

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:20:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818909.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_SRR1818909 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818909.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:19:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818909.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,238,202
Mapped reads	2,209,189 / 98.7%
Unmapped reads	29,013 / 1.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,441 / 1.58%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	579,325 / 25.88%
Duplication rate	22.08%
Clipped reads	2,217,752 / 99.09%

2.2. ACGT Content

Number/percentage of A's	58,429,891 / 28.6%
Number/percentage of C's	44,286,855 / 21.68%
Number/percentage of T's	57,608,120 / 28.2%
Number/percentage of G's	43,945,206 / 21.51%
Number/percentage of N's	3,006 / 0%
GC Percentage	43.19%

2.3. Coverage

Mean	0.066

Standard Deviation	0.8175
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2.4. Mapping Quality

Mean Mapping Quality	49.1
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2.5. Mismatches and indels

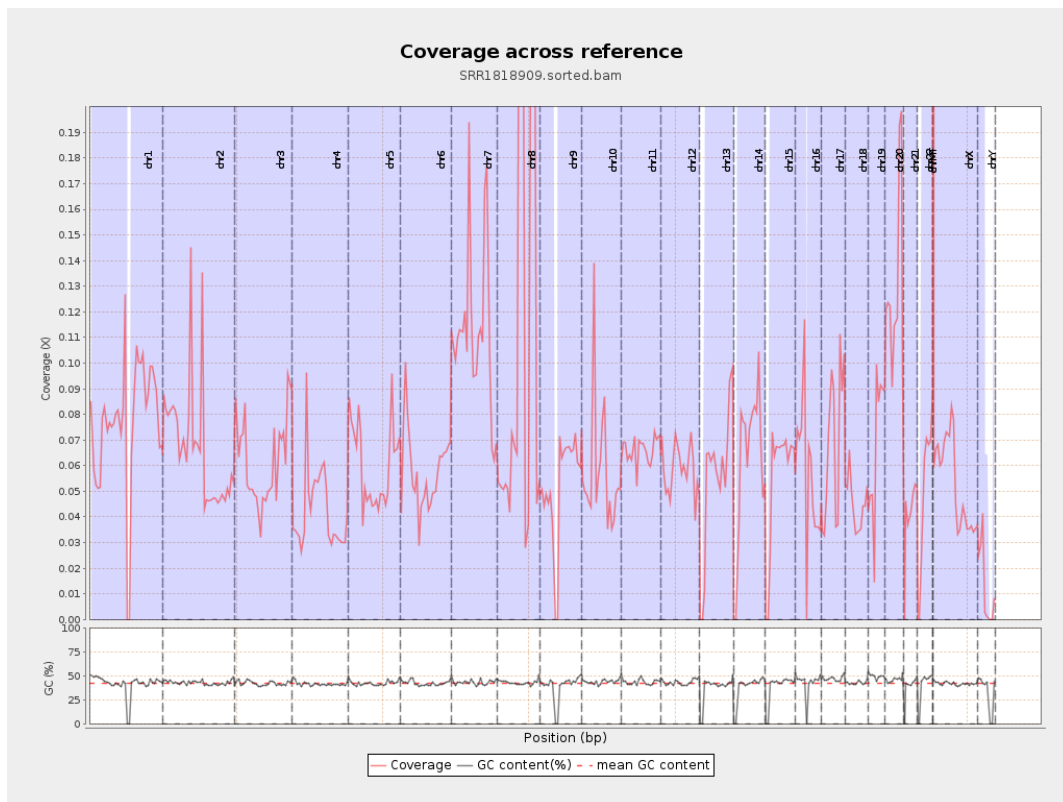
General error rate	0.66%
Mismatches	1,276,336
Insertions	31,517
Mapped reads with at least one insertion	1.38%
Deletions	70,104
Mapped reads with at least one deletion	3.1%
Homopolymer indels	40.62%

2.6. Chromosome stats

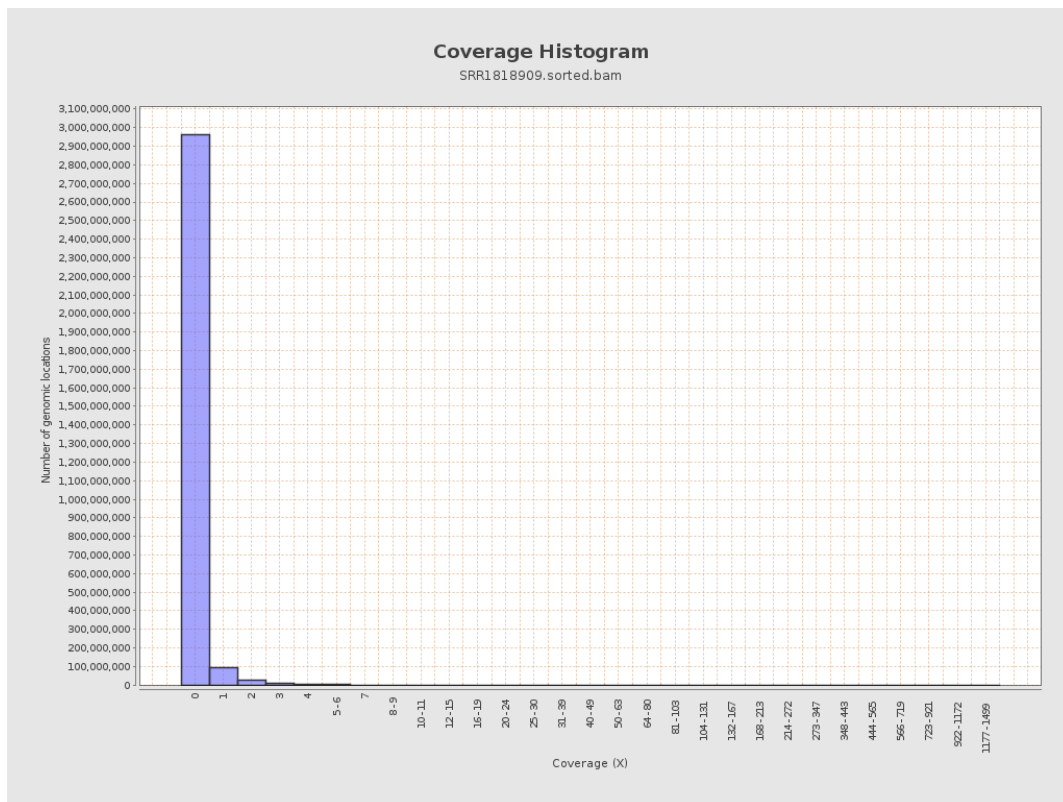
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19129627	0.0767	1.2196
chr2	243199373	16226796	0.0667	1.3078
chr3	198022430	12231203	0.0618	0.3528
chr4	191154276	8152776	0.0427	0.4416
chr5	180915260	10918704	0.0604	0.3851
chr6	171115067	9911293	0.0579	0.3874
chr7	159138663	17901225	0.1125	1.7549

chr8	146364022	18943192	0.1294	0.6555
chr9	141213431	7353010	0.0521	0.6
chr10	135534747	7660345	0.0565	1.0046
chr11	135006516	8907254	0.066	0.4594
chr12	133851895	7888028	0.0589	0.3449
chr13	115169878	6425857	0.0558	0.3307
chr14	107349540	6785289	0.0632	0.4009
chr15	102531392	5606493	0.0547	0.3295
chr16	90354753	5079875	0.0562	0.97
chr17	81195210	5450452	0.0671	0.4695
chr18	78077248	3539978	0.0453	0.7274
chr19	59128983	4001783	0.0677	0.9801
chr20	63025520	8433943	0.1338	0.573
chr21	48129895	2008742	0.0417	0.3552
chr22	51304566	2464399	0.048	0.35
chrMT	16571	402182	24.2702	14.1164
chrX	155270560	8221090	0.0529	0.423
chrY	59373566	766663	0.0129	1.0477

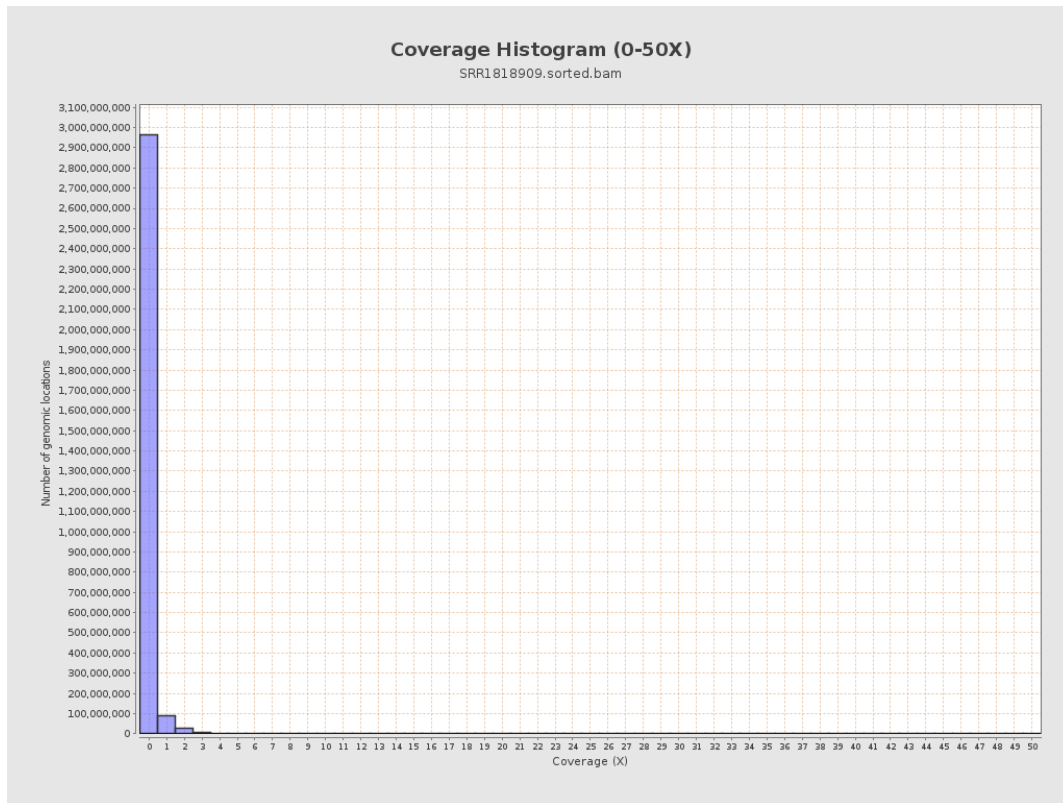
3. Results : Coverage across reference



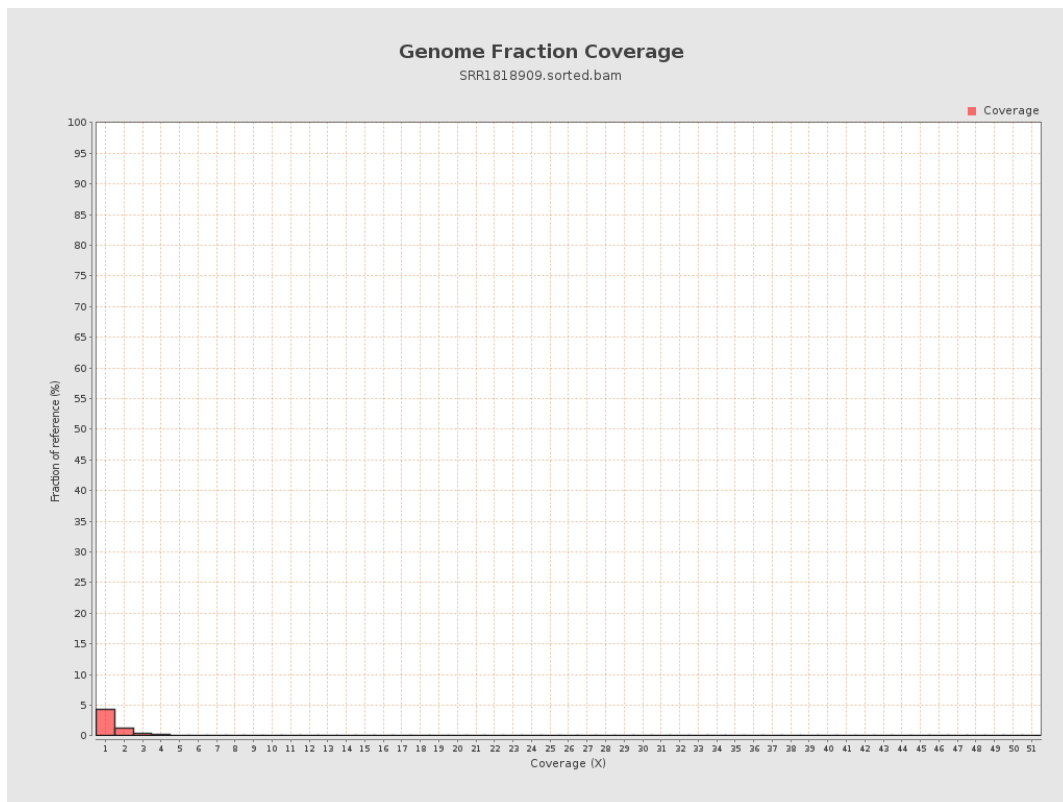
4. Results : Coverage Histogram



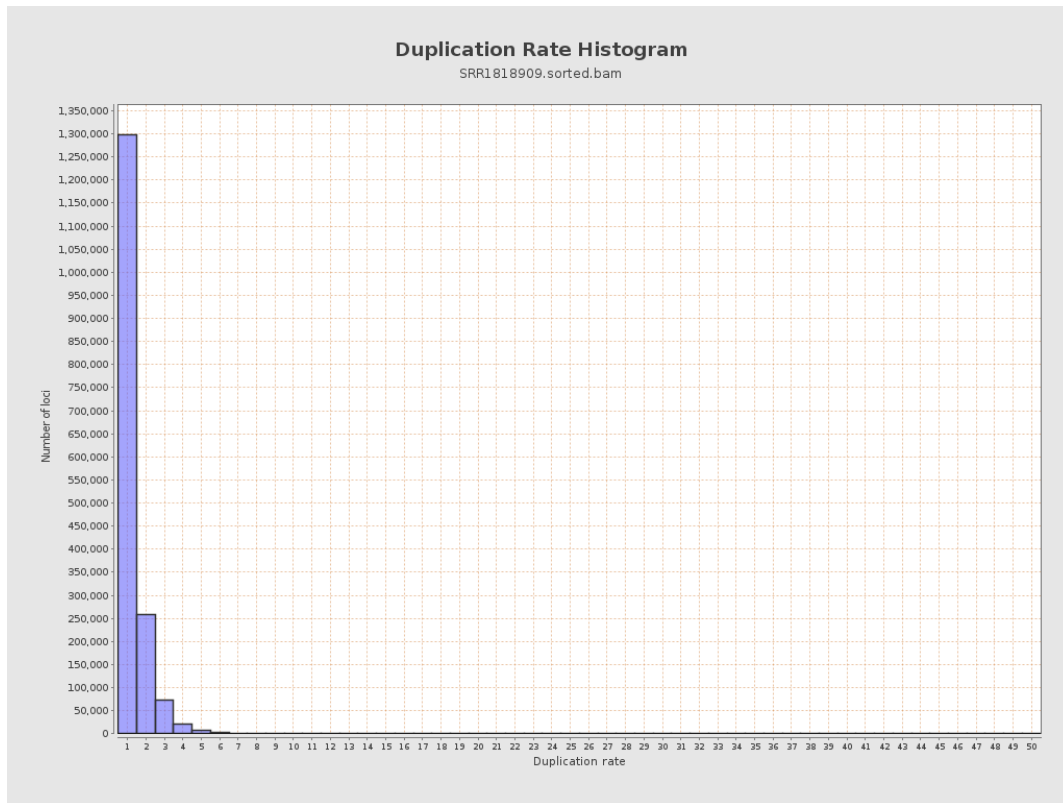
5. Results : Coverage Histogram (0-50X)



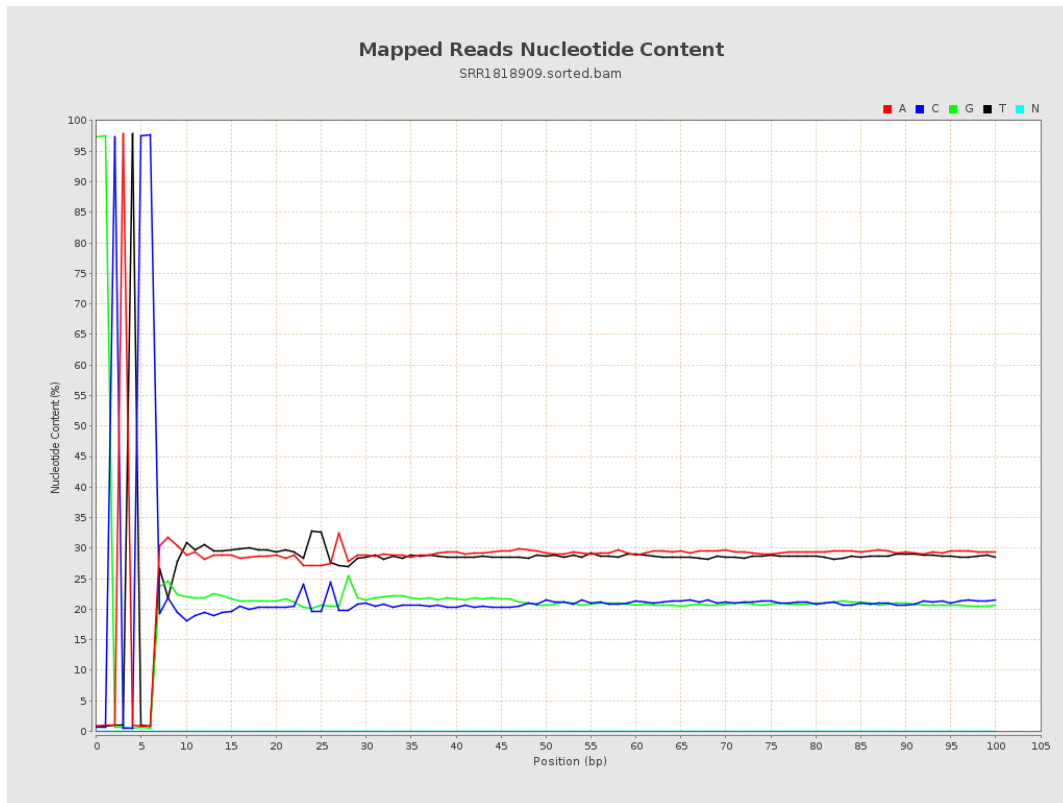
6. Results : Genome Fraction Coverage



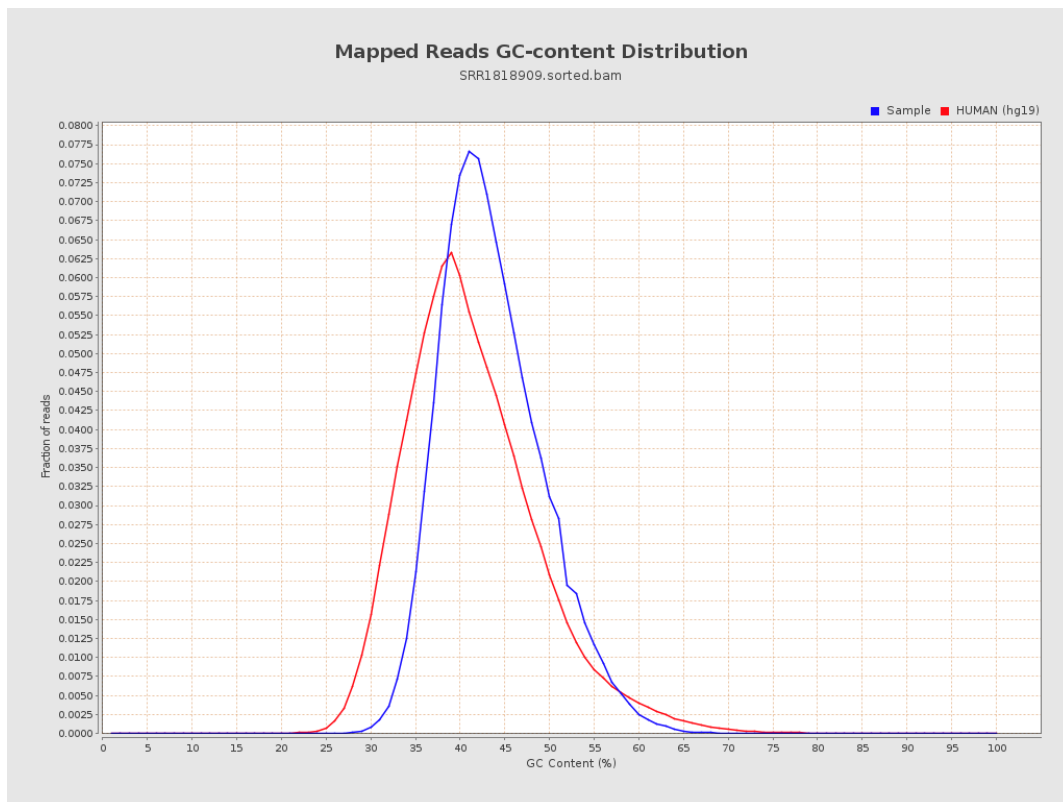
7. Results : Duplication Rate Histogram



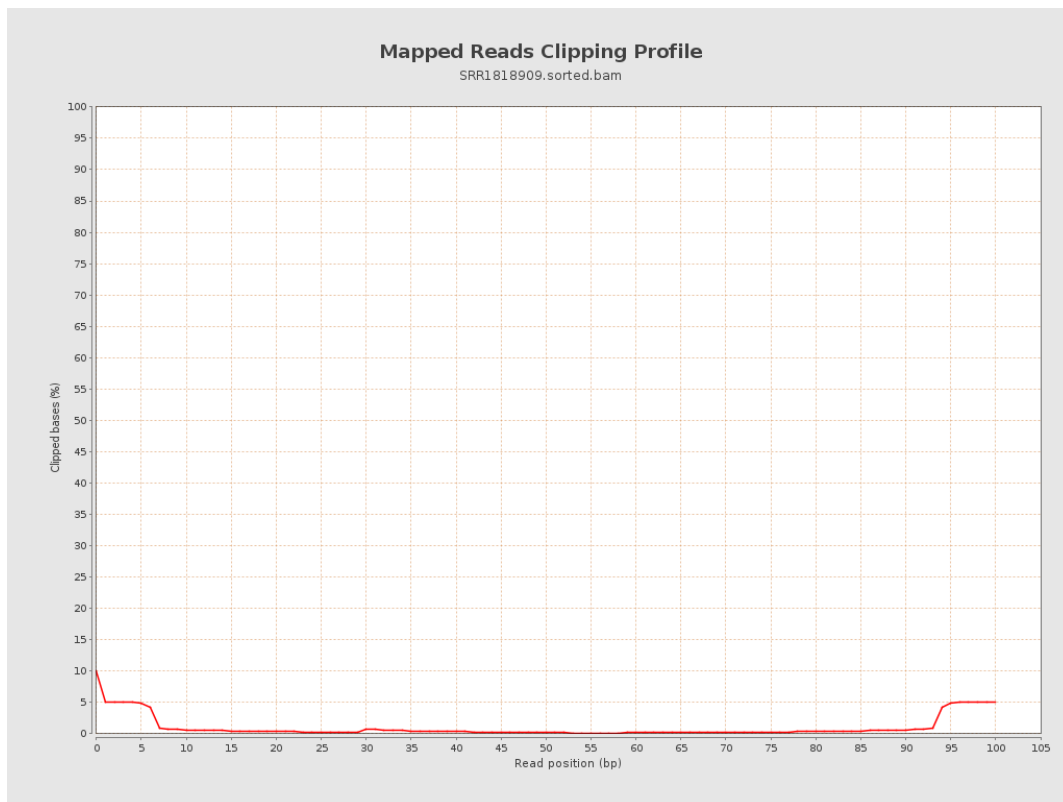
8. Results : Mapped Reads Nucleotide Content



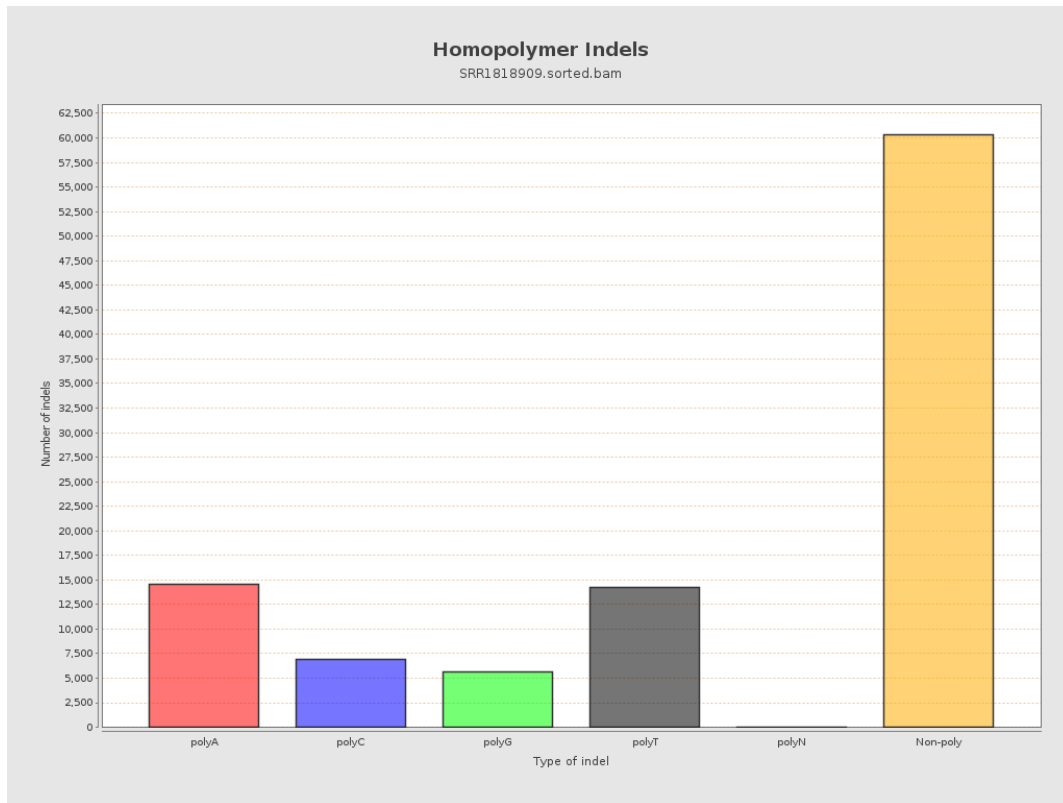
9. Results : Mapped Reads GC-content Distribution



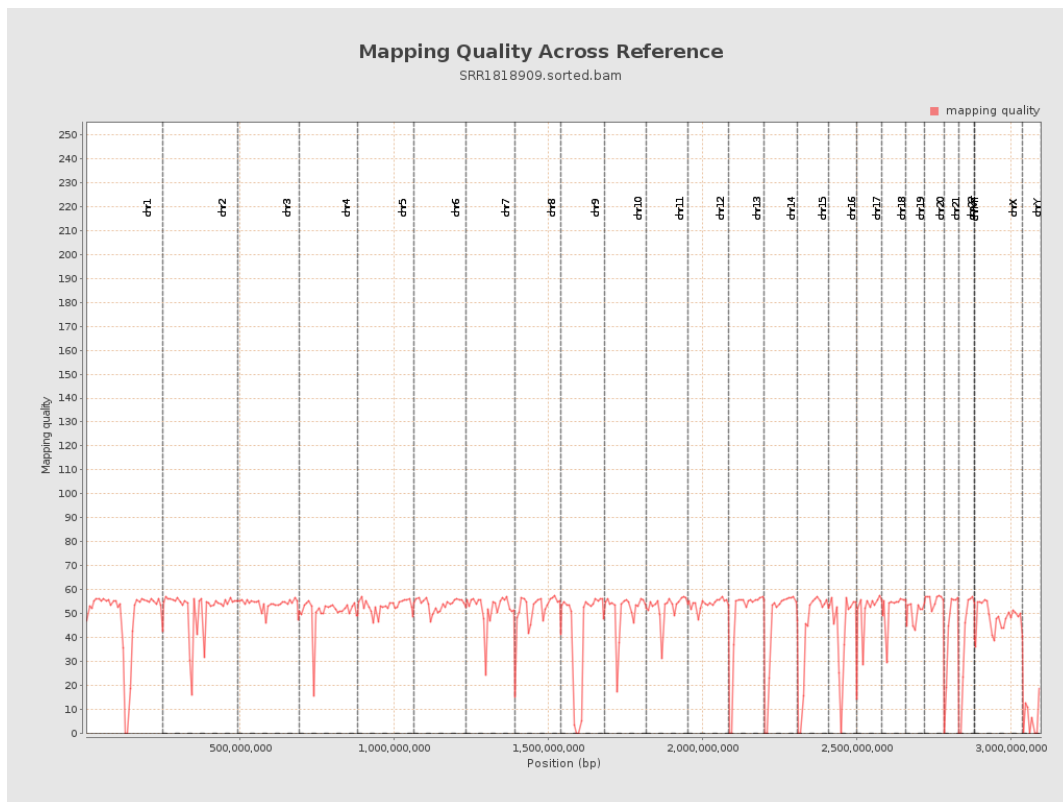
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

