

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 15:43:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618660.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_SRR618660 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618660.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 15:43:03 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618660.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,446,248
Mapped reads	32,955,624 / 92.97%
Unmapped reads	2,490,624 / 7.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	101,478 / 0.29%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	14,226,387 / 40.14%
Duplication rate	34.54%
Clipped reads	3,626,818 / 10.23%

2.2. ACGT Content

Number/percentage of A's	876,555,641 / 27.29%
Number/percentage of C's	709,068,663 / 22.07%
Number/percentage of T's	892,643,705 / 27.79%
Number/percentage of G's	702,243,146 / 21.86%
Number/percentage of N's	31,892,053 / 0.99%
GC Percentage	43.93%

2.3. Coverage

Mean	1.0384

Standard Deviation	4.3167
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2.4. Mapping Quality

Mean Mapping Quality	49.73
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2.5. Mismatches and indels

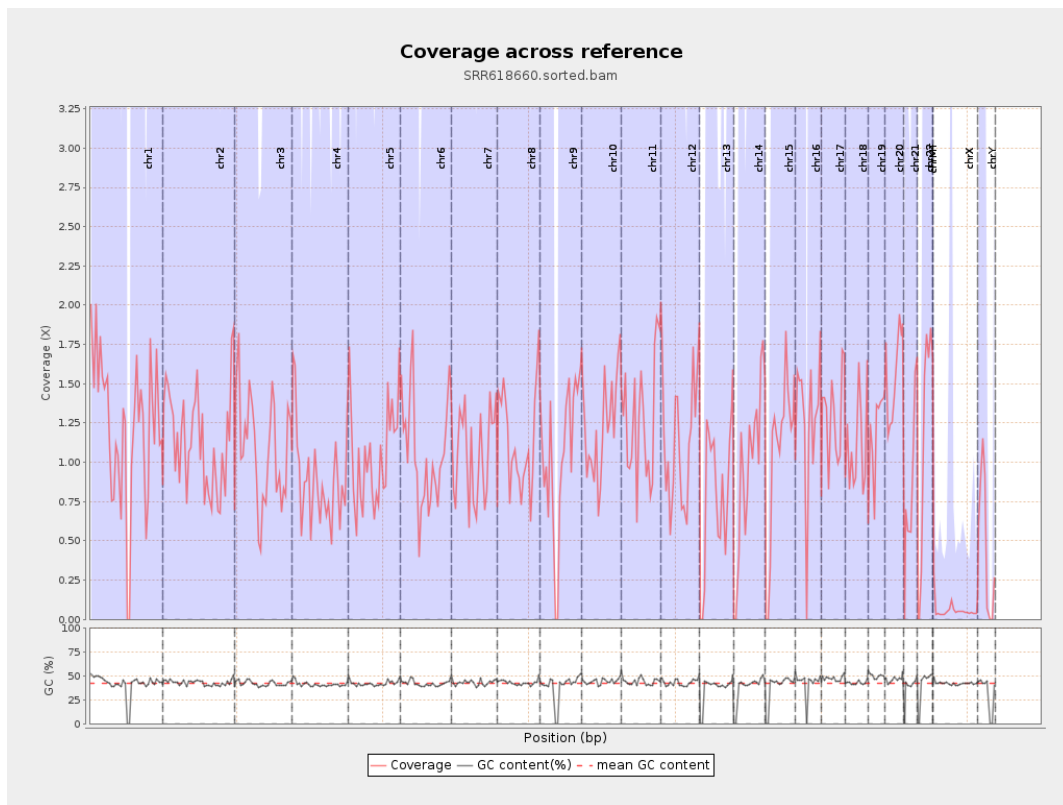
General error rate	1.99%
Mismatches	63,049,246
Insertions	597,922
Mapped reads with at least one insertion	1.79%
Deletions	1,638,293
Mapped reads with at least one deletion	4.85%
Homopolymer indels	53.05%

2.6. Chromosome stats

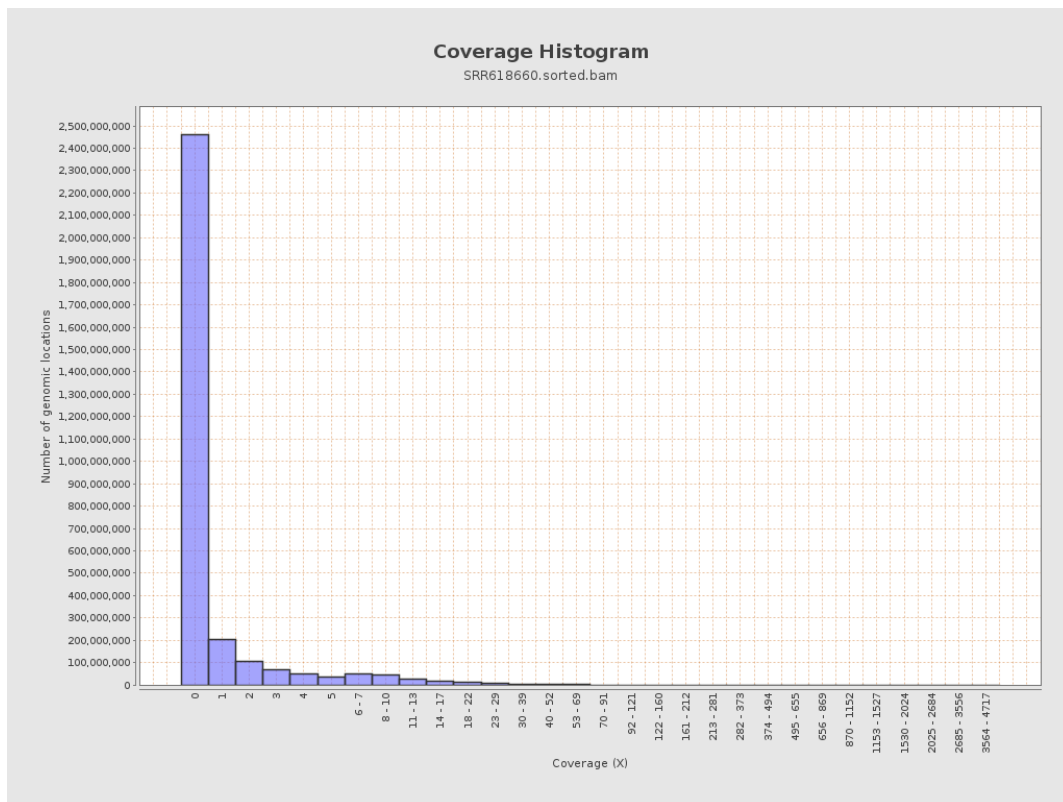
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	302416038	1.2133	5.0533
chr2	243199373	276768337	1.138	4.8931
chr3	198022430	212269242	1.0719	3.7885
chr4	191154276	169511256	0.8868	3.8236
chr5	180915260	190601323	1.0535	3.7115
chr6	171115067	180810847	1.0567	3.7722
chr7	159138663	168061422	1.0561	3.8825

chr8	146364022	166531772	1.1378	3.9524
chr9	141213431	145926050	1.0334	4.2996
chr10	135534747	165088223	1.2181	4.1454
chr11	135006516	170291998	1.2614	4.9513
chr12	133851895	152102957	1.1364	4.0098
chr13	115169878	90770370	0.7881	3.1063
chr14	107349540	103196815	0.9613	3.6481
chr15	102531392	108212553	1.0554	3.9091
chr16	90354753	114320481	1.2652	7.6743
chr17	81195210	105061503	1.2939	4.6215
chr18	78077248	85287331	1.0923	5.0701
chr19	59128983	70245405	1.188	4.586
chr20	63025520	97710930	1.5503	4.9702
chr21	48129895	42416002	0.8813	6.1245
chr22	51304566	59082284	1.1516	4.4584
chrMT	16571	25743	1.5535	6.3157
chrX	155270560	9074406	0.0584	1.2503
chrY	59373566	28897493	0.4867	3.1086

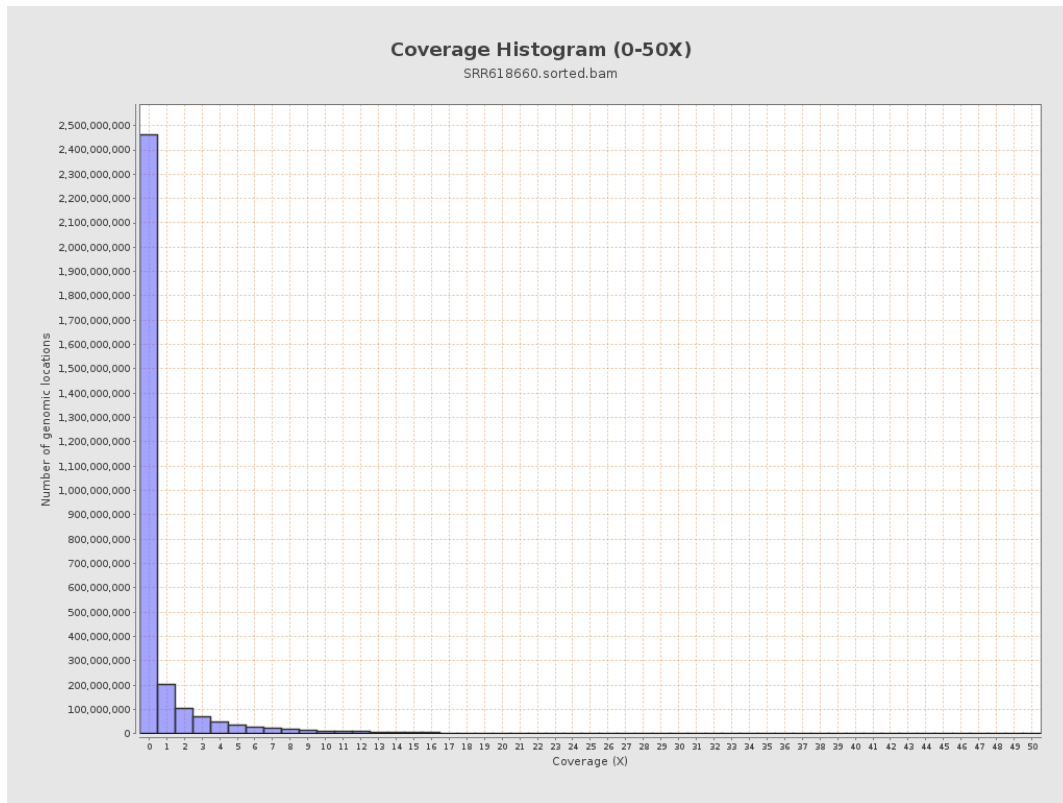
3. Results : Coverage across reference



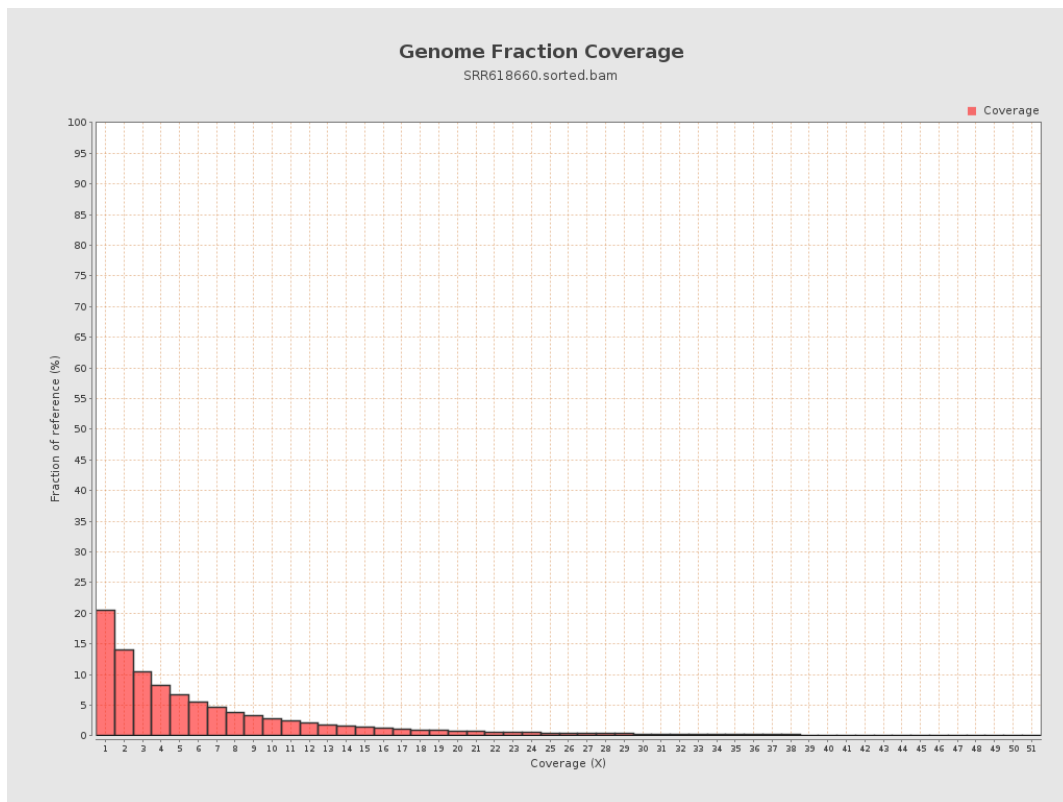
4. Results : Coverage Histogram



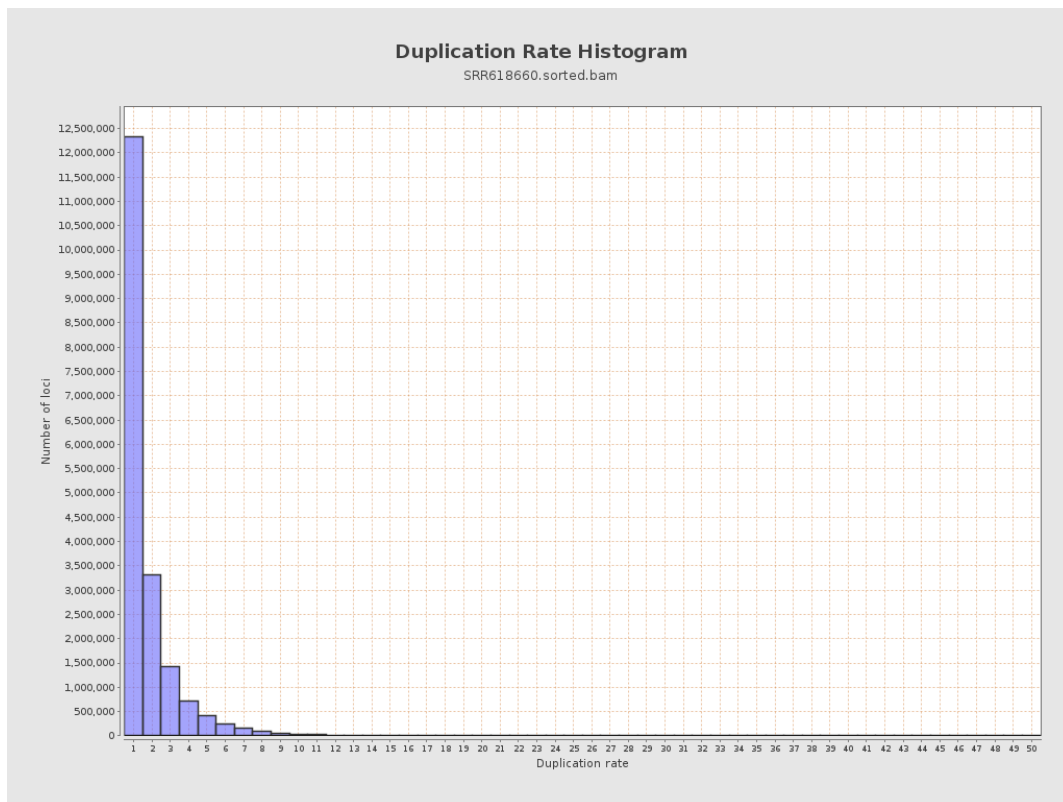
5. Results : Coverage Histogram (0-50X)



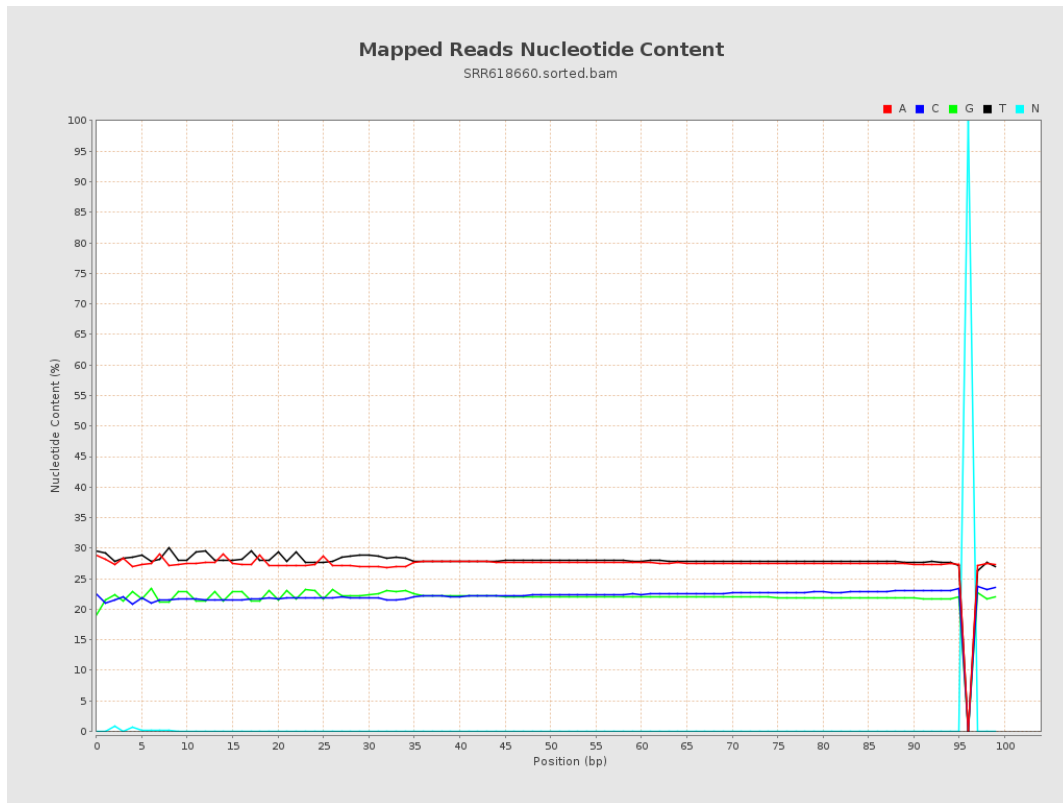
6. Results : Genome Fraction Coverage



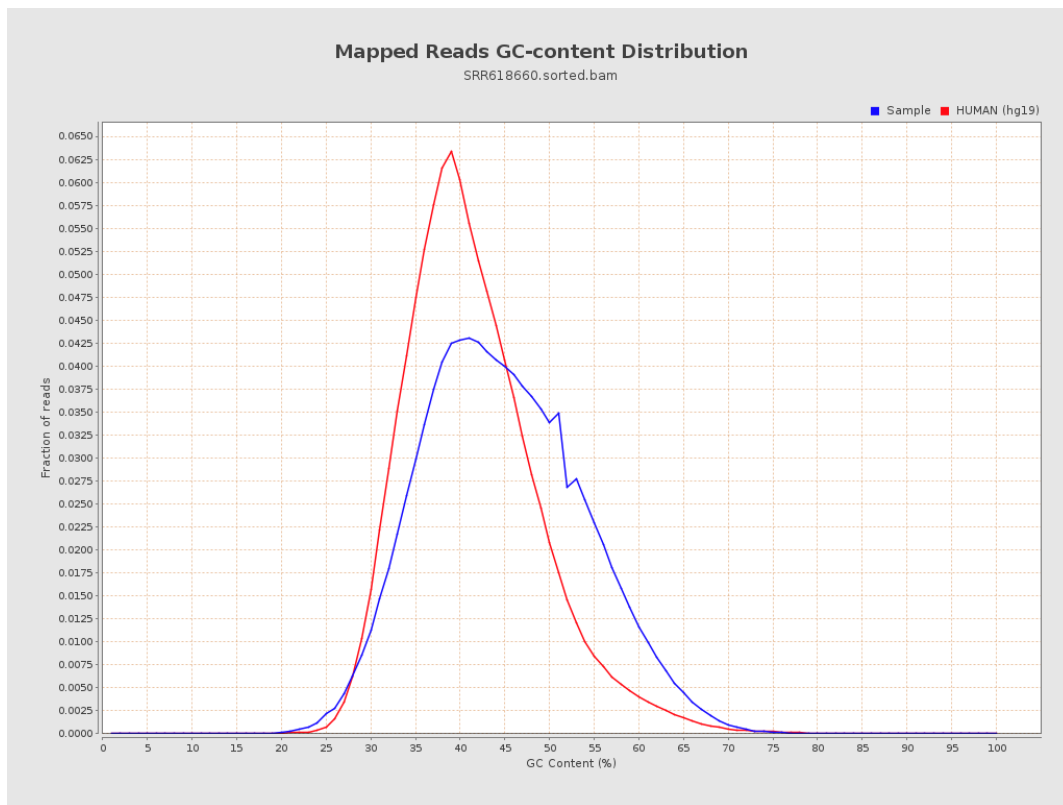
7. Results : Duplication Rate Histogram



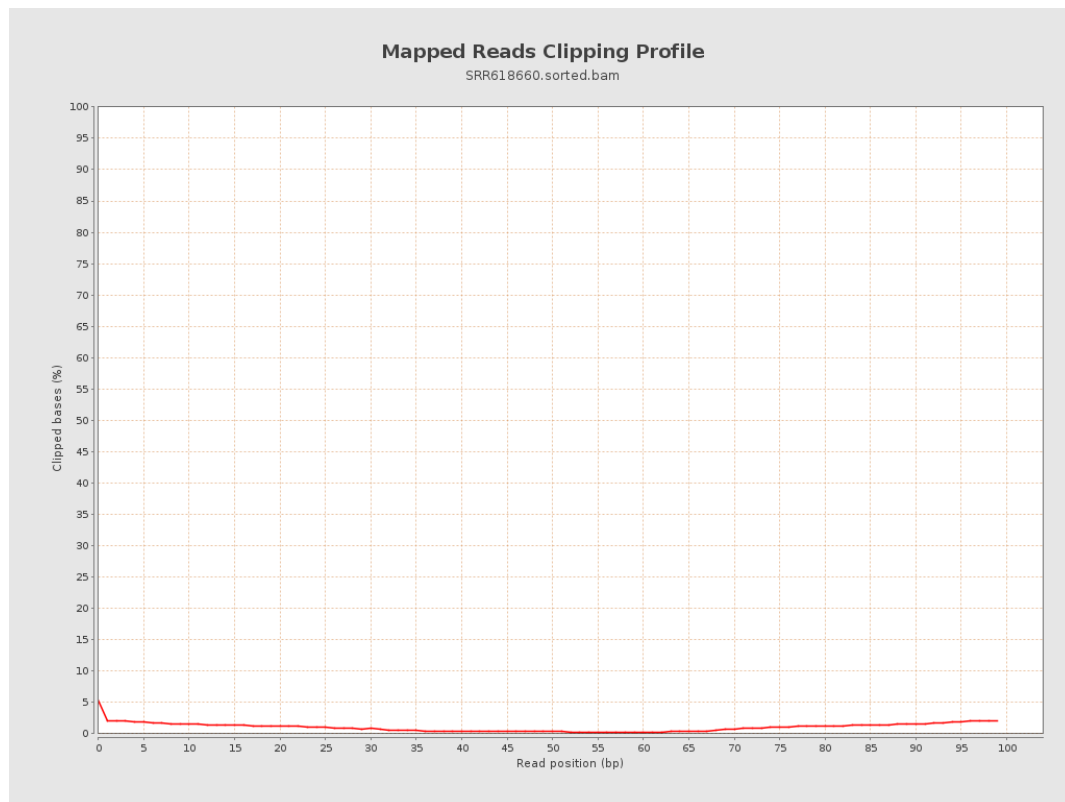
8. Results : Mapped Reads Nucleotide Content



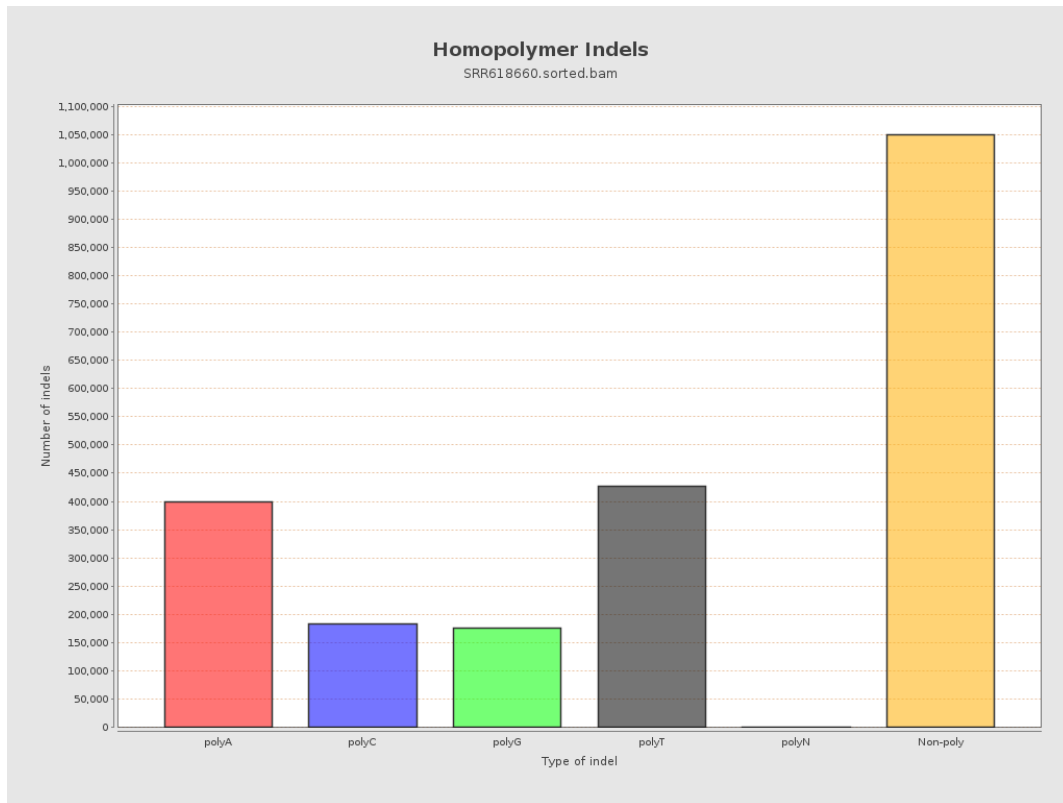
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

