

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:53:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818943.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_SRR1818943 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818943.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:53:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818943.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,318,763
Mapped reads	2,164,553 / 93.35%
Unmapped reads	154,210 / 6.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,237 / 1.13%
Read min/max/mean length	30 / 101 / 101.44
Duplicated reads (estimated)	936,581 / 40.39%
Duplication rate	36.19%
Clipped reads	2,182,451 / 94.12%

2.2. ACGT Content

Number/percentage of A's	58,479,491 / 29.17%
Number/percentage of C's	41,887,397 / 20.9%
Number/percentage of T's	57,497,252 / 28.68%
Number/percentage of G's	42,578,261 / 21.24%
Number/percentage of N's	9,744 / 0%
GC Percentage	42.14%

2.3. Coverage

Mean	0.0648

Standard Deviation	0.7137
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2.4. Mapping Quality

Mean Mapping Quality	49.39
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2.5. Mismatches and indels

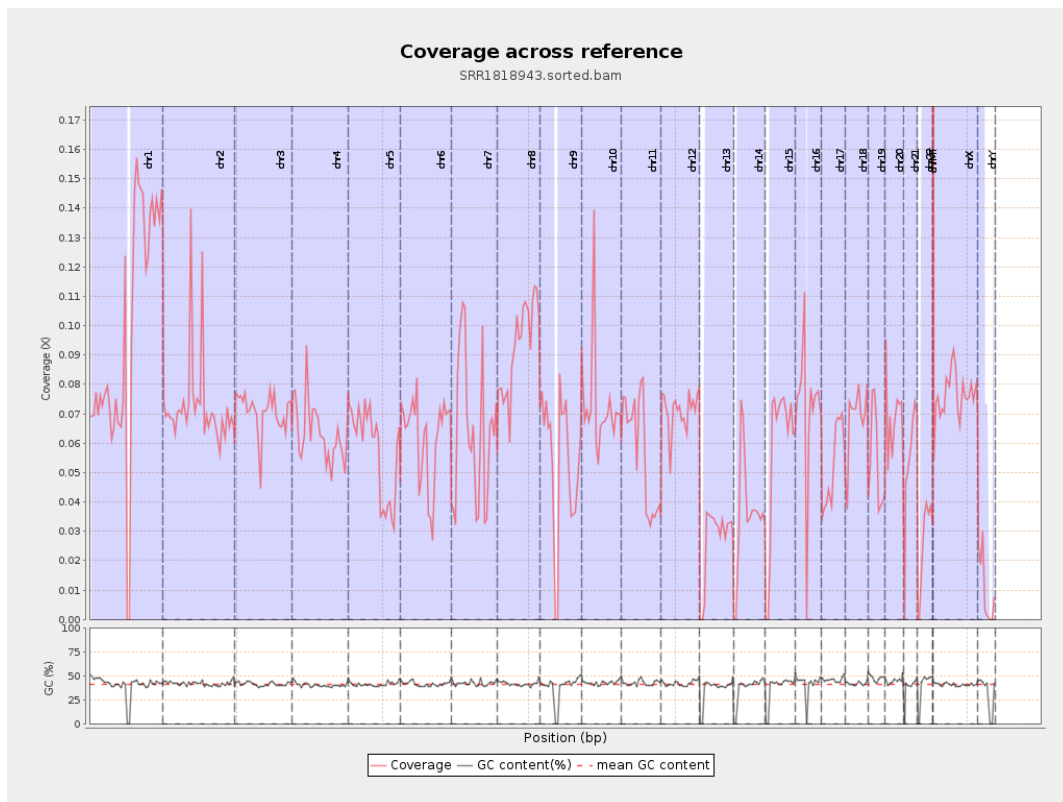
General error rate	0.67%
Mismatches	1,282,458
Insertions	26,032
Mapped reads with at least one insertion	1.17%
Deletions	61,660
Mapped reads with at least one deletion	2.79%
Homopolymer indels	41.89%

2.6. Chromosome stats

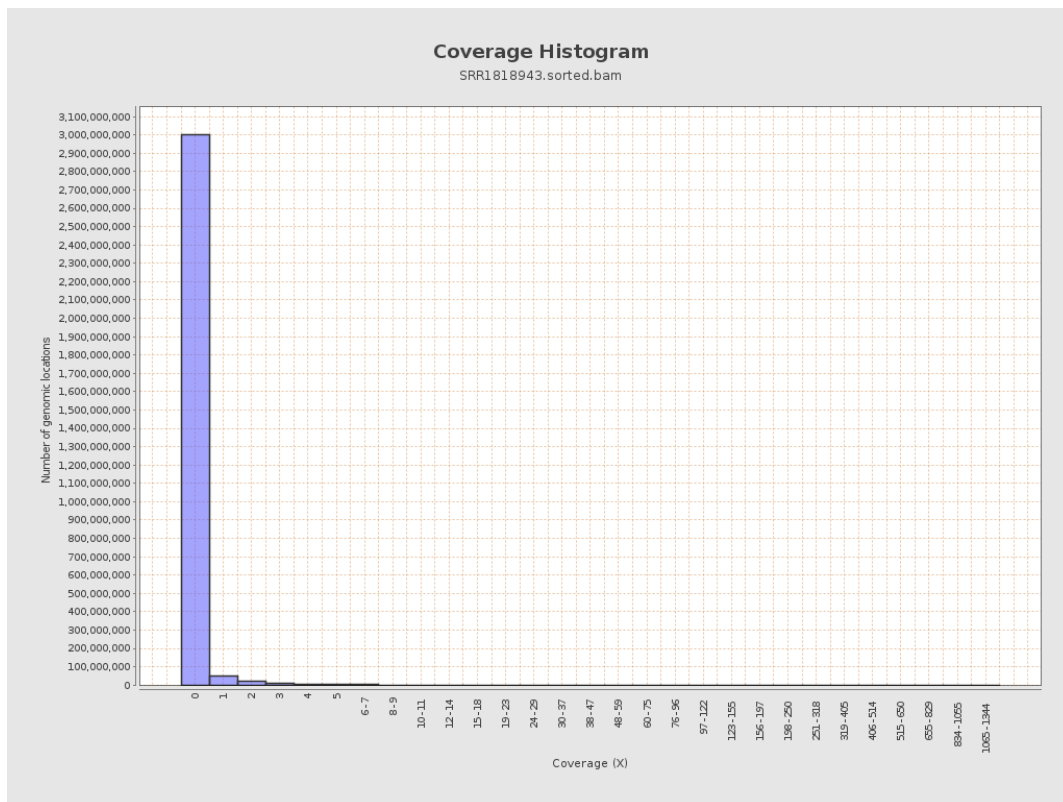
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24315553	0.0976	1.2642
chr2	243199373	17685694	0.0727	1.0036
chr3	198022430	13944832	0.0704	0.495
chr4	191154276	12183867	0.0637	0.5068
chr5	180915260	10391450	0.0574	0.4569
chr6	171115067	10650984	0.0622	0.4932
chr7	159138663	10138953	0.0637	0.6058

chr8	146364022	13616957	0.093	0.6318
chr9	141213431	7624010	0.054	0.7662
chr10	135534747	9776641	0.0721	0.9056
chr11	135006516	7675200	0.0569	0.496
chr12	133851895	9533274	0.0712	0.5063
chr13	115169878	3155828	0.0274	0.3003
chr14	107349540	3980864	0.0371	0.3986
chr15	102531392	5871702	0.0573	0.445
chr16	90354753	6417412	0.071	0.8252
chr17	81195210	4278332	0.0527	0.4775
chr18	78077248	5306098	0.068	0.9695
chr19	59128983	3245765	0.0549	1.0971
chr20	63025520	4322082	0.0686	0.5206
chr21	48129895	2647843	0.055	0.4652
chr22	51304566	1340617	0.0261	0.3347
chrMT	16571	12340	0.7447	1.5763
chrX	155270560	11855026	0.0764	0.5613
chrY	59373566	595432	0.01	0.618

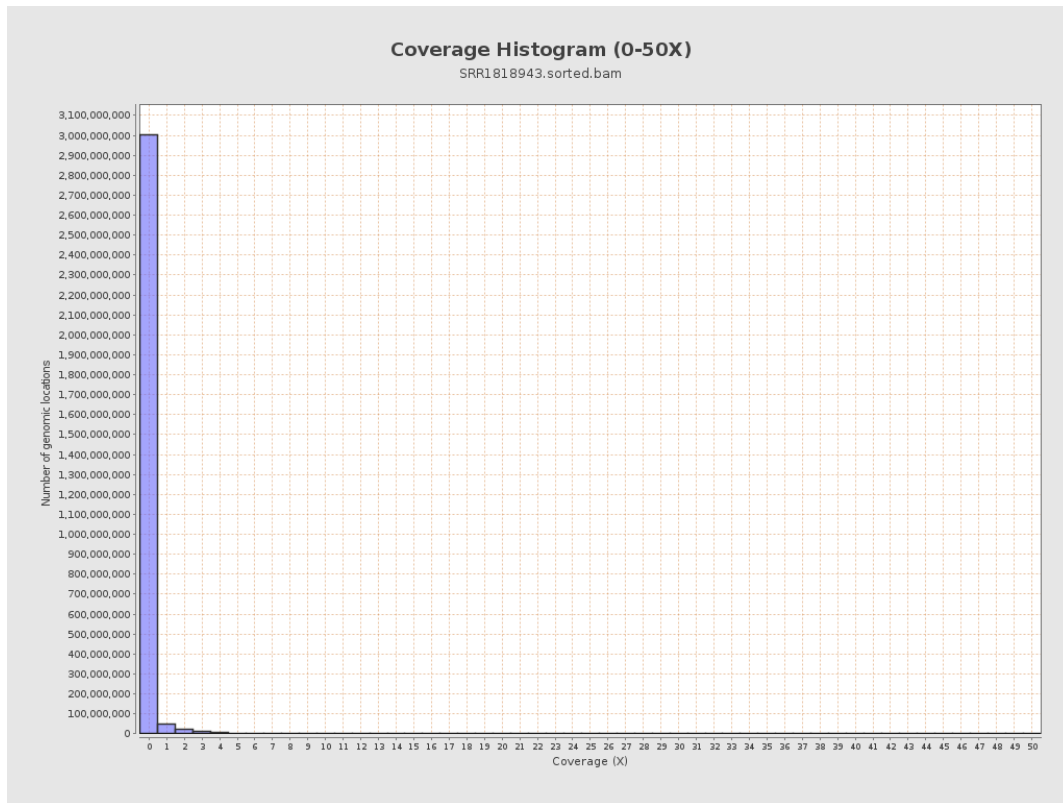
3. Results : Coverage across reference



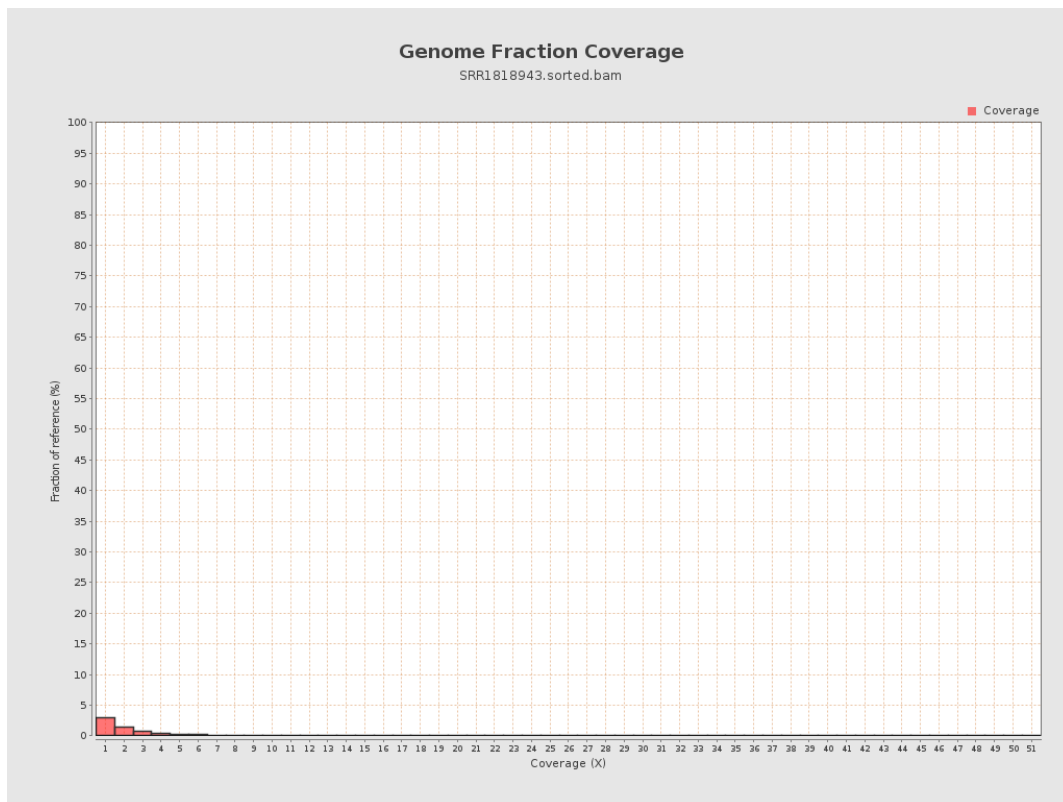
4. Results : Coverage Histogram



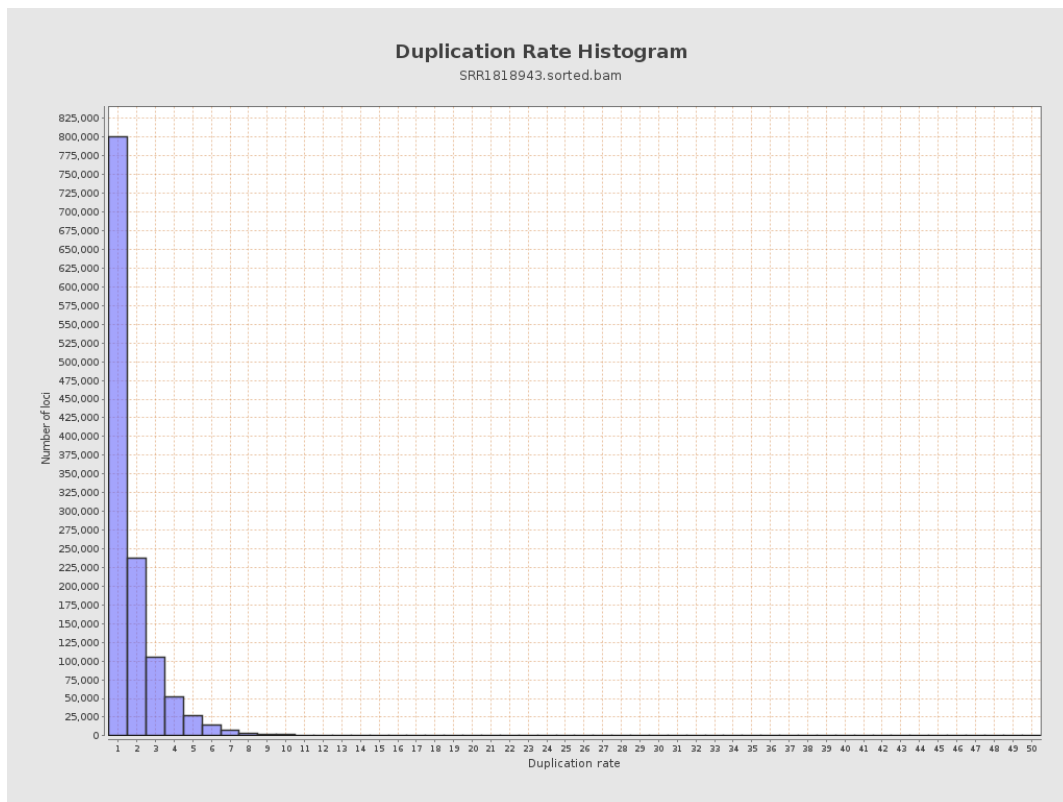
5. Results : Coverage Histogram (0-50X)



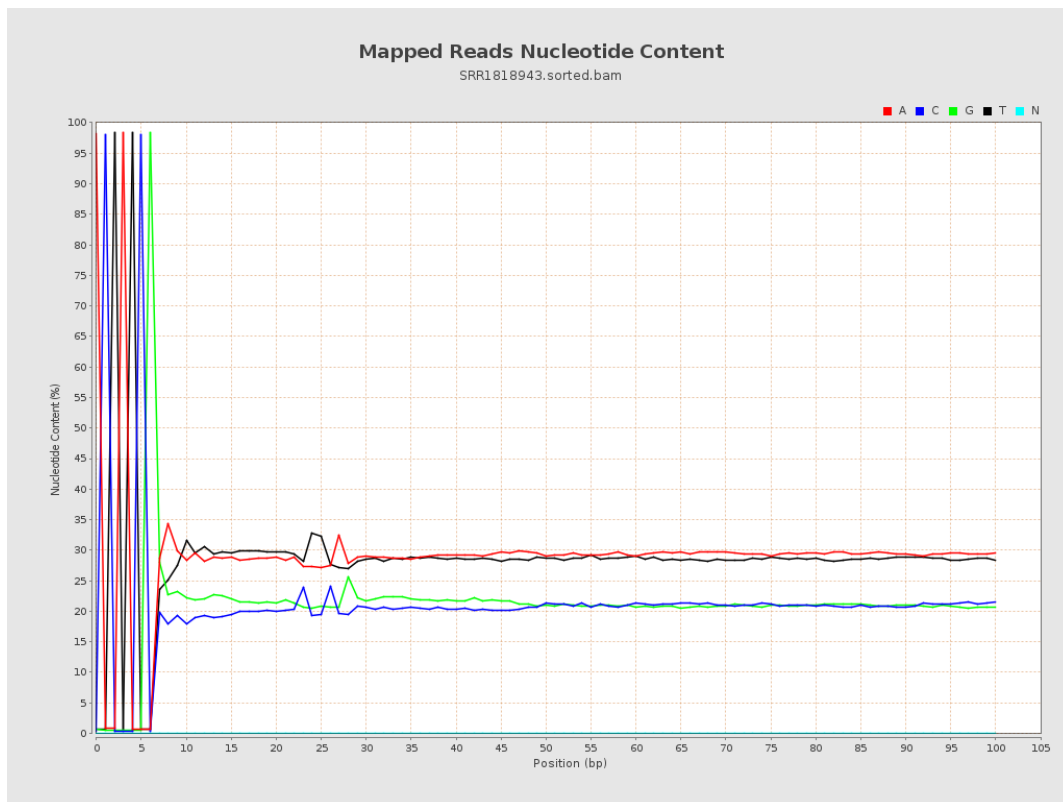
6. Results : Genome Fraction Coverage



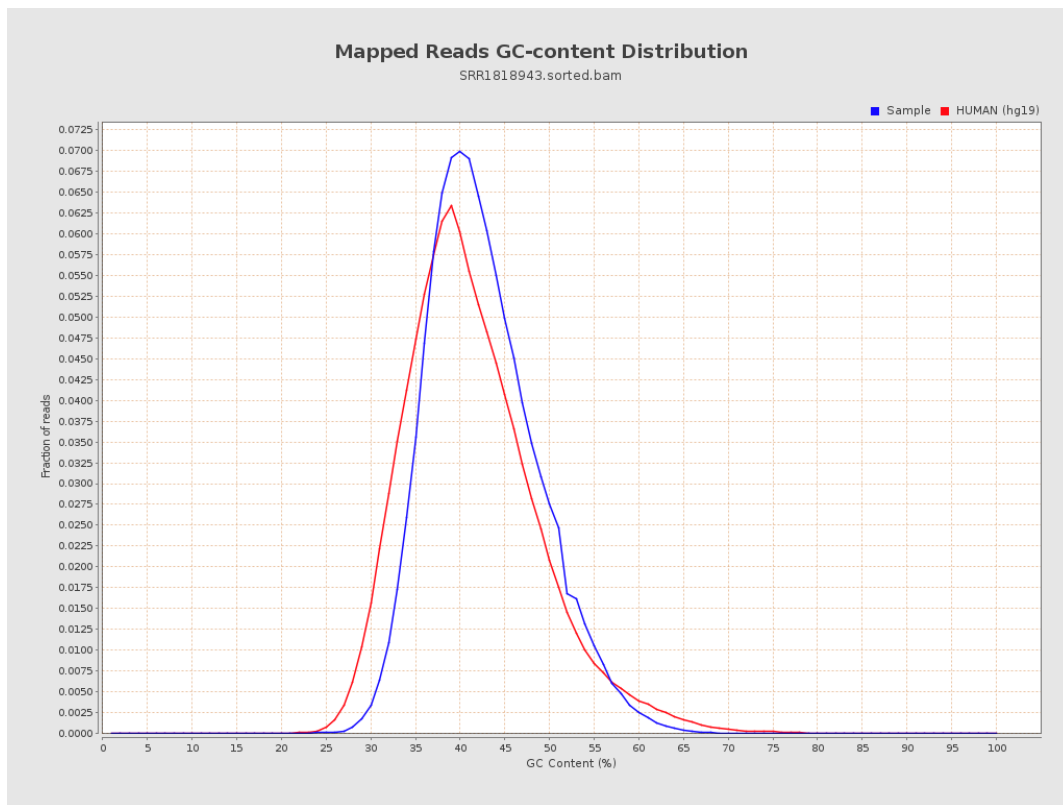
7. Results : Duplication Rate Histogram



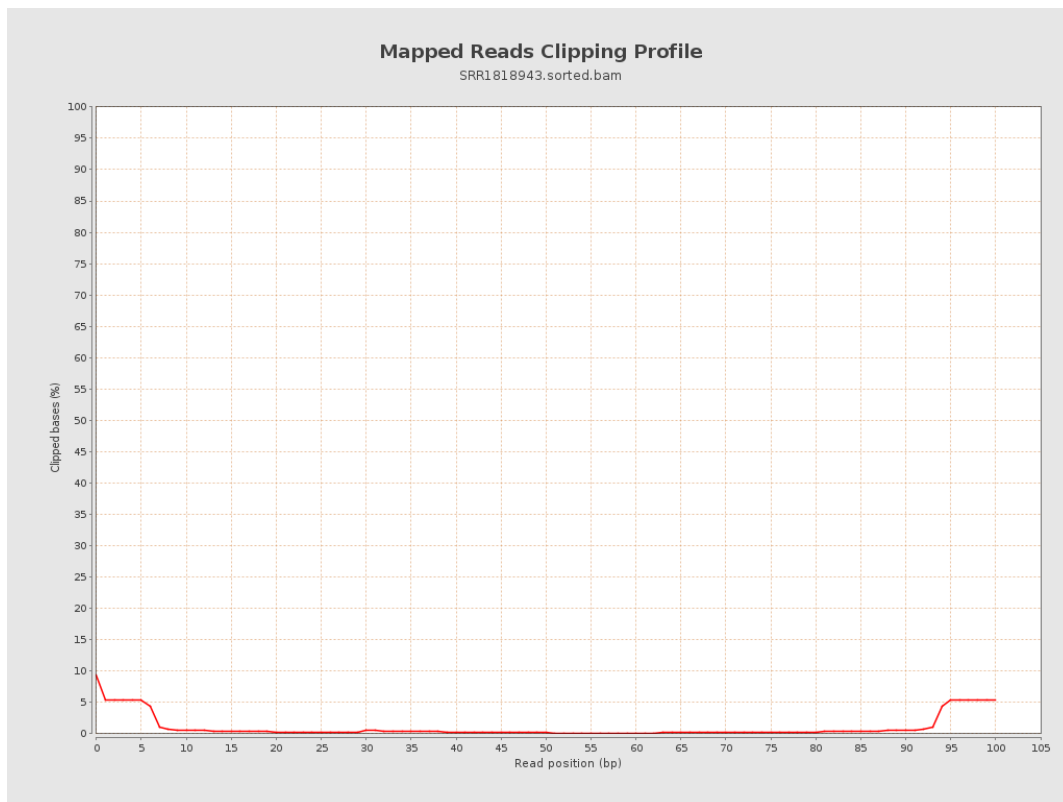
8. Results : Mapped Reads Nucleotide Content



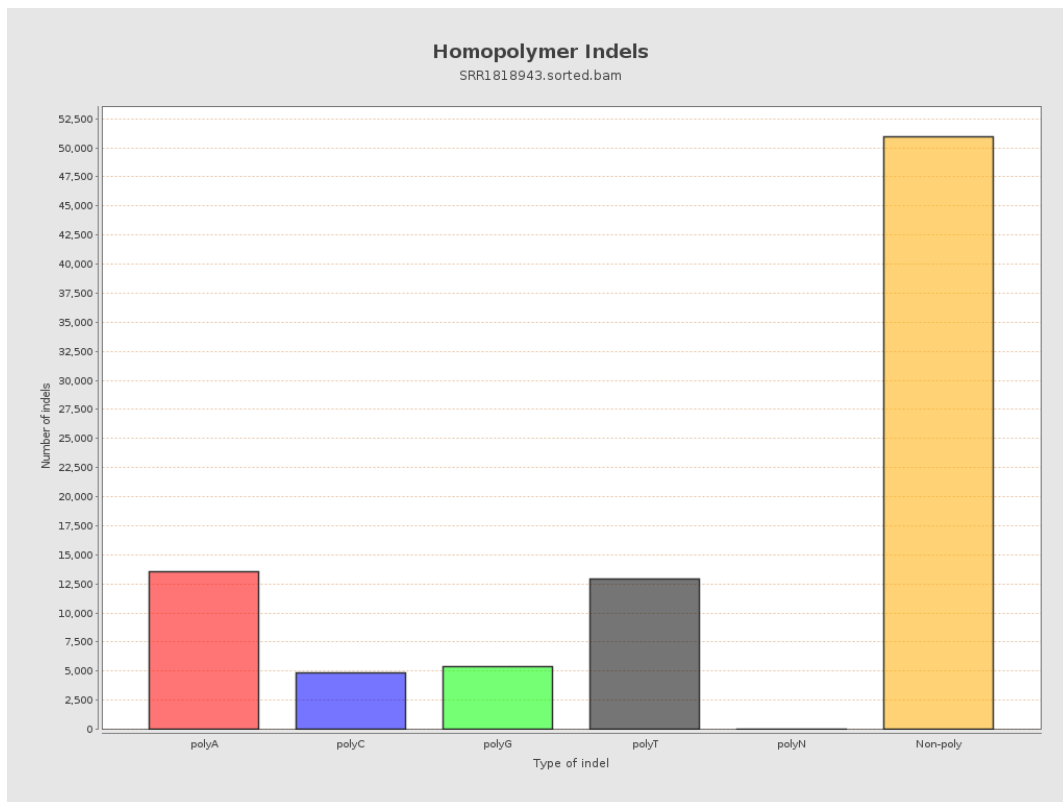
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

