

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 13:08:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618655.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_SRR618655 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618655.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 13:08:41 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618655.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,291,343
Mapped reads	53,031,208 / 89.44%
Unmapped reads	6,260,135 / 10.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	321,703 / 0.54%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	34,317,462 / 57.88%
Duplication rate	48.42%
Clipped reads	14,188,024 / 23.93%

2.2. ACGT Content

Number/percentage of A's	1,284,843,727 / 26.19%
Number/percentage of C's	1,189,144,736 / 24.24%
Number/percentage of T's	1,529,684,845 / 31.18%
Number/percentage of G's	900,296,789 / 18.35%
Number/percentage of N's	2,042,489 / 0.04%
GC Percentage	42.59%

2.3. Coverage

Mean	1.5861

Standard Deviation	177.682
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2.4. Mapping Quality

Mean Mapping Quality	48.86
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2.5. Mismatches and indels

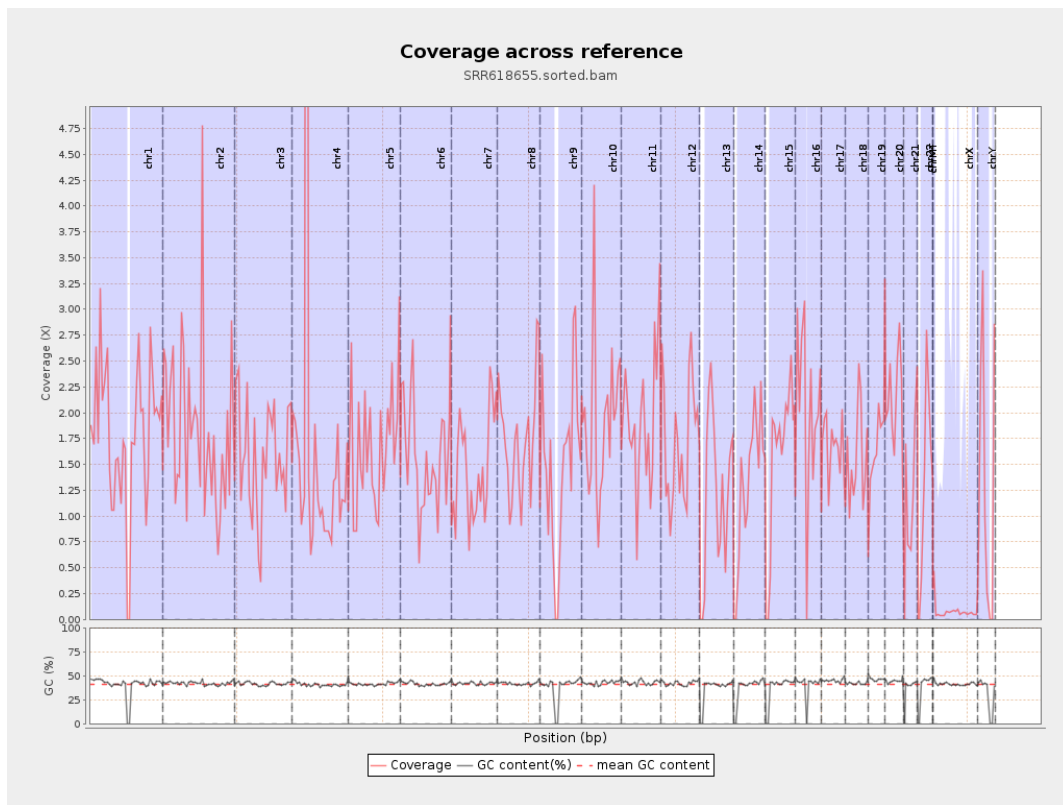
General error rate	1.33%
Mismatches	62,621,080
Insertions	1,230,043
Mapped reads with at least one insertion	2.23%
Deletions	2,374,110
Mapped reads with at least one deletion	4.33%
Homopolymer indels	45.7%

2.6. Chromosome stats

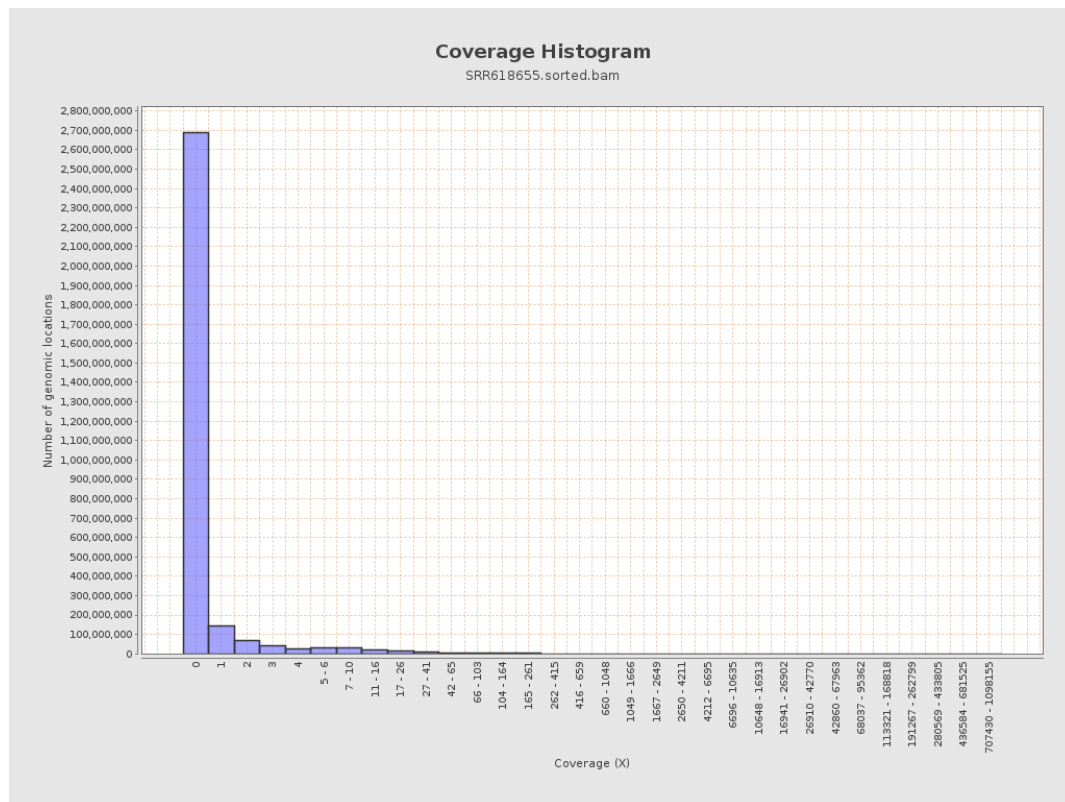
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	447487066	1.7953	43.0241
chr2	243199373	445164317	1.8305	67.826
chr3	198022430	311275259	1.5719	27.8833
chr4	191154276	352994918	1.8466	684.3202
chr5	180915260	302495704	1.672	29.0949
chr6	171115067	271710004	1.5879	25.451
chr7	159138663	230789525	1.4502	25.7937

chr8	146364022	252553200	1.7255	30.5243
chr9	141213431	210458355	1.4904	37.5931
chr10	135534747	255968891	1.8886	158.3831
chr11	135006516	258898033	1.9177	30.8267
chr12	133851895	233576165	1.745	32.8302
chr13	115169878	138337635	1.2012	24.3842
chr14	107349540	142858502	1.3308	21.9787
chr15	102531392	158699524	1.5478	29.1164
chr16	90354753	179669311	1.9885	62.1772
chr17	81195210	137727197	1.6962	29.5833
chr18	78077248	120167292	1.5391	23.1735
chr19	59128983	100379876	1.6976	41.8398
chr20	63025520	136711487	2.1691	32.2782
chr21	48129895	60620843	1.2595	56.543
chr22	51304566	69037220	1.3456	99.4842
chrMT	16571	4823	0.2911	1.0601
chrX	155270560	11931295	0.0768	6.96
chrY	59373566	80663321	1.3586	100.2417

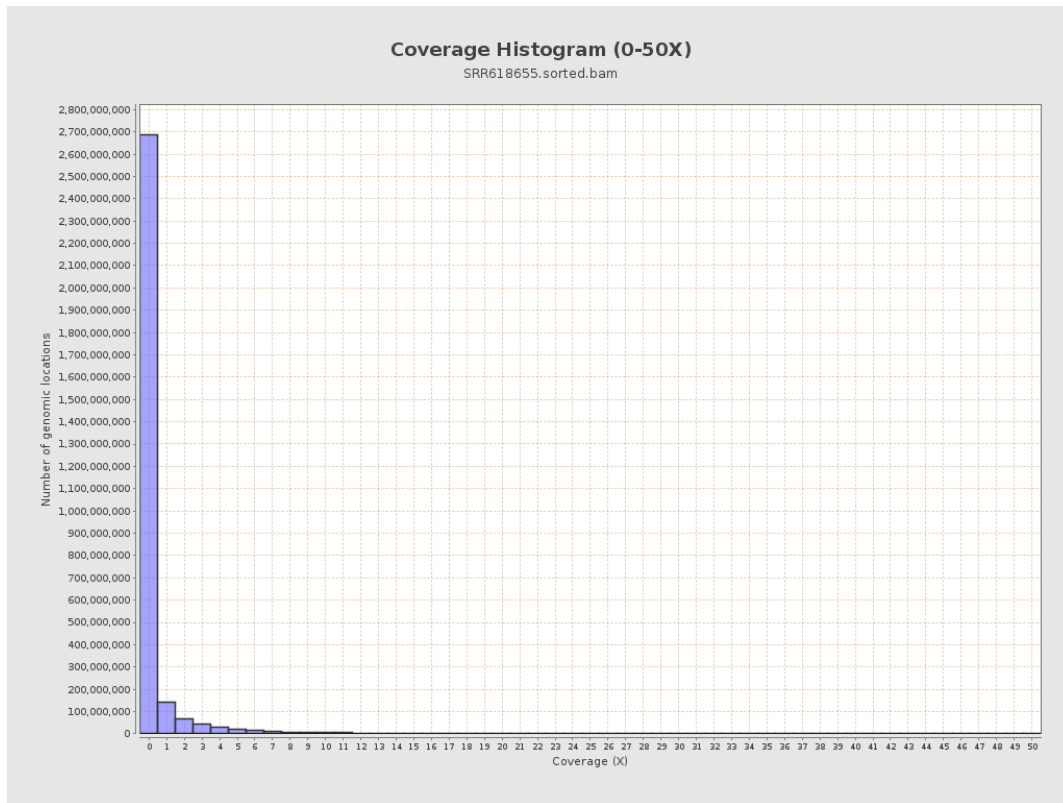
3. Results : Coverage across reference



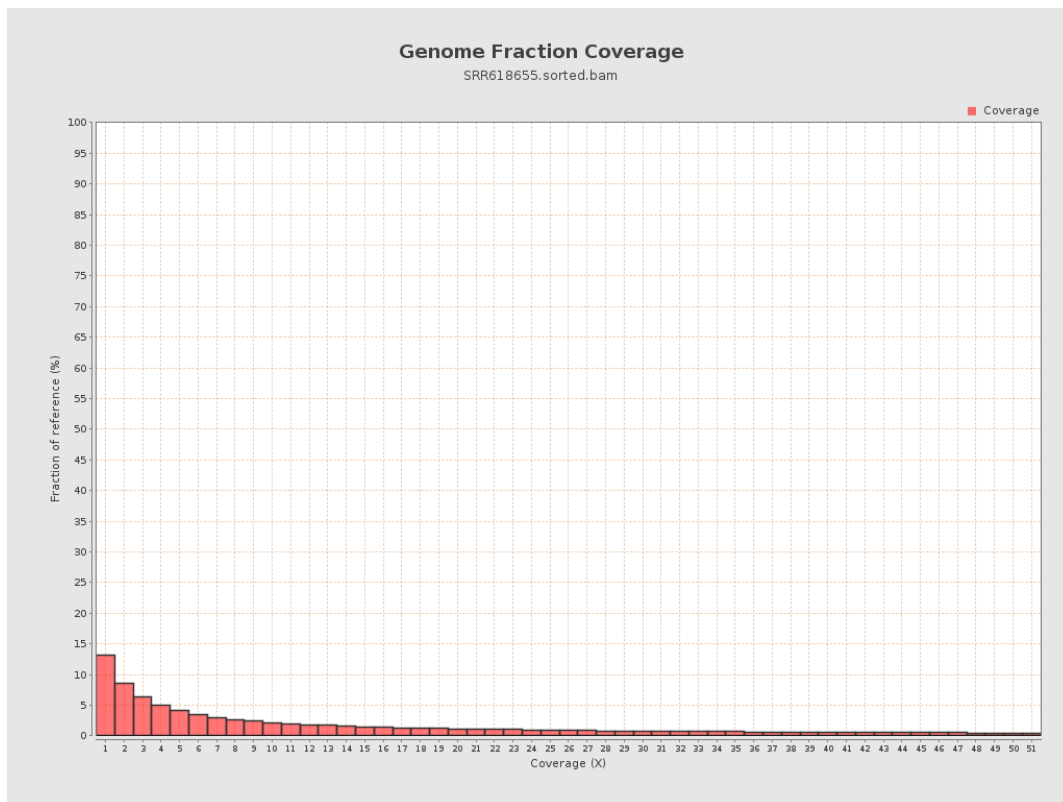
4. Results : Coverage Histogram



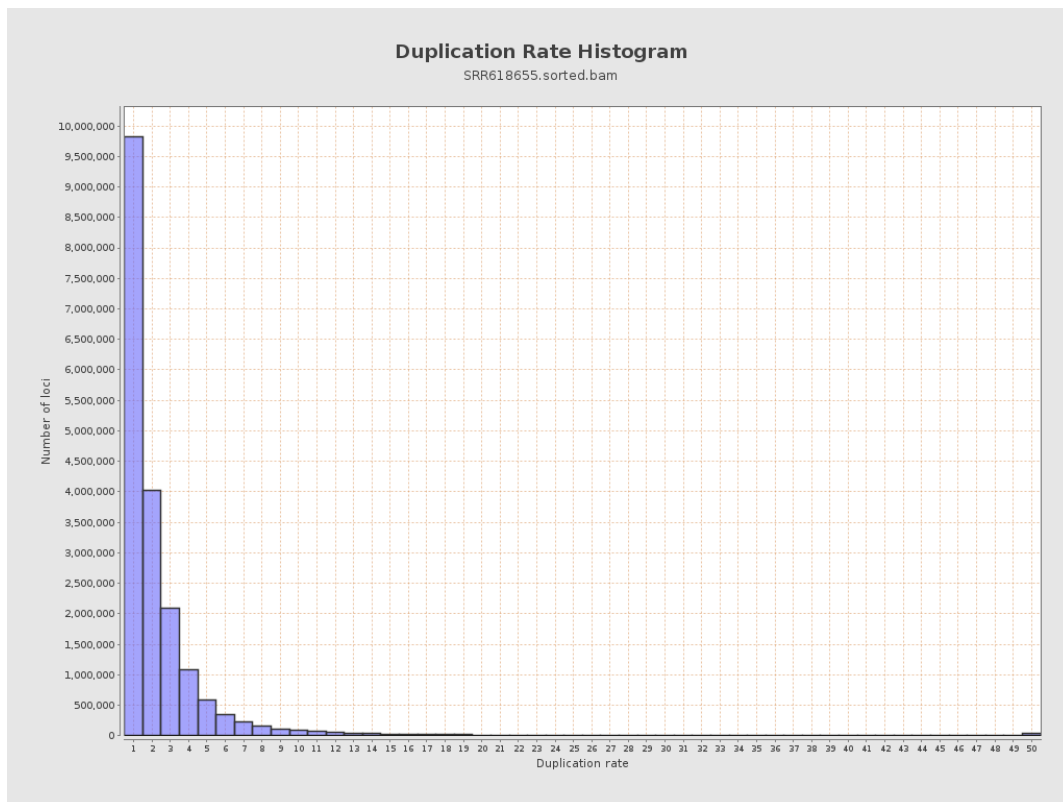
5. Results : Coverage Histogram (0-50X)



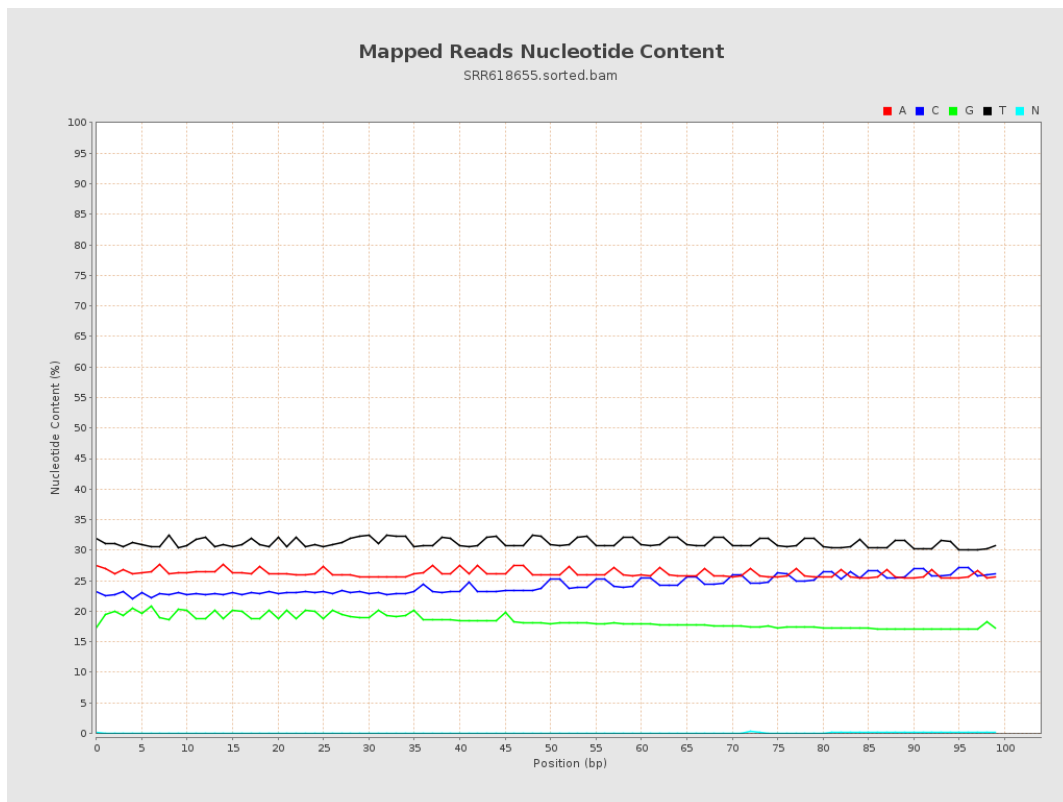
6. Results : Genome Fraction Coverage



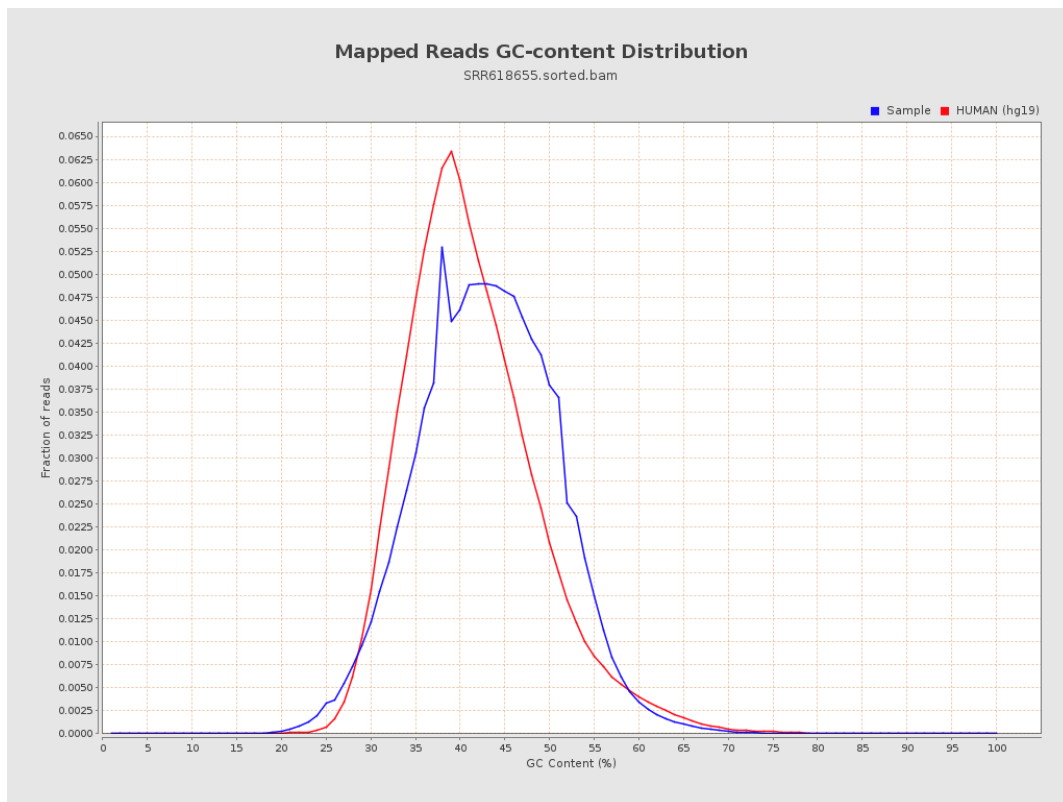
7. Results : Duplication Rate Histogram



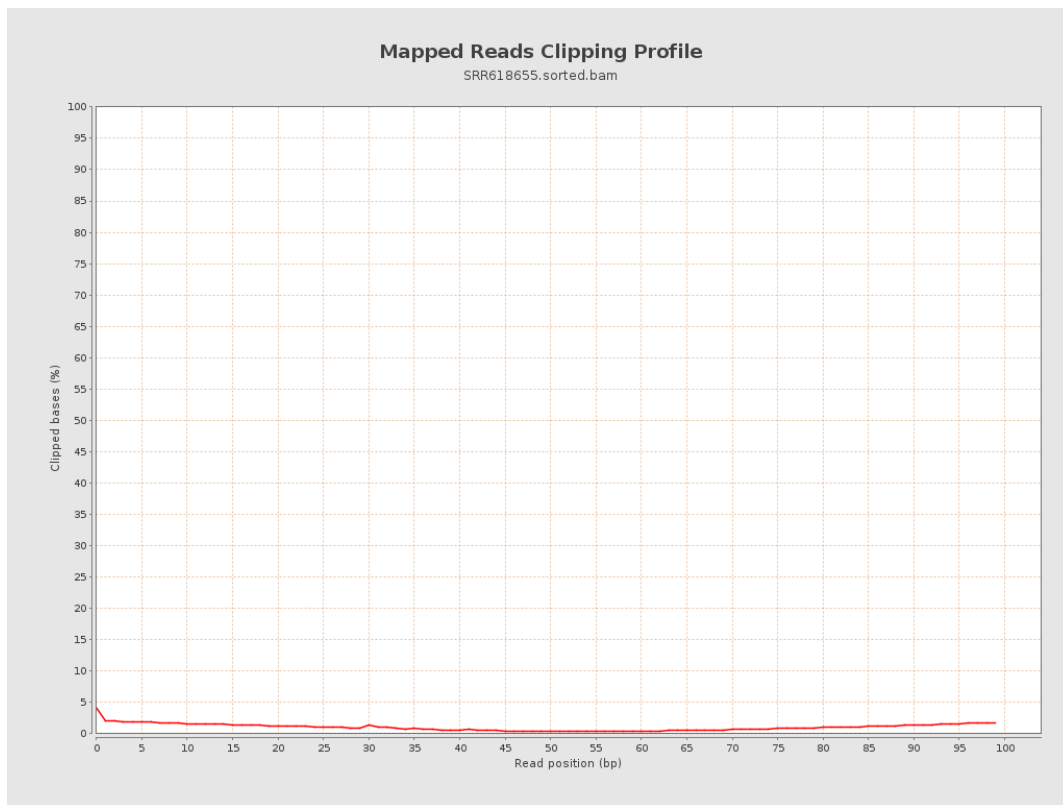
8. Results : Mapped Reads Nucleotide Content



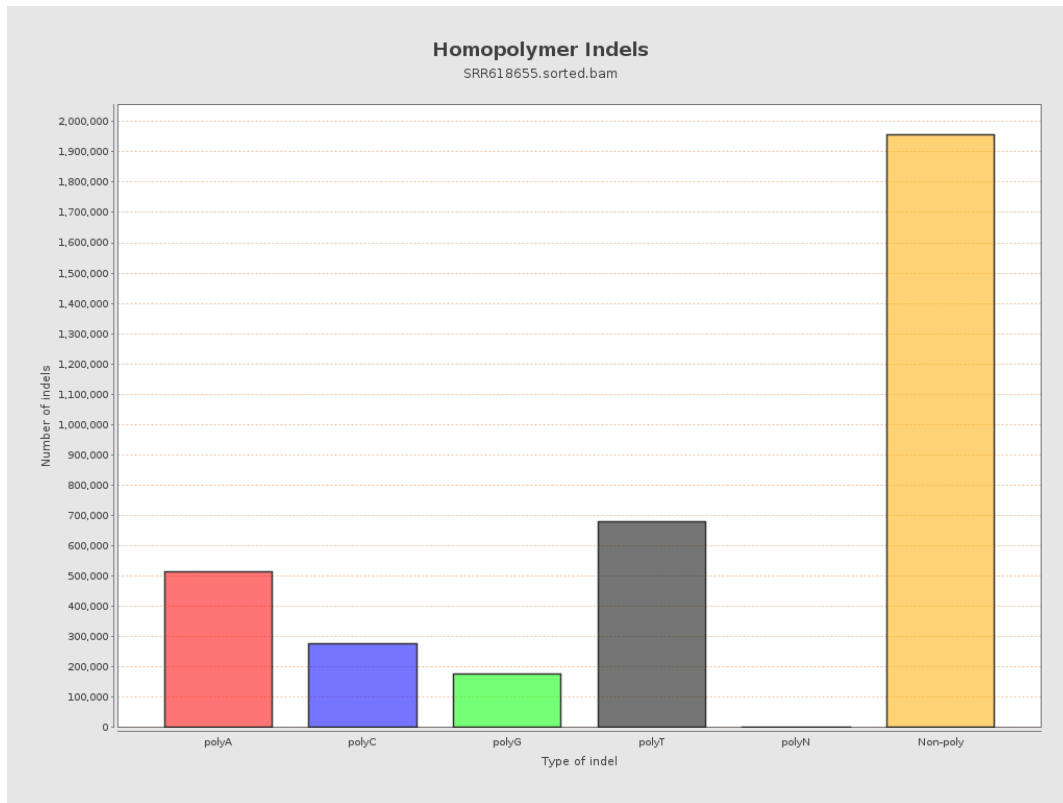
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

