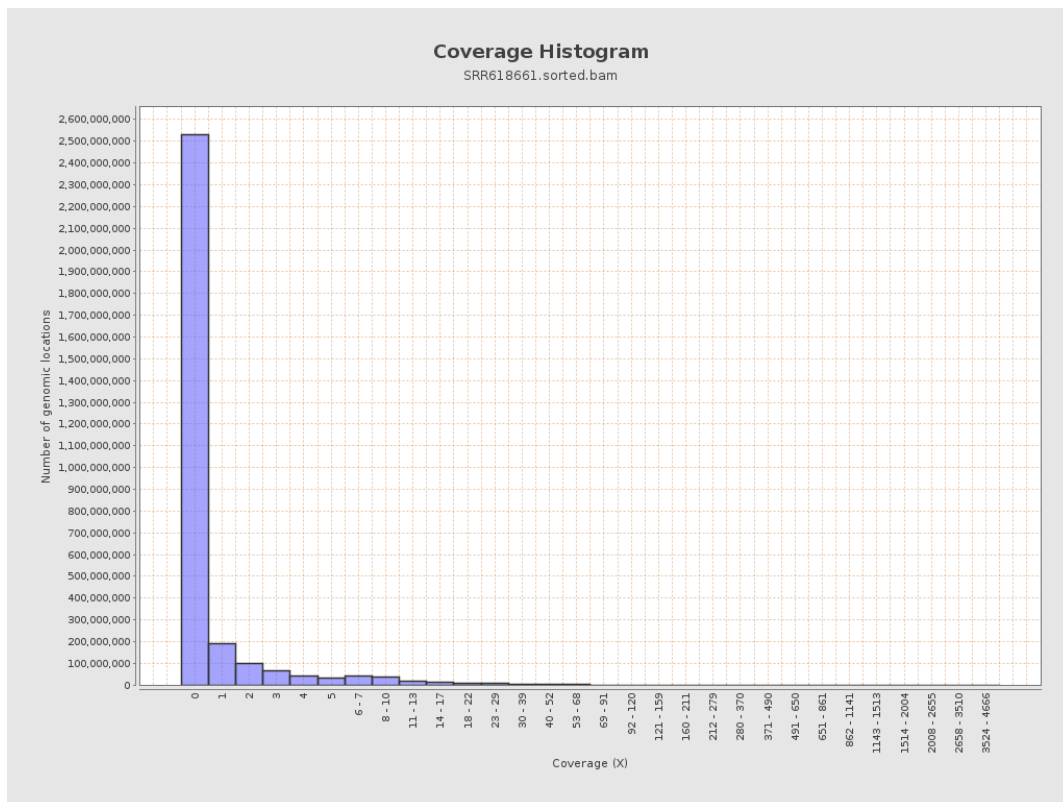
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	222937164	0.8944	4.4761
chr2	243199373	196166495	0.8066	3.9413
chr3	198022430	187403594	0.9464	4.2679
chr4	191154276	152691230	0.7988	3.4663
chr5	180915260	195730441	1.0819	3.6291
chr6	171115067	139550802	0.8155	3.3555
chr7	159138663	155228872	0.9754	3.6357

chr8	146364022	106838653	0.73	3.1618
chr9	141213431	113777844	0.8057	3.5211
chr10	135534747	83719201	0.6177	2.9544
chr11	135006516	160270173	1.1871	4.716
chr12	133851895	119497515	0.8928	3.5489
chr13	115169878	49964283	0.4338	2.2479
chr14	107349540	82293330	0.7666	3.2953
chr15	102531392	113007444	1.1022	3.9937
chr16	90354753	86447176	0.9568	5.87
chr17	81195210	93021072	1.1456	4.4134
chr18	78077248	60862891	0.7795	3.4722
chr19	59128983	70771236	1.1969	4.7004
chr20	63025520	86753219	1.3765	4.6018
chr21	48129895	39720628	0.8253	5.2657
chr22	51304566	55372061	1.0793	4.3694
chrMT	16571	5920	0.3573	1.0959
chrX	155270560	125985914	0.8114	3.3408
chrY	59373566	3813306	0.0642	1.619

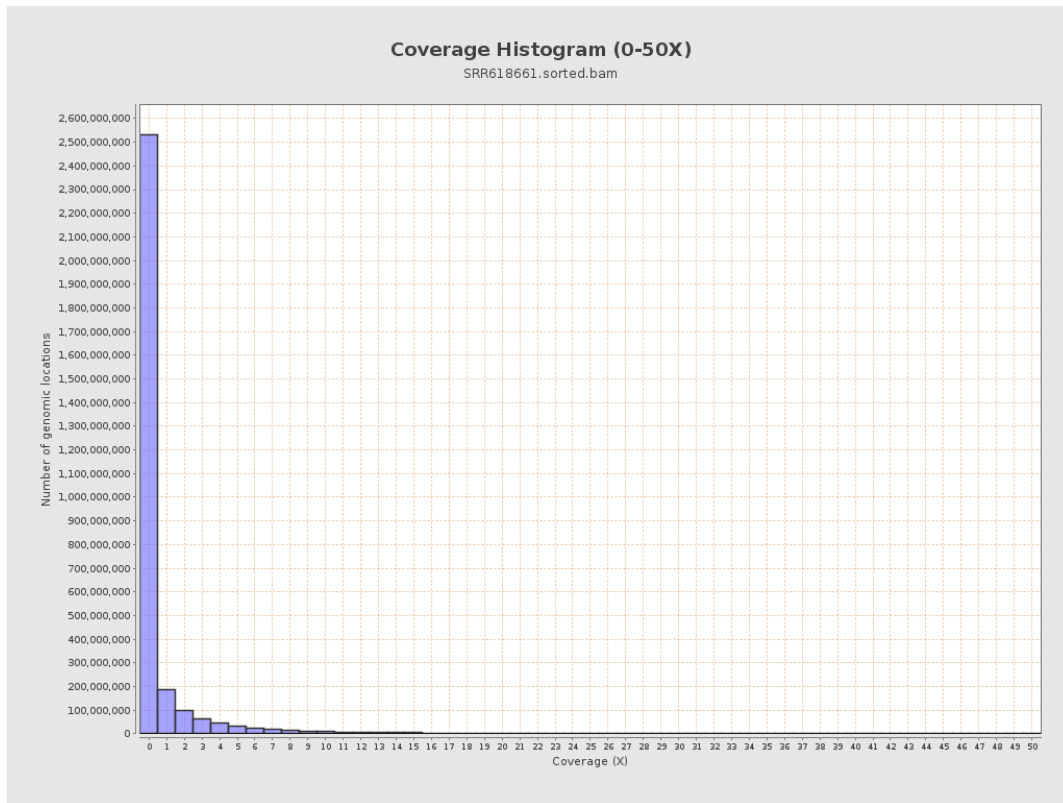
3. Results : Coverage across reference



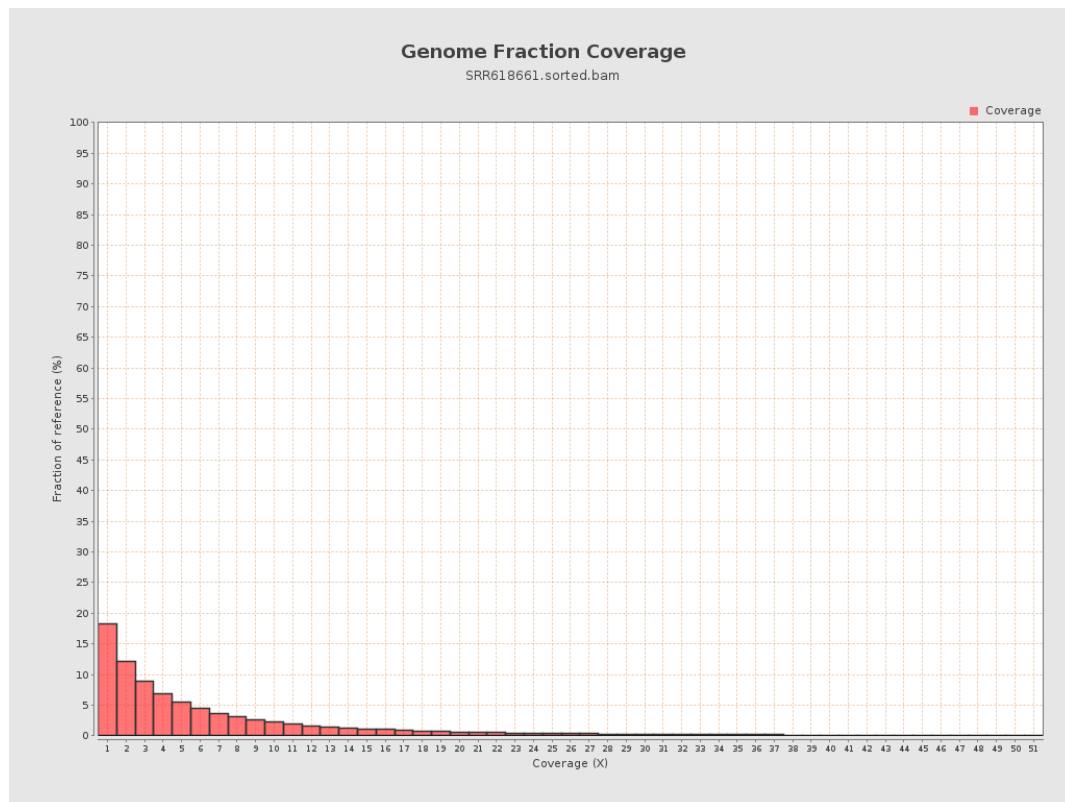
4. Results : Coverage Histogram



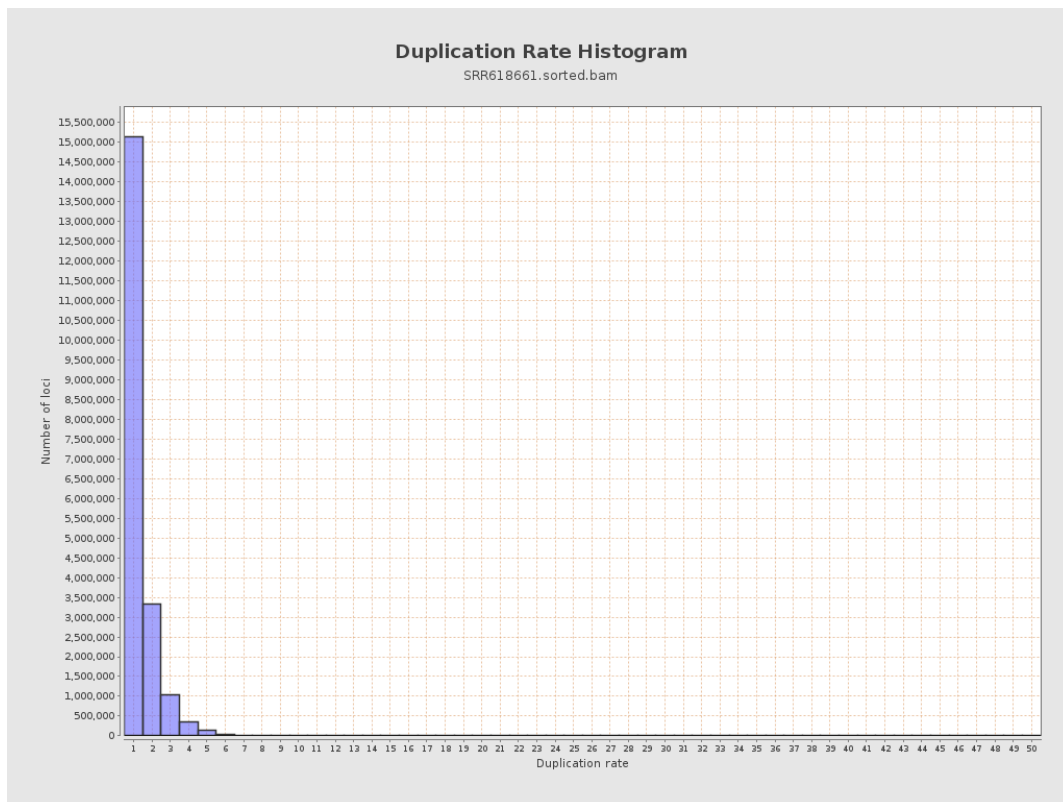
5. Results : Coverage Histogram (0-50X)



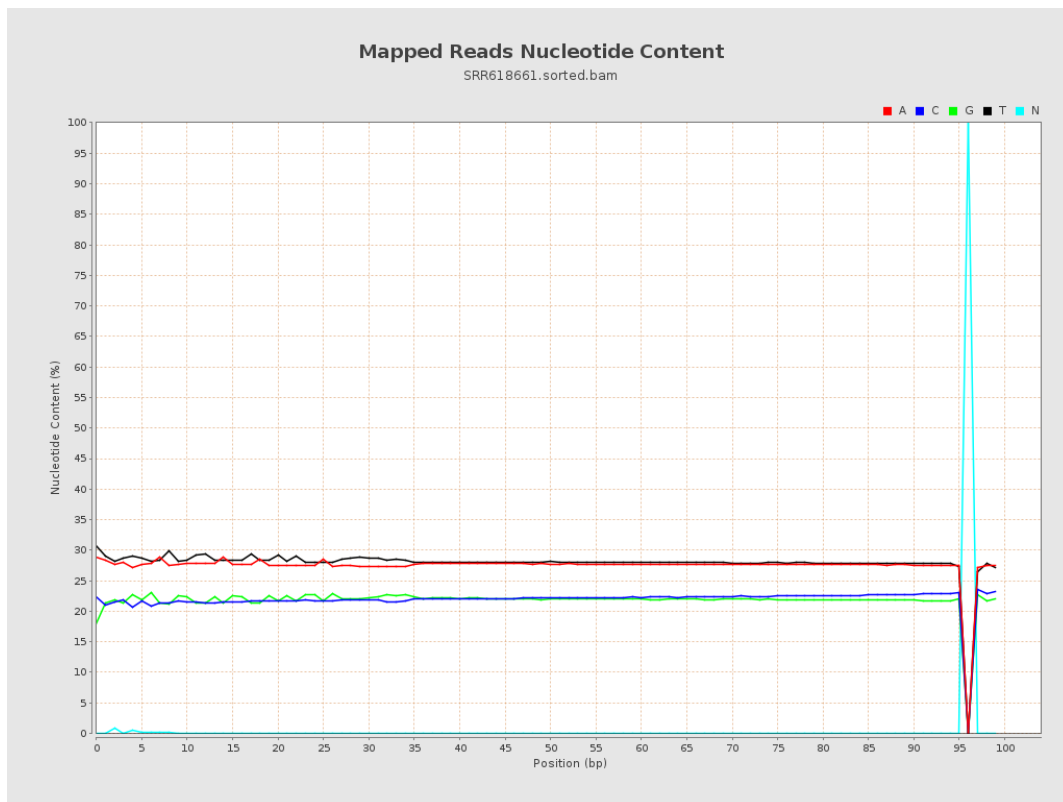
6. Results : Genome Fraction Coverage



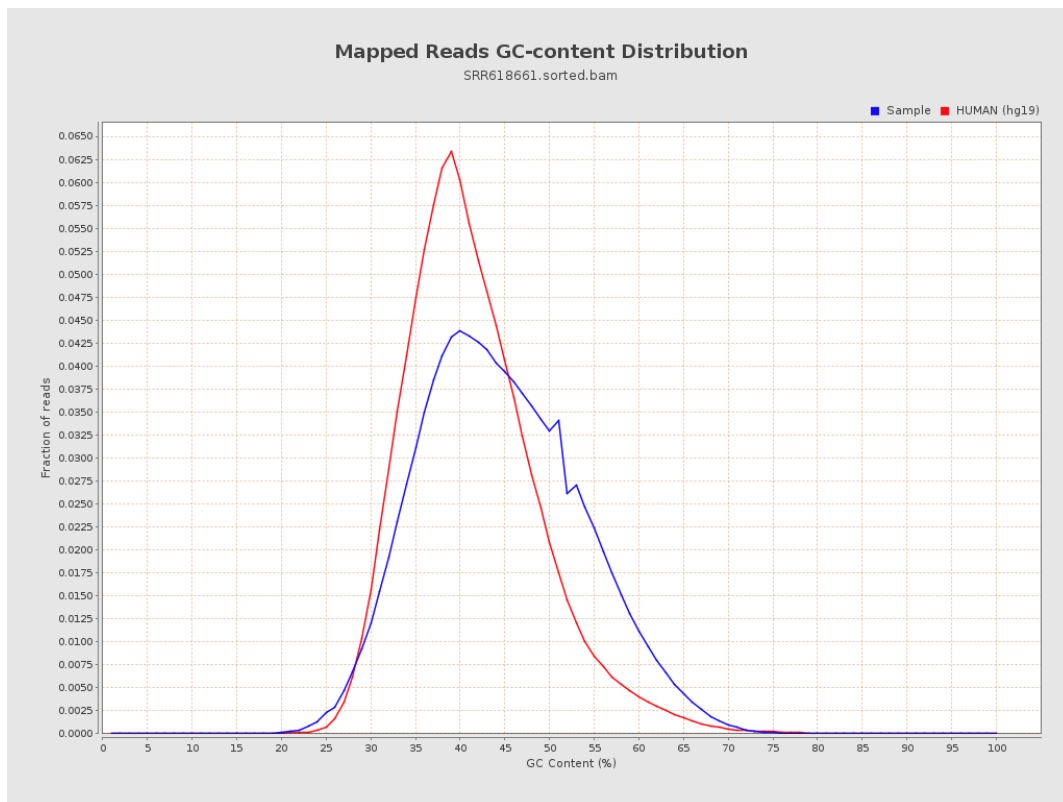
7. Results : Duplication Rate Histogram



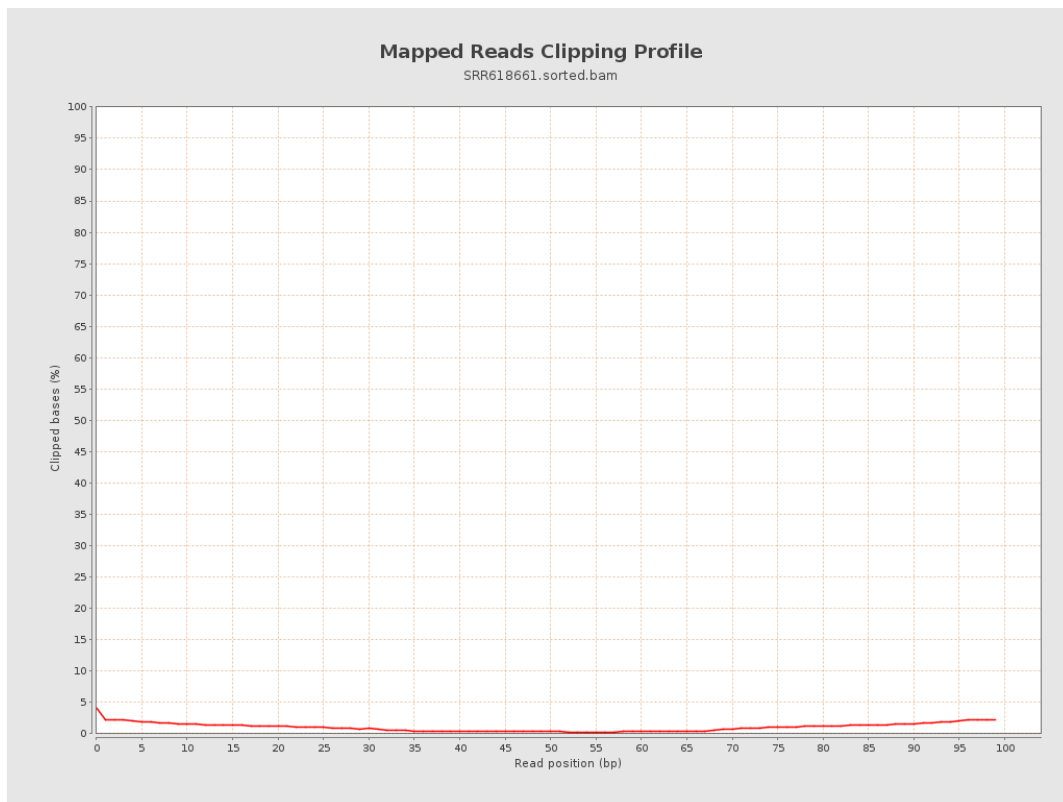
8. Results : Mapped Reads Nucleotide Content



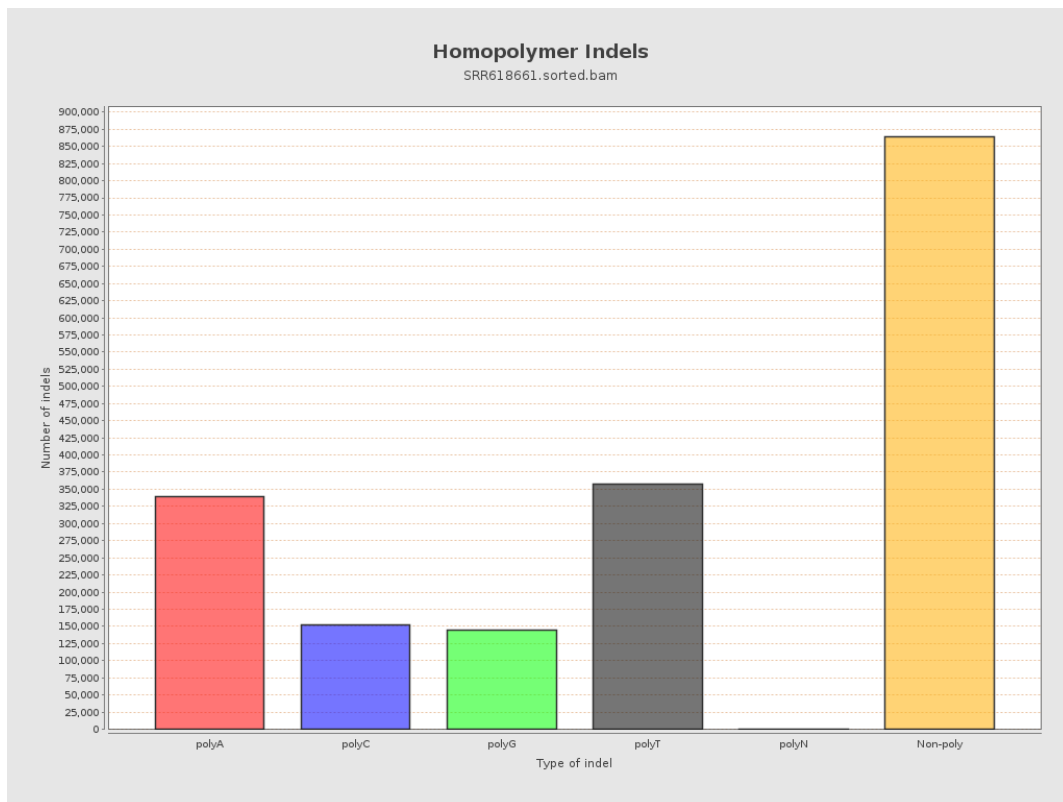
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

