

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 11:51:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618653.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_SRR618653 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618653.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 11:51:14 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618653.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	70,279,999
Mapped reads	62,312,541 / 88.66%
Unmapped reads	7,967,458 / 11.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	291,600 / 0.41%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	38,947,096 / 55.42%
Duplication rate	48.29%
Clipped reads	21,073,694 / 29.99%

2.2. ACGT Content

Number/percentage of A's	1,475,818,833 / 25.88%
Number/percentage of C's	1,370,849,989 / 24.04%
Number/percentage of T's	1,770,976,403 / 31.06%
Number/percentage of G's	1,082,935,281 / 18.99%
Number/percentage of N's	1,860,171 / 0.03%
GC Percentage	43.03%

2.3. Coverage

Mean	1.8434

Standard Deviation	35.4206
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2.4. Mapping Quality

Mean Mapping Quality	50.98
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2.5. Mismatches and indels

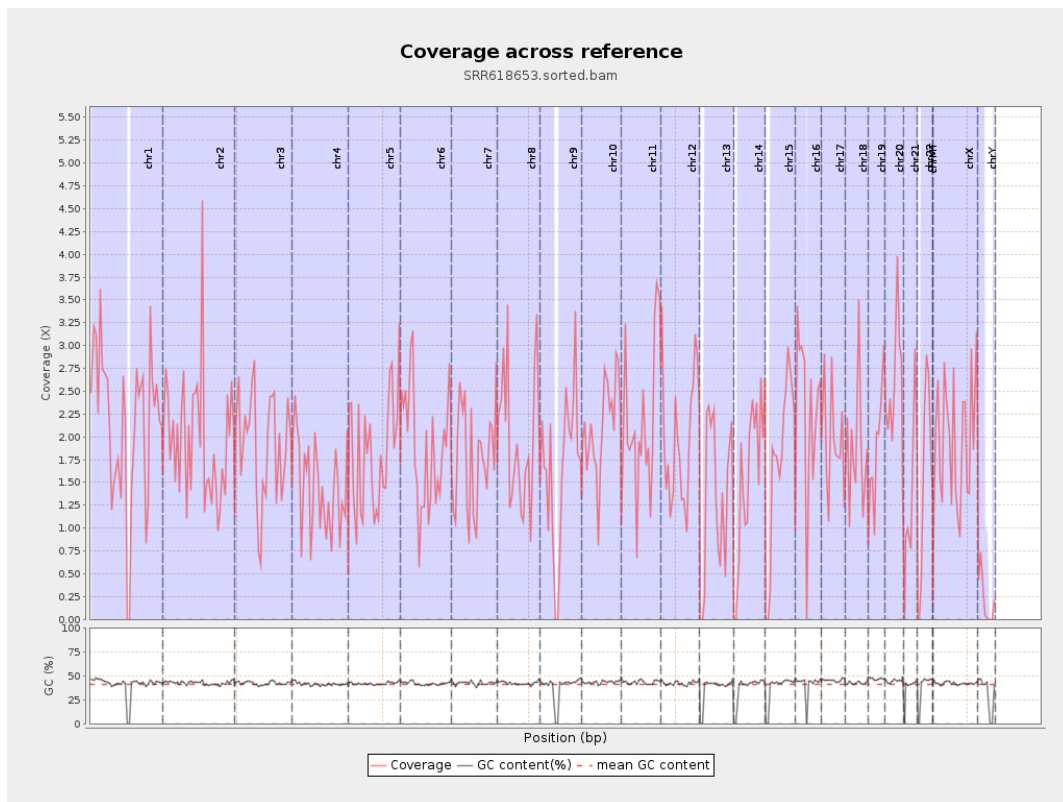
General error rate	1.74%
Mismatches	97,167,957
Insertions	1,265,960
Mapped reads with at least one insertion	1.98%
Deletions	2,626,501
Mapped reads with at least one deletion	4.11%
Homopolymer indels	46.57%

2.6. Chromosome stats

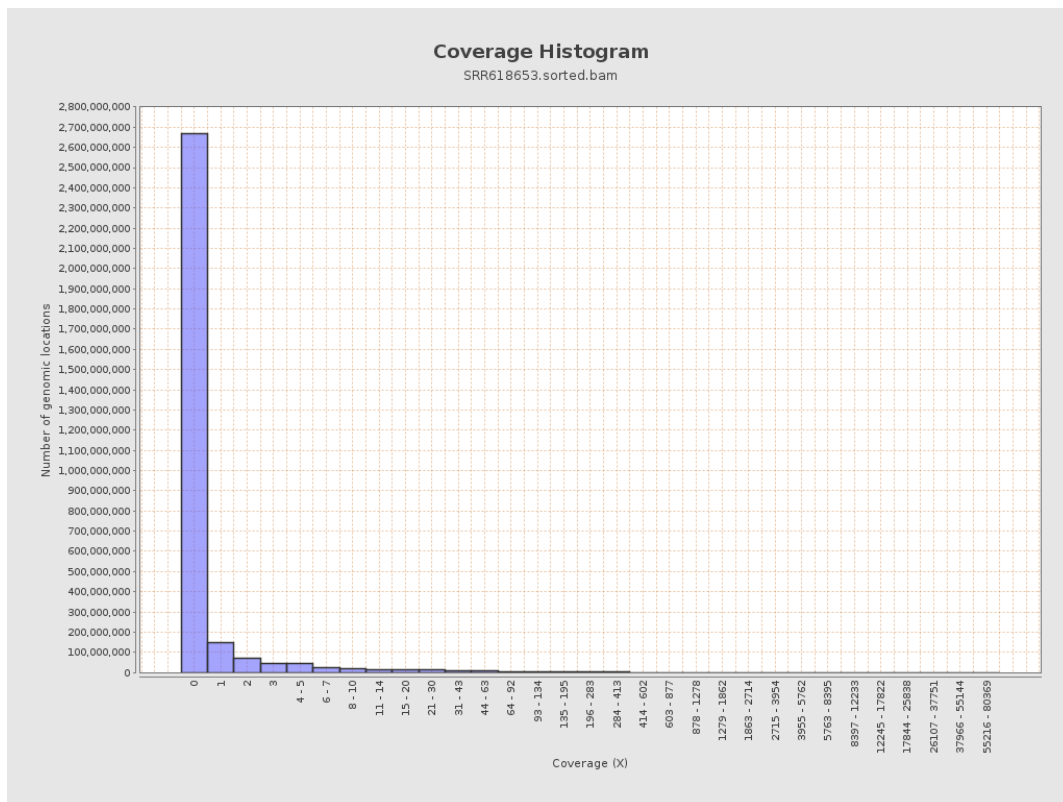
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	532184453	2.1351	35.2936
chr2	243199373	480165620	1.9744	58.7222
chr3	198022430	374268985	1.89	28.4782
chr4	191154276	278682446	1.4579	26.3744
chr5	180915260	331130412	1.8303	32.6876
chr6	171115067	320800736	1.8748	27.0469
chr7	159138663	281946508	1.7717	30.793

chr8	146364022	288699480	1.9725	43.3837
chr9	141213431	232213131	1.6444	26.814
chr10	135534747	286243392	2.112	41.8278
chr11	135006516	291170319	2.1567	29.9969
chr12	133851895	265586367	1.9842	34.0912
chr13	115169878	153762756	1.3351	22.0543
chr14	107349540	165500414	1.5417	26.2095
chr15	102531392	176819534	1.7245	25.662
chr16	90354753	200845083	2.2229	58.2248
chr17	81195210	161158722	1.9848	27.8546
chr18	78077248	143397248	1.8366	26.9478
chr19	59128983	111685583	1.8888	32.5911
chr20	63025520	162828679	2.5835	37.6193
chr21	48129895	67611166	1.4048	32.5201
chr22	51304566	81812539	1.5946	27.6129
chrMT	16571	3186	0.1923	1.0723
chrX	155270560	305158151	1.9653	32.4844
chrY	59373566	13053911	0.2199	29.3605

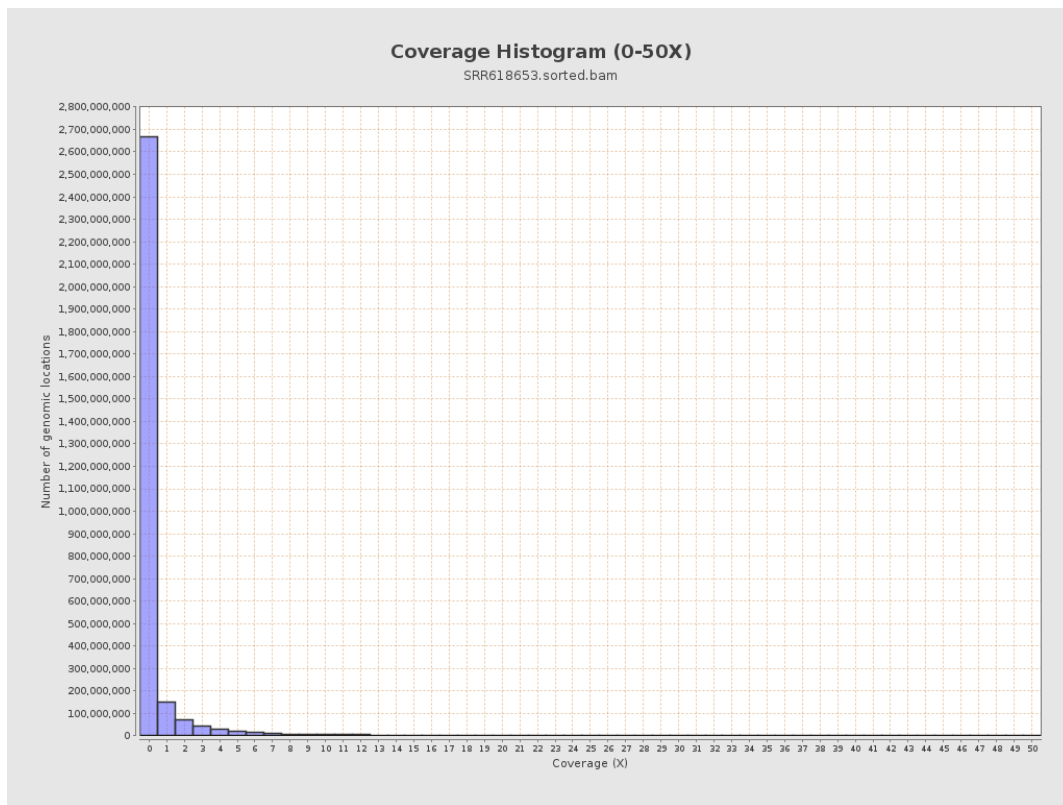
3. Results : Coverage across reference



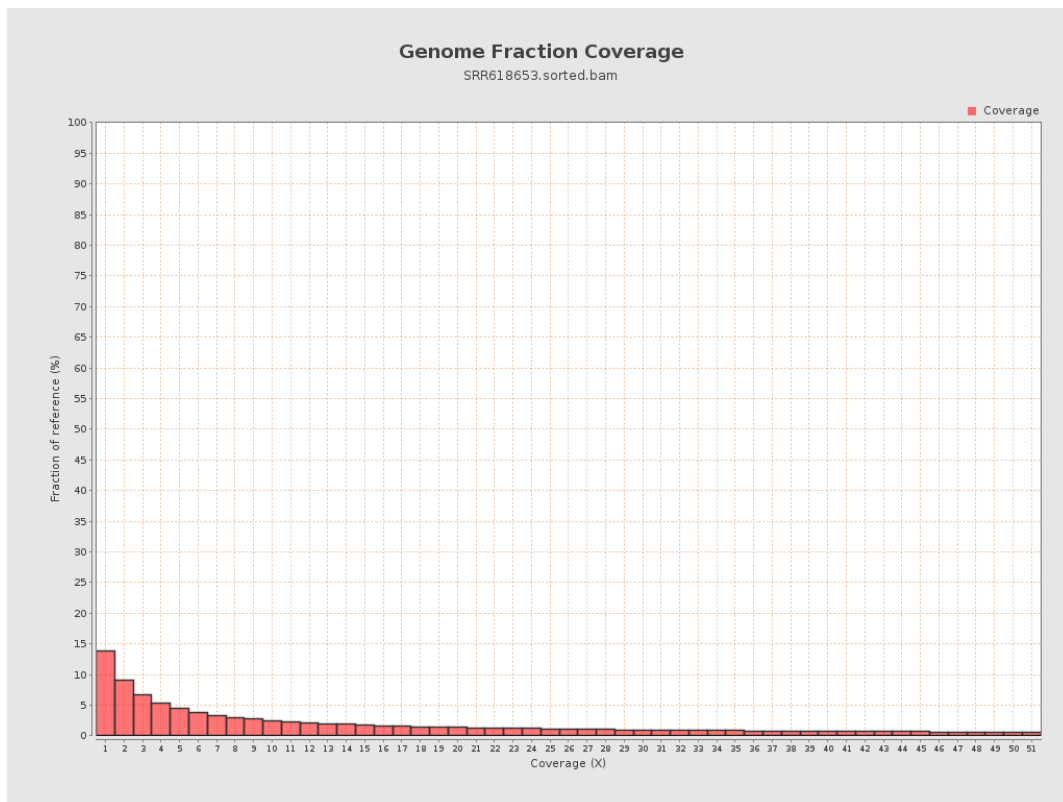
4. Results : Coverage Histogram



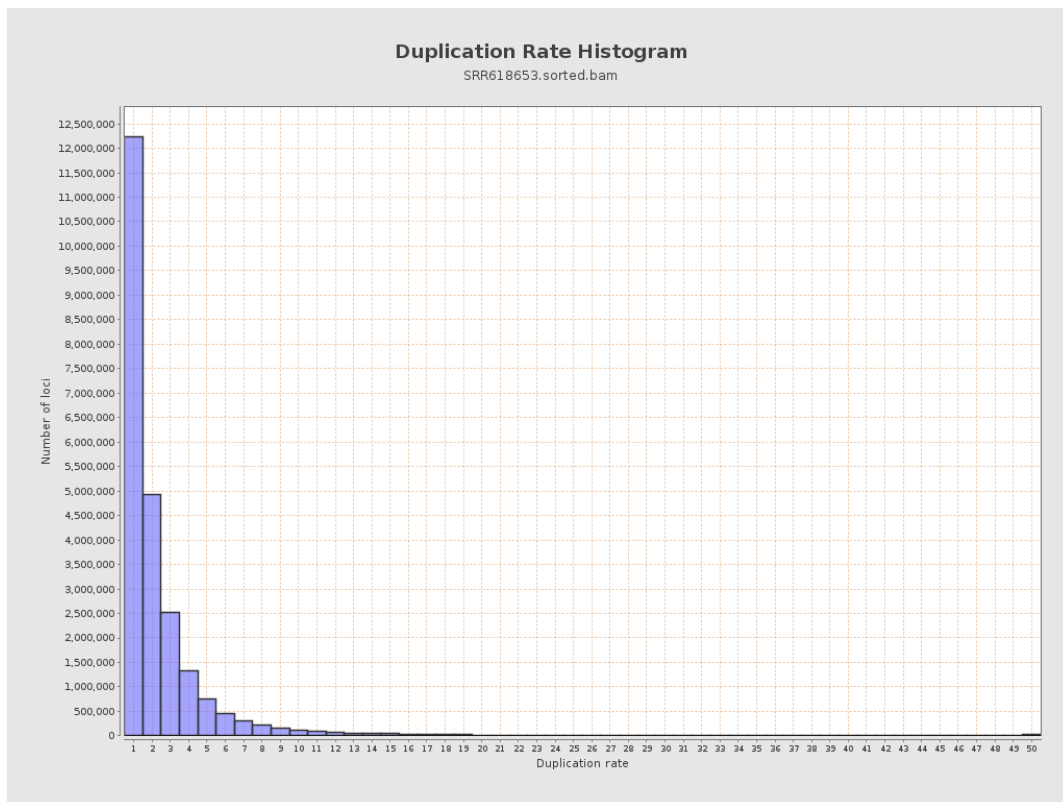
5. Results : Coverage Histogram (0-50X)



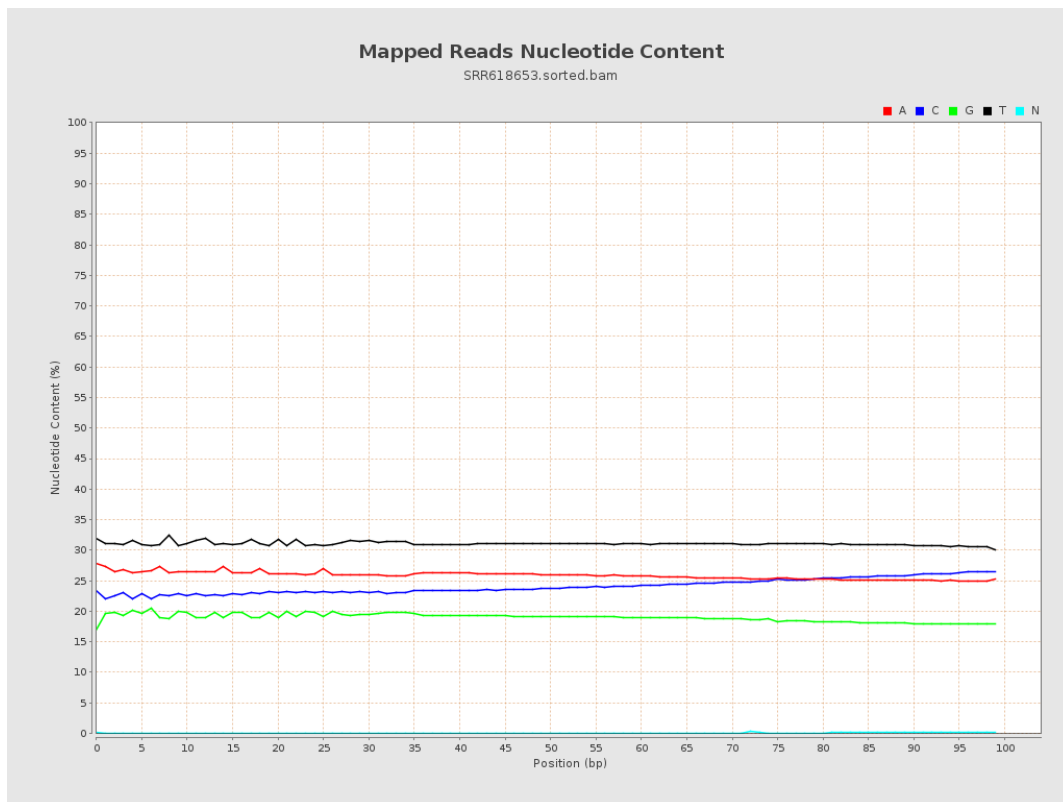
6. Results : Genome Fraction Coverage



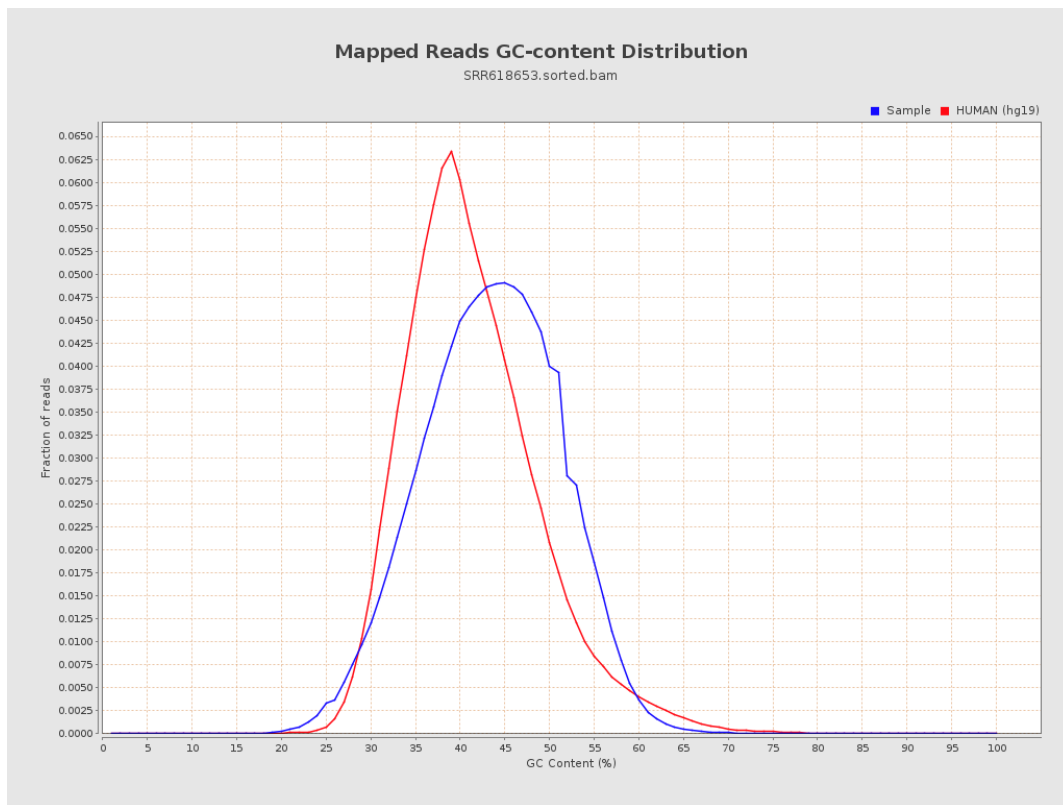
7. Results : Duplication Rate Histogram



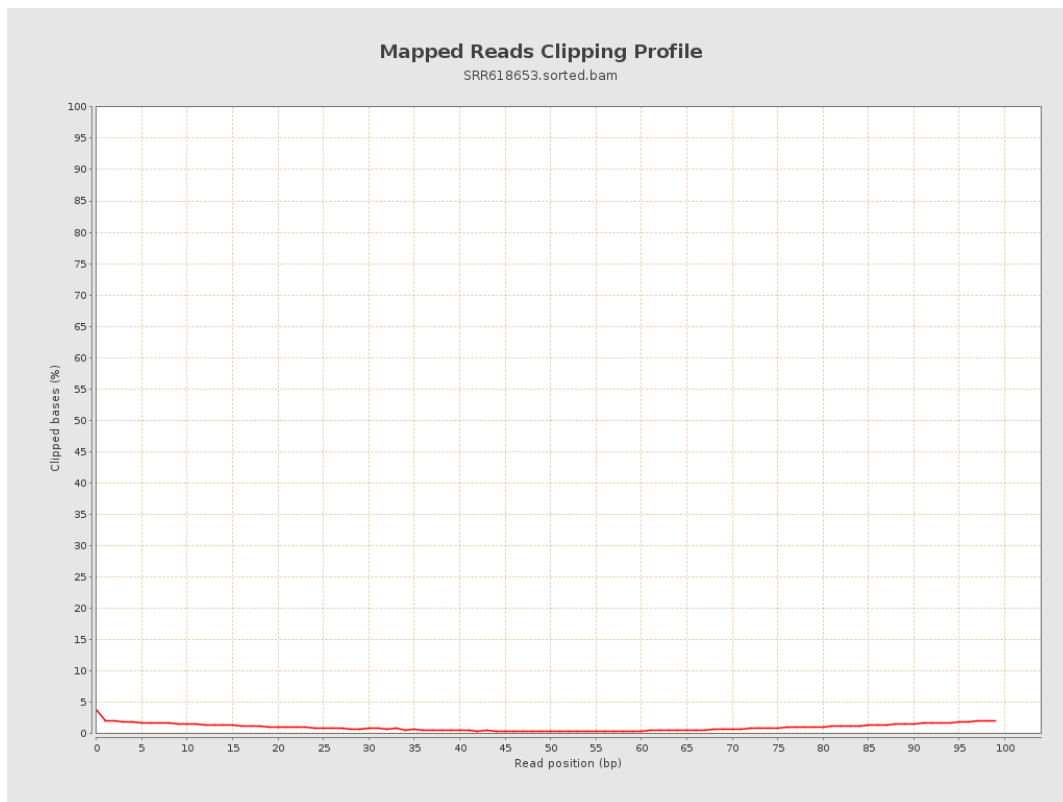
8. Results : Mapped Reads Nucleotide Content



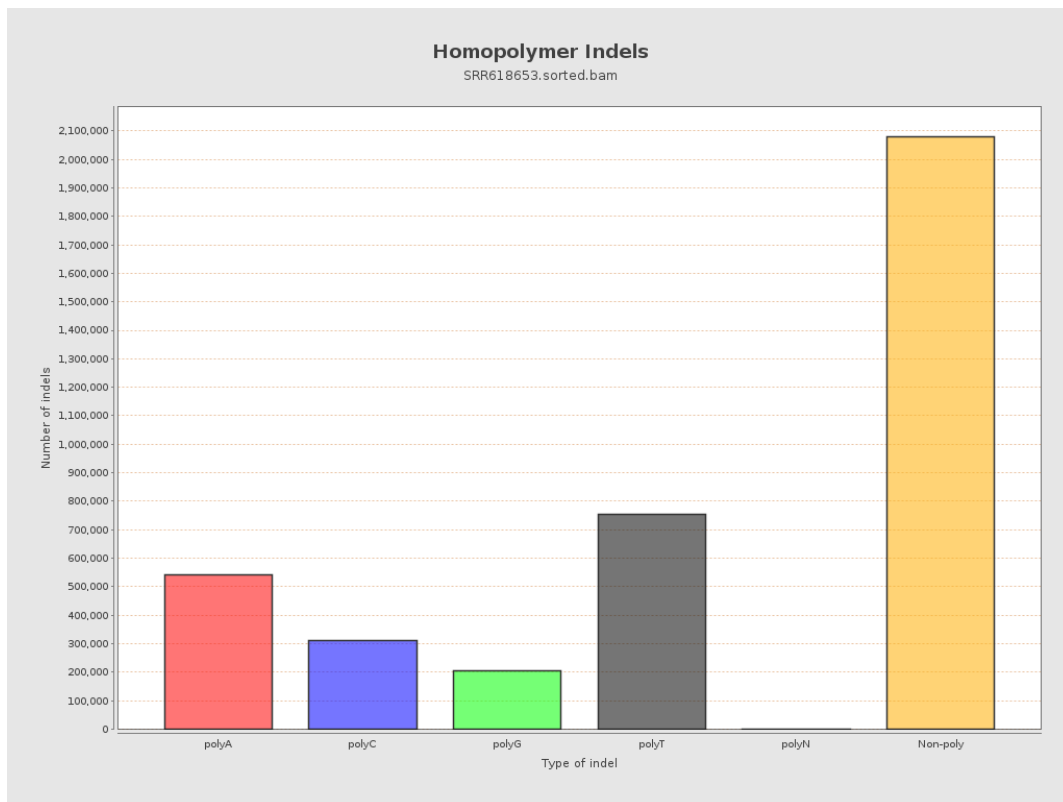
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

