

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 00:23:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818857.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_SRR1818857 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818857.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 00:23:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818857.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,421,835
Mapped reads	1,392,941 / 97.97%
Unmapped reads	28,894 / 2.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,206 / 1.56%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	293,514 / 20.64%
Duplication rate	17.92%
Clipped reads	1,412,867 / 99.37%

2.2. ACGT Content

Number/percentage of A's	36,623,631 / 28.45%
Number/percentage of C's	27,914,325 / 21.68%
Number/percentage of T's	36,323,861 / 28.22%
Number/percentage of G's	27,865,608 / 21.65%
Number/percentage of N's	1,776 / 0%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0416

Standard Deviation	0.5175
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2.4. Mapping Quality

Mean Mapping Quality	49.39
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2.5. Mismatches and indels

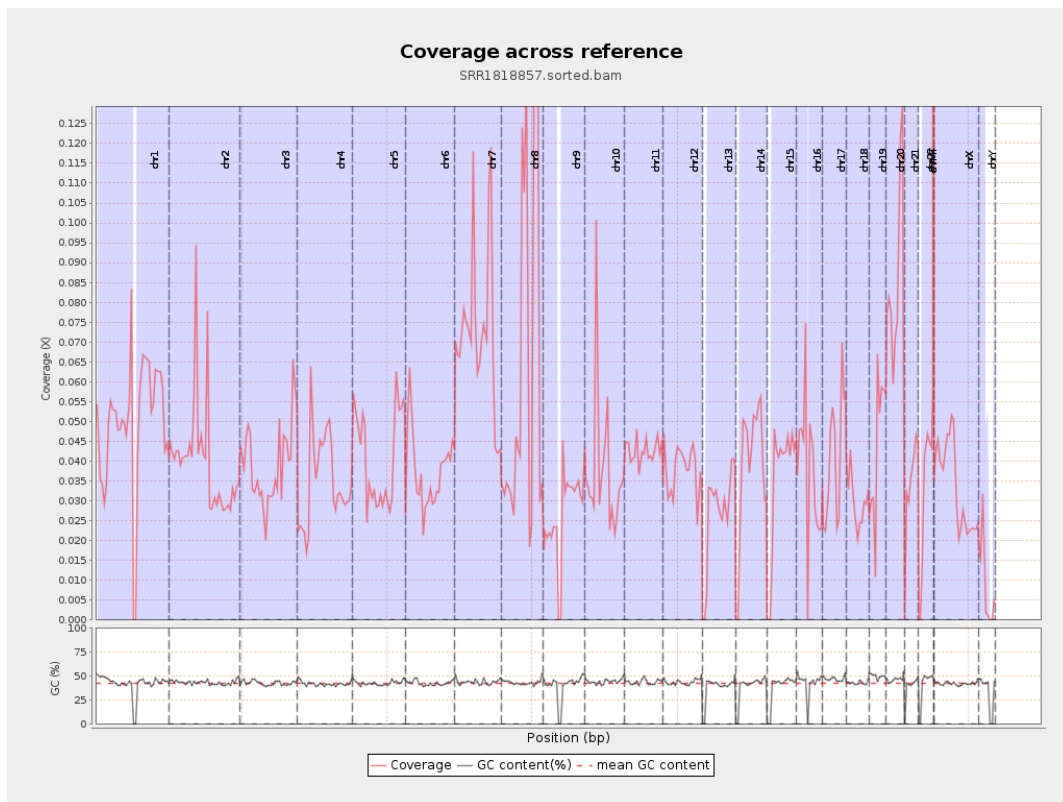
General error rate	0.64%
Mismatches	783,554
Insertions	16,209
Mapped reads with at least one insertion	1.12%
Deletions	41,610
Mapped reads with at least one deletion	2.91%
Homopolymer indels	40.5%

2.6. Chromosome stats

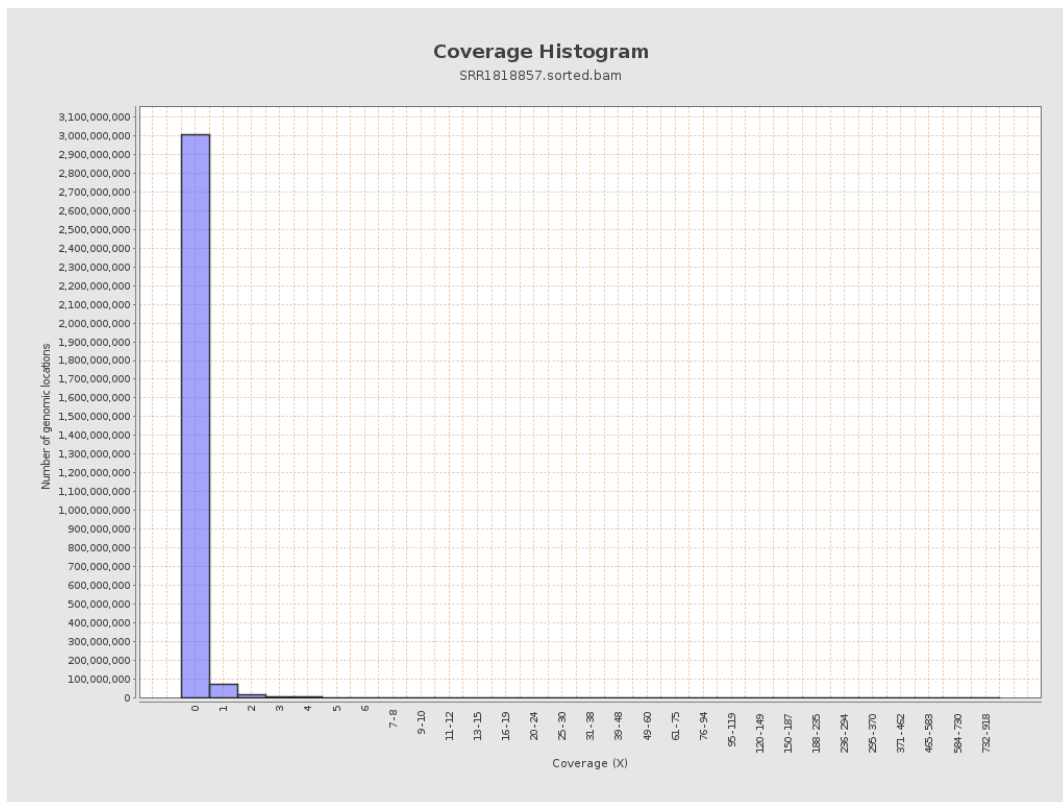
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12296842	0.0493	0.7881
chr2	243199373	9727107	0.04	0.7892
chr3	198022430	7730160	0.039	0.2581
chr4	191154276	6598682	0.0345	0.326
chr5	180915260	7350979	0.0406	0.2776
chr6	171115067	6377036	0.0373	0.2736
chr7	159138663	11612671	0.073	1.0249

chr8	146364022	10605518	0.0725	0.4407
chr9	141213431	3710625	0.0263	0.3926
chr10	135534747	5029539	0.0371	0.6758
chr11	135006516	5721674	0.0424	0.3232
chr12	133851895	5099945	0.0381	0.26
chr13	115169878	3055263	0.0265	0.2092
chr14	107349540	4143362	0.0386	0.2763
chr15	102531392	3633397	0.0354	0.2481
chr16	90354753	3325490	0.0368	0.5536
chr17	81195210	3336836	0.0411	0.3382
chr18	78077248	2345829	0.03	0.4682
chr19	59128983	2565556	0.0434	0.7151
chr20	63025520	5406930	0.0858	0.412
chr21	48129895	1650222	0.0343	0.2914
chr22	51304566	1593336	0.0311	0.2555
chrMT	16571	175877	10.6135	7.0633
chrX	155270560	5210561	0.0336	0.2897
chrY	59373566	508489	0.0086	0.6038

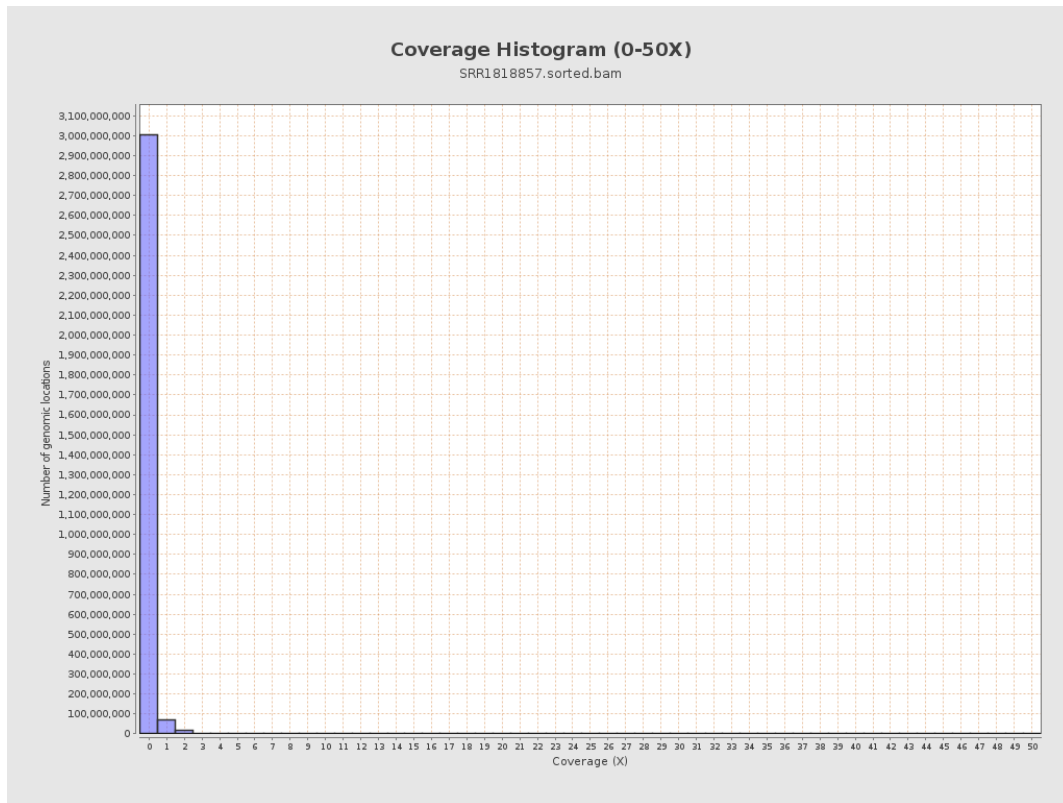
3. Results : Coverage across reference



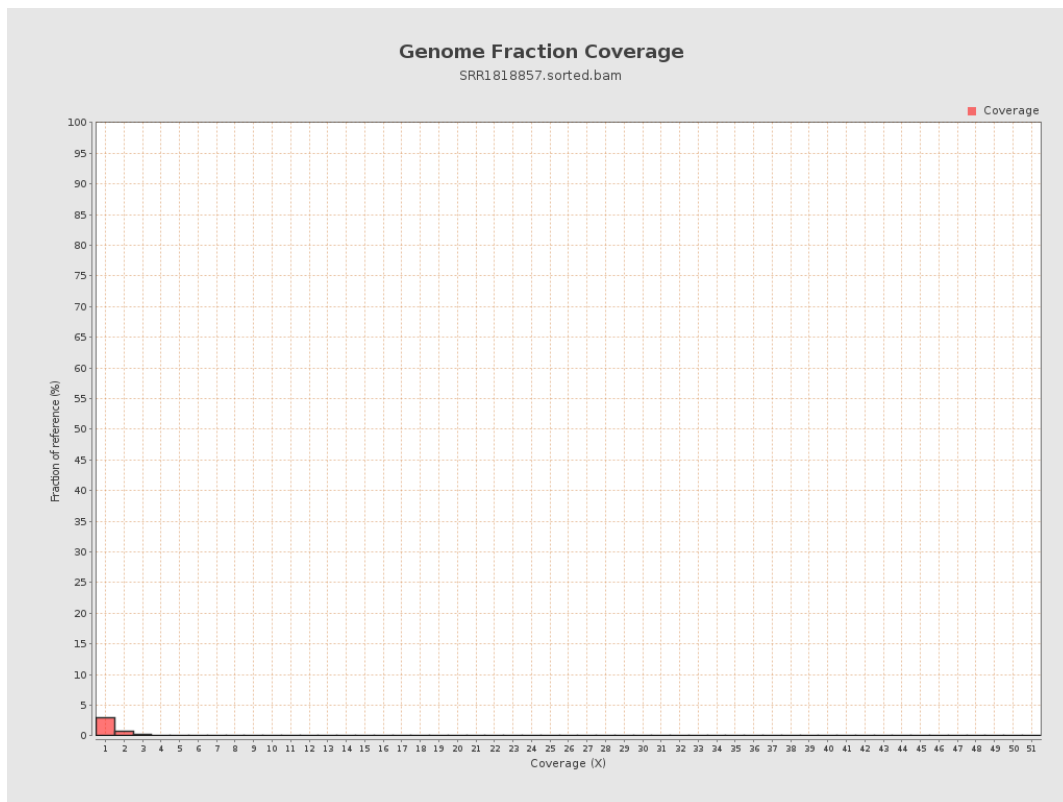
4. Results : Coverage Histogram



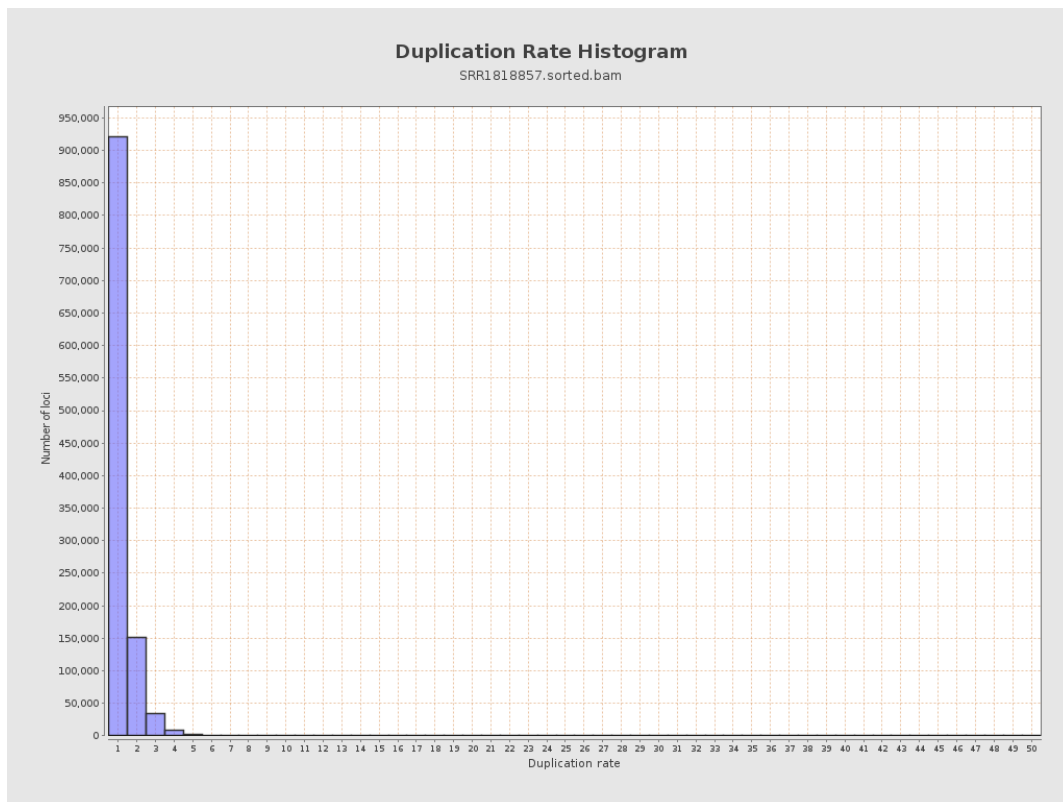
5. Results : Coverage Histogram (0-50X)



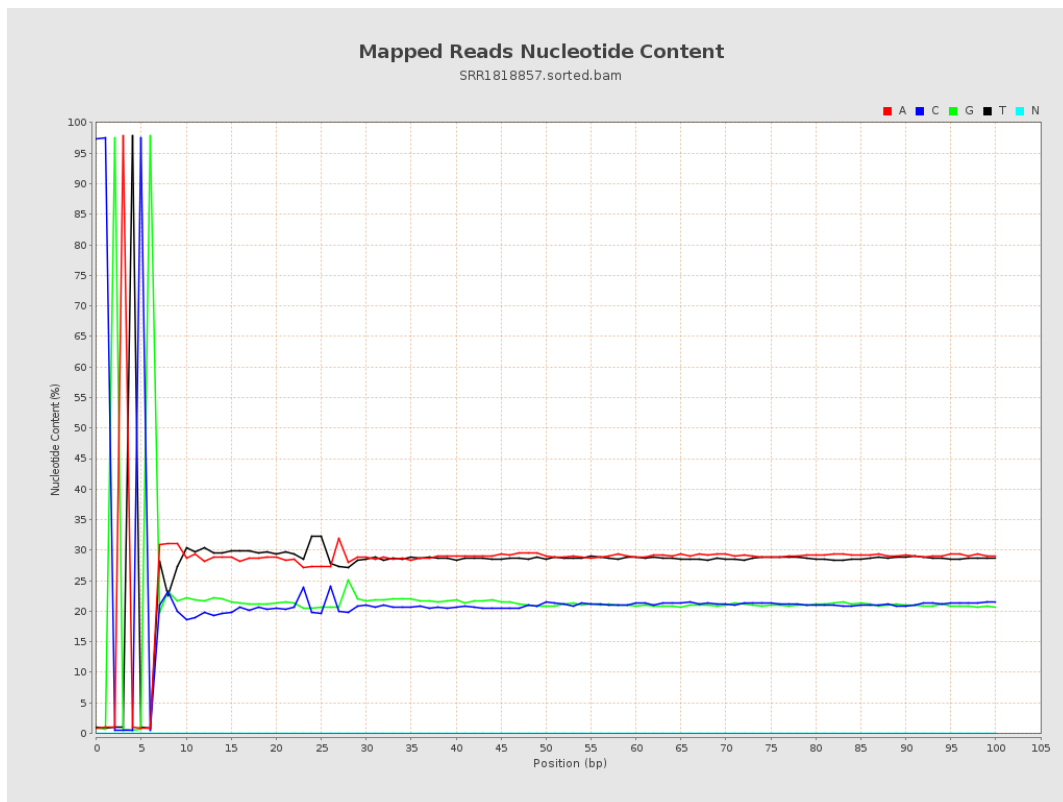
6. Results : Genome Fraction Coverage



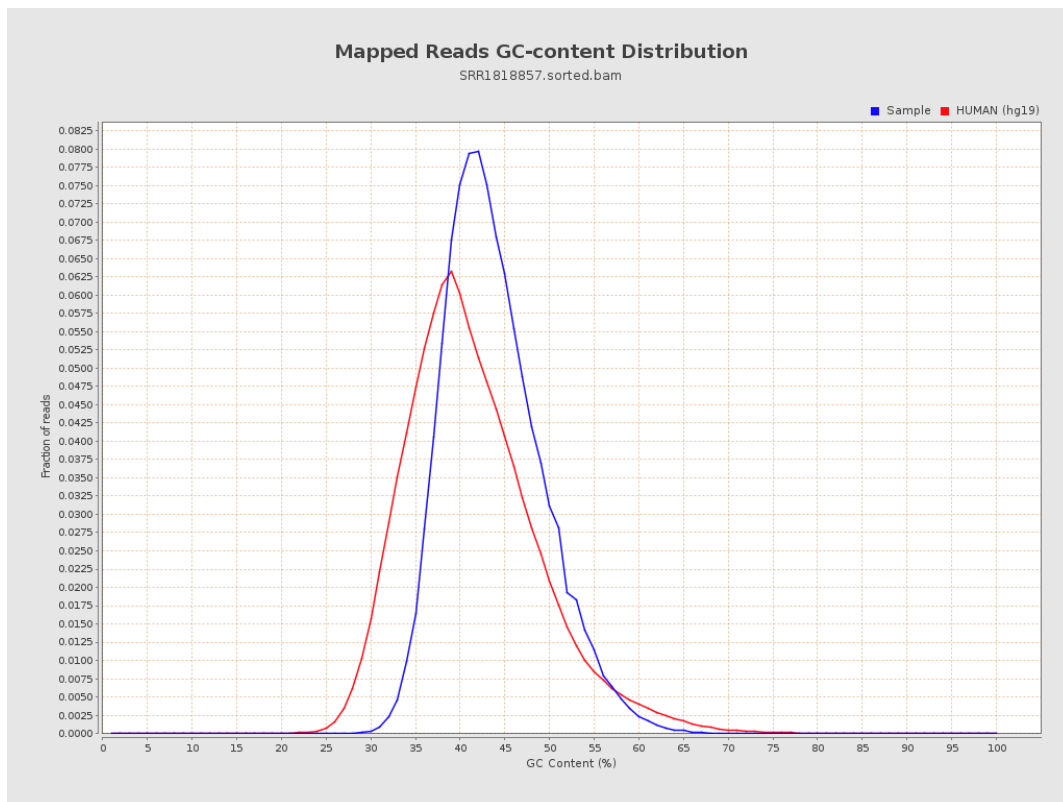
7. Results : Duplication Rate Histogram



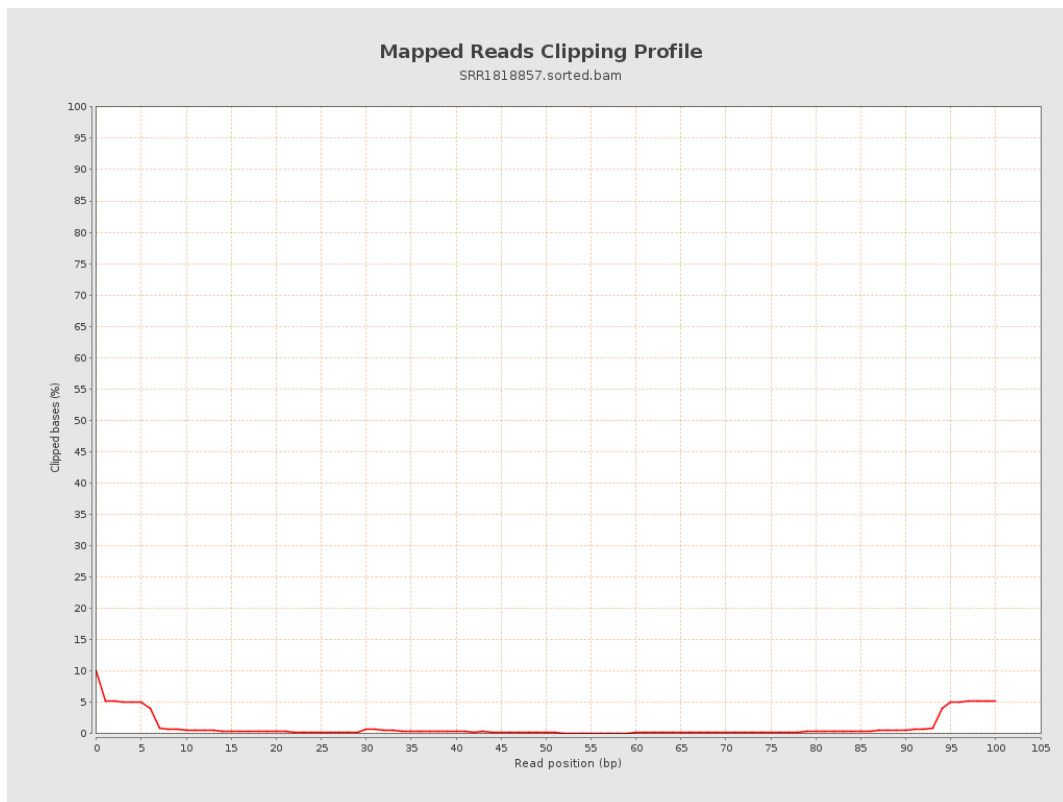
8. Results : Mapped Reads Nucleotide Content



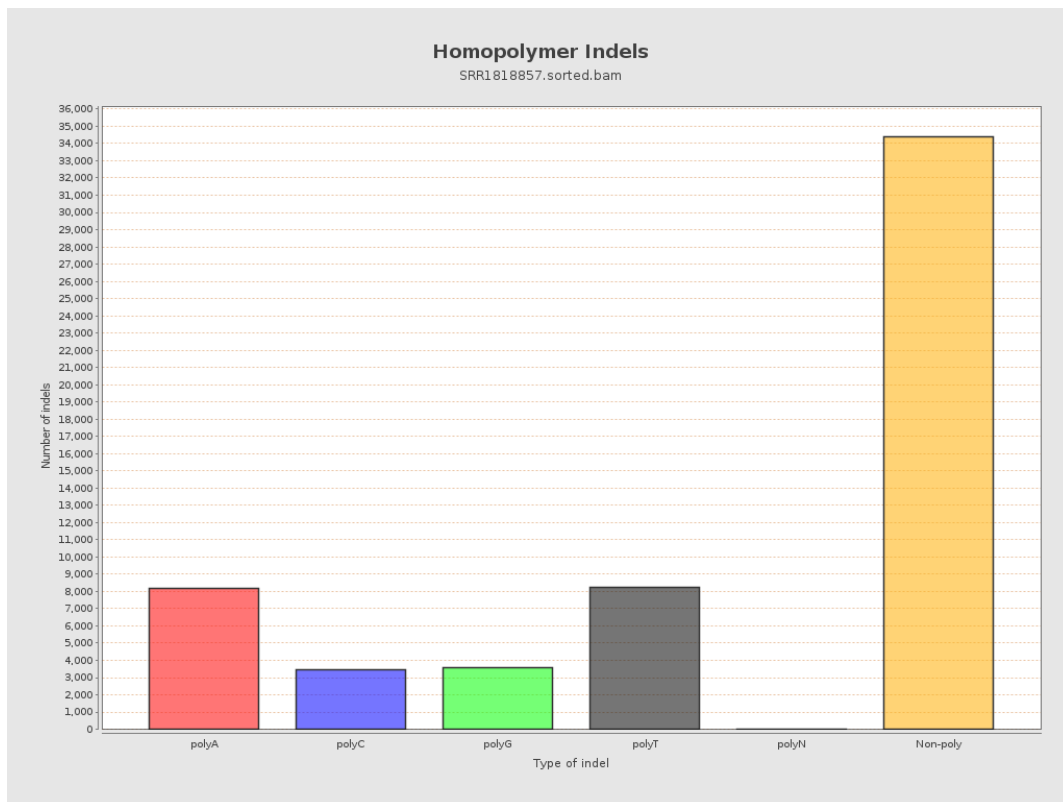
9. Results : Mapped Reads GC-content Distribution



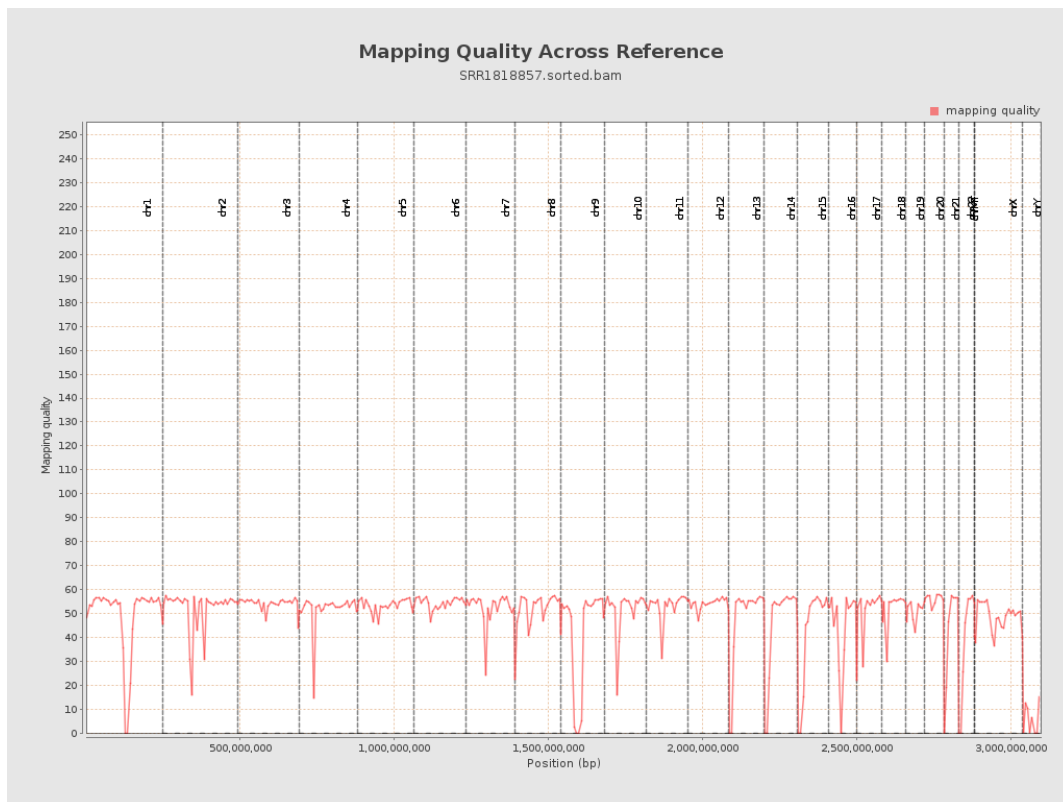
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

