

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:53:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080909.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_SRR3080909 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080909.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:53:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080909.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,339,628
Mapped reads	2,994,355 / 89.66%
Unmapped reads	345,273 / 10.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,251 / 1.15%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	140,213 / 4.2%
Duplication rate	3.88%
Clipped reads	1,017,918 / 30.48%

2.2. ACGT Content

Number/percentage of A's	60,666,963 / 29.26%
Number/percentage of C's	36,655,286 / 17.68%
Number/percentage of T's	66,598,976 / 32.12%
Number/percentage of G's	42,430,999 / 20.46%
Number/percentage of N's	985,615 / 0.48%
GC Percentage	38.14%

2.3. Coverage

Mean	0.067

Standard Deviation	0.4407
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2.4. Mapping Quality

Mean Mapping Quality	48.09
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2.5. Mismatches and indels

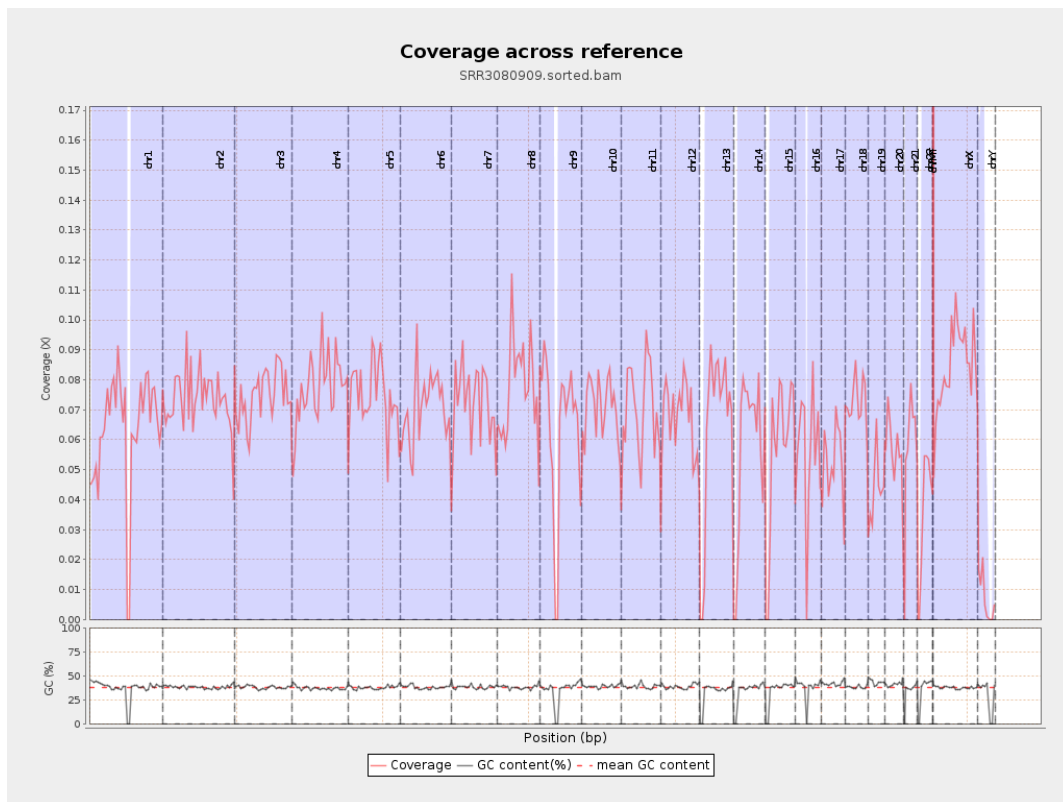
General error rate	1.15%
Mismatches	2,364,466
Insertions	15,882
Mapped reads with at least one insertion	0.53%
Deletions	45,722
Mapped reads with at least one deletion	1.51%
Homopolymer indels	50.07%

2.6. Chromosome stats

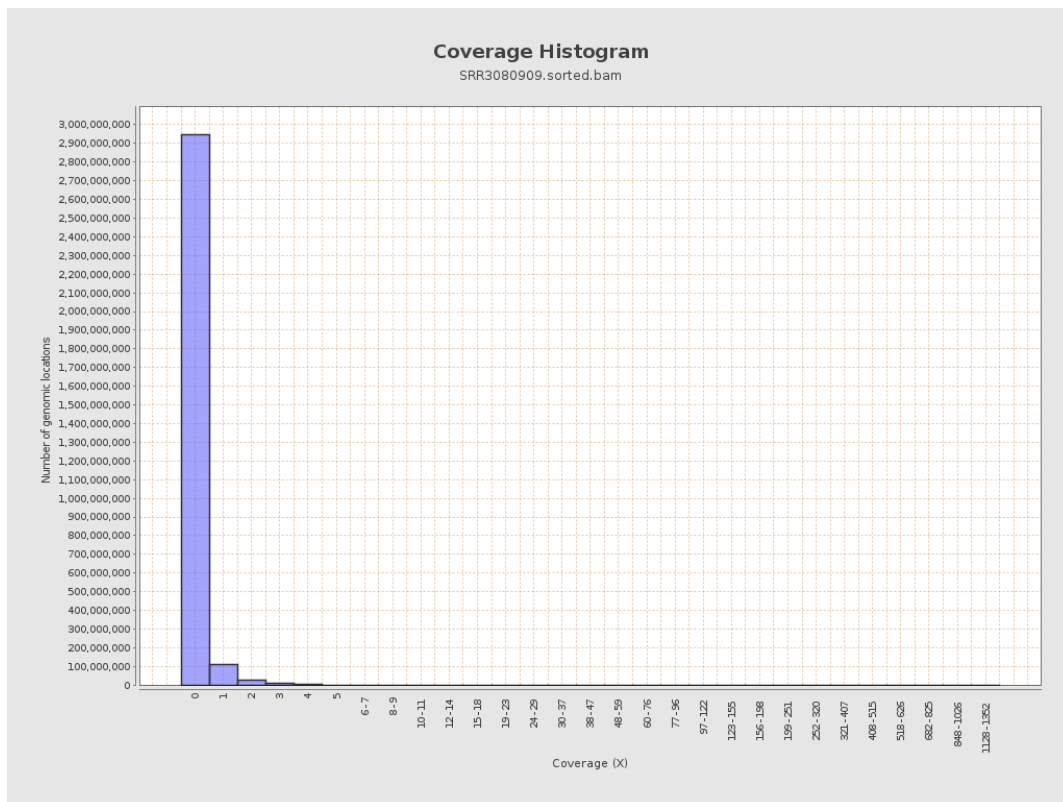
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15818041	0.0635	0.5691
chr2	243199373	17845951	0.0734	0.4394
chr3	198022430	14827928	0.0749	0.3616
chr4	191154276	14886877	0.0779	0.3781
chr5	180915260	13435776	0.0743	0.3604
chr6	171115067	12104563	0.0707	0.4056
chr7	159138663	11411561	0.0717	0.4746

chr8	146364022	11307316	0.0773	0.899
chr9	141213431	9016923	0.0639	0.3921
chr10	135534747	9605239	0.0709	0.4122
chr11	135006516	9486018	0.0703	0.3975
chr12	133851895	9038287	0.0675	0.3447
chr13	115169878	7356847	0.0639	0.3351
chr14	107349540	6163892	0.0574	0.3243
chr15	102531392	5714438	0.0557	0.31
chr16	90354753	4976700	0.0551	0.3172
chr17	81195210	4293362	0.0529	0.3146
chr18	78077248	5702008	0.073	0.6133
chr19	59128983	2628926	0.0445	0.4201
chr20	63025520	3622287	0.0575	0.3231
chr21	48129895	2761938	0.0574	0.3278
chr22	51304566	1845169	0.036	0.2456
chrMT	16571	42525	2.5662	2.3961
chrX	155270560	13101704	0.0844	0.4021
chrY	59373566	418568	0.007	0.134

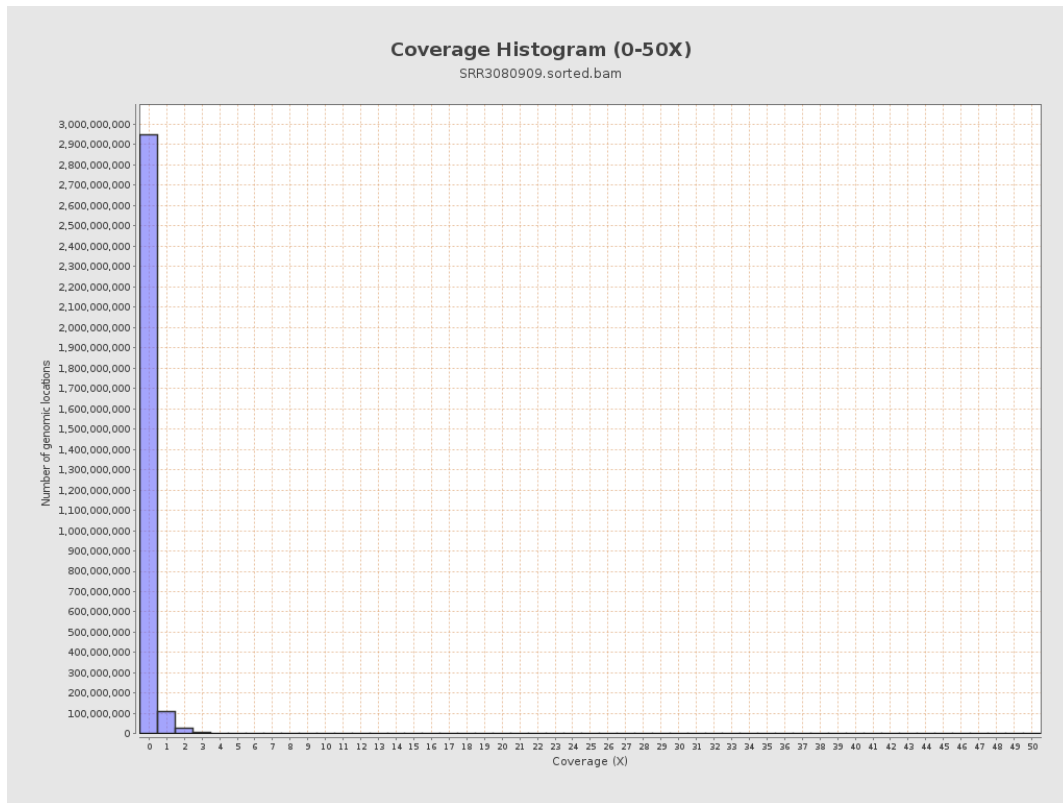
3. Results : Coverage across reference



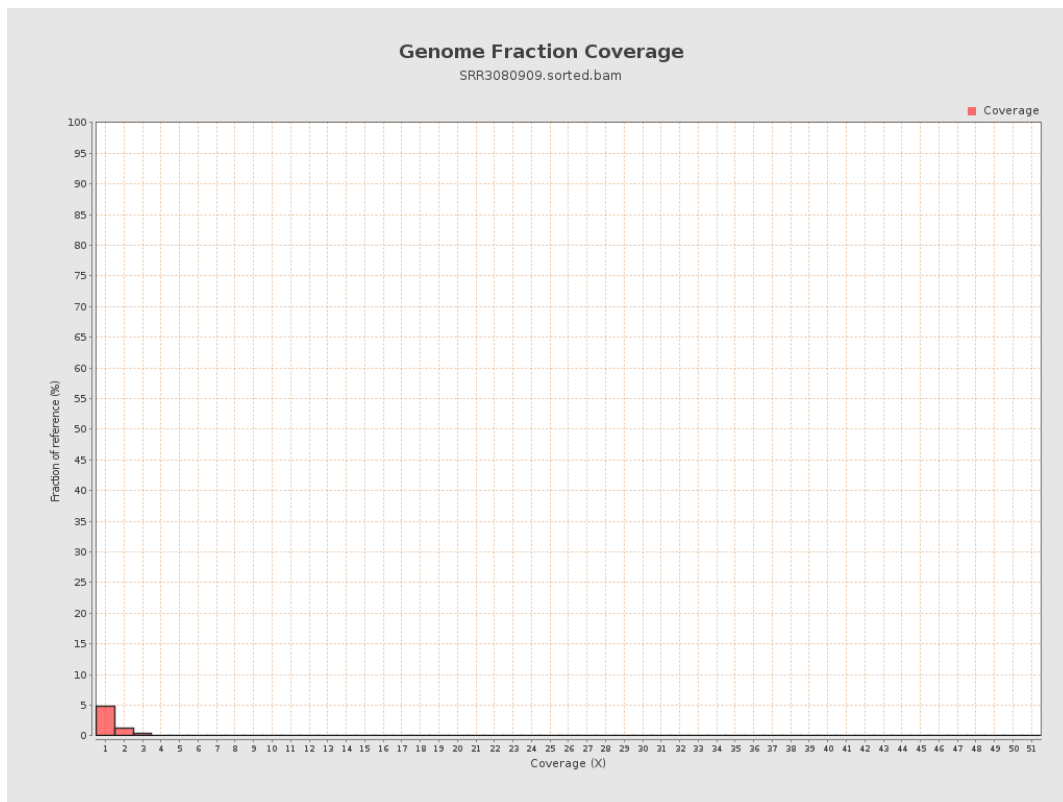
4. Results : Coverage Histogram



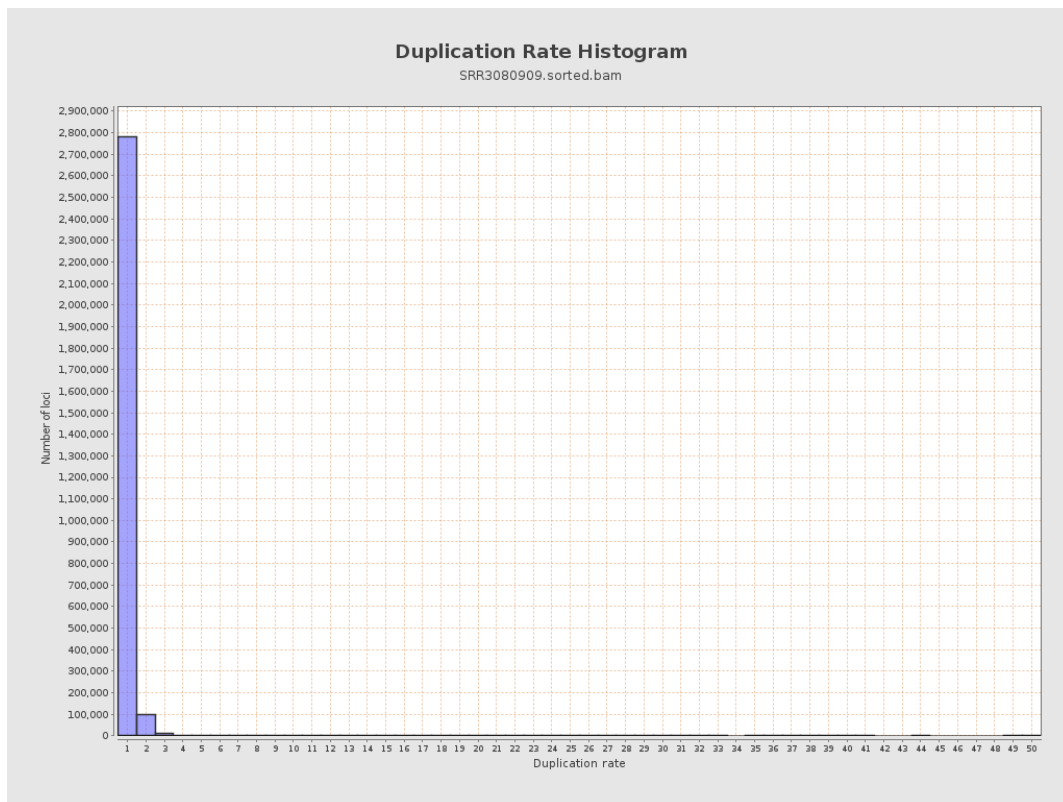
5. Results : Coverage Histogram (0-50X)



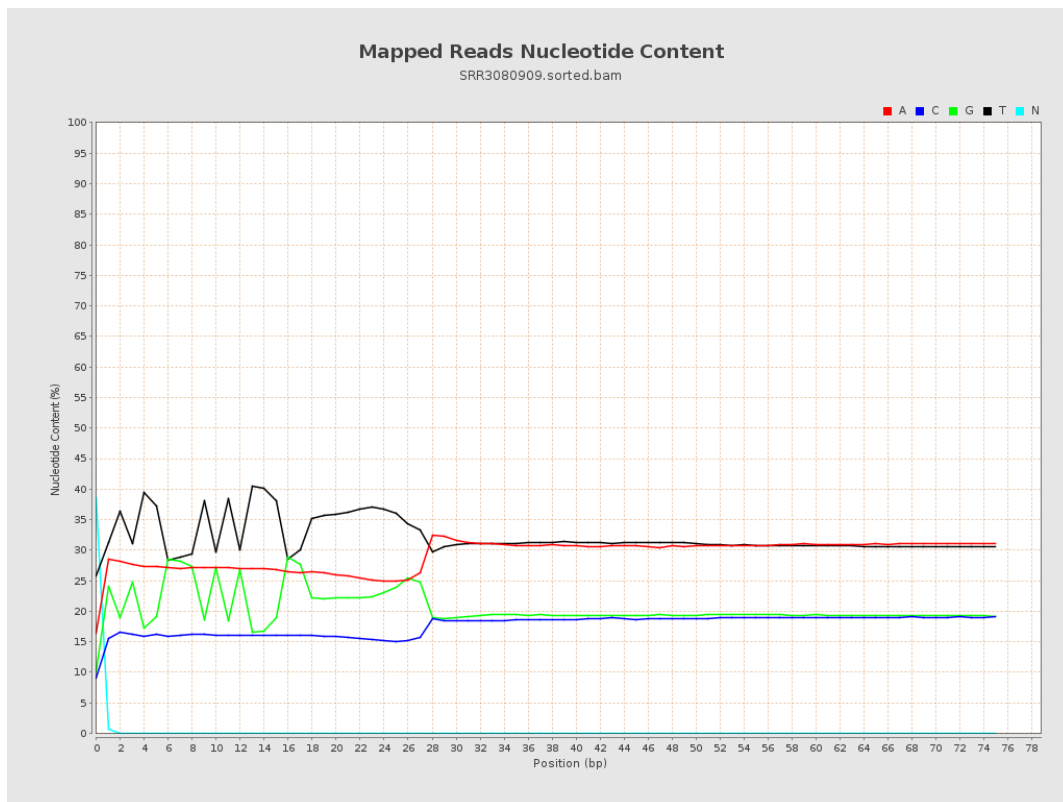
6. Results : Genome Fraction Coverage



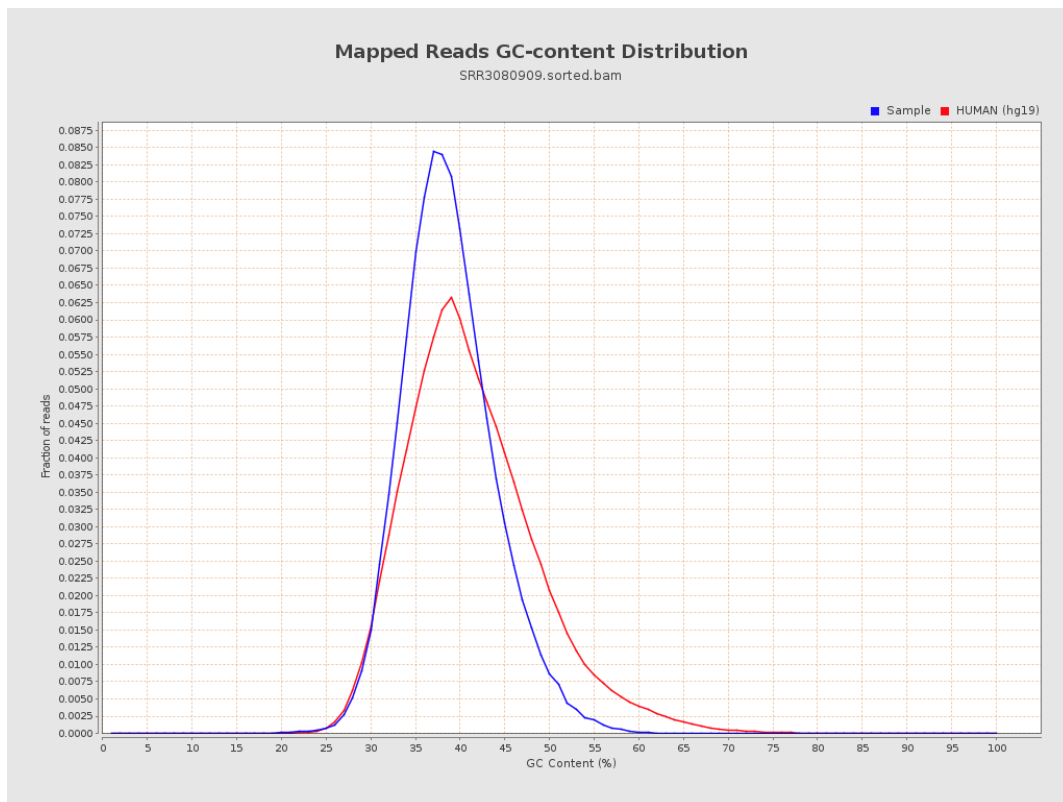
7. Results : Duplication Rate Histogram



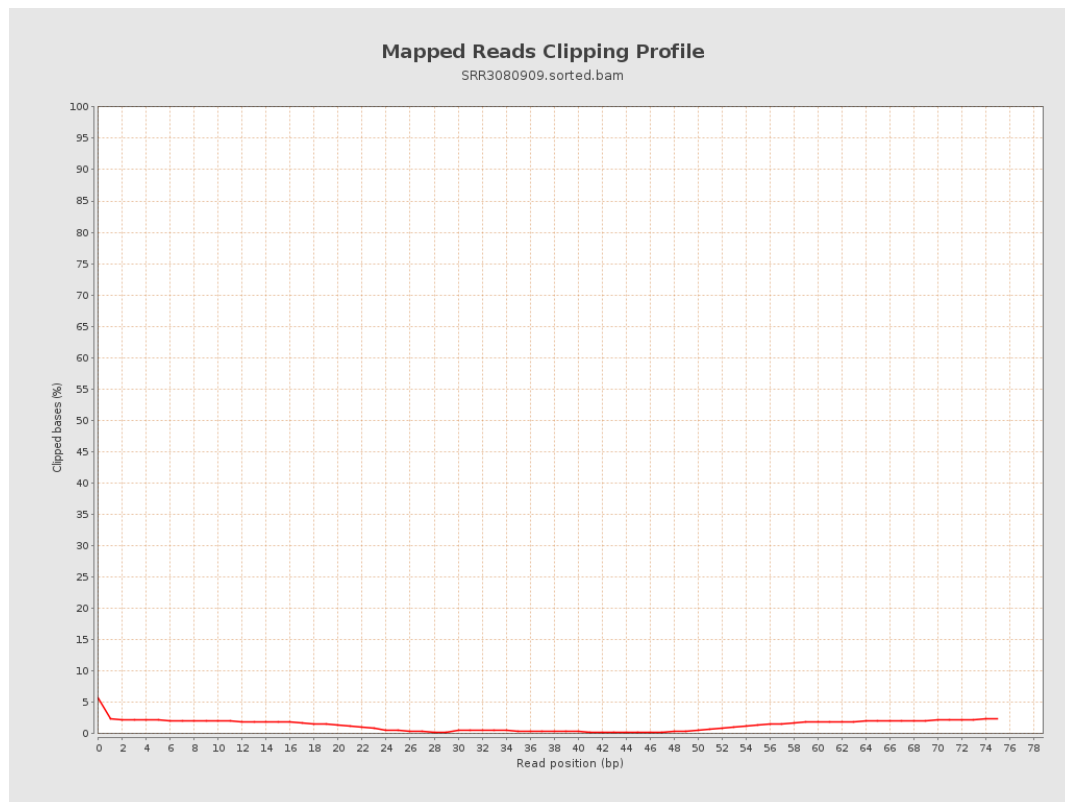
8. Results : Mapped Reads Nucleotide Content



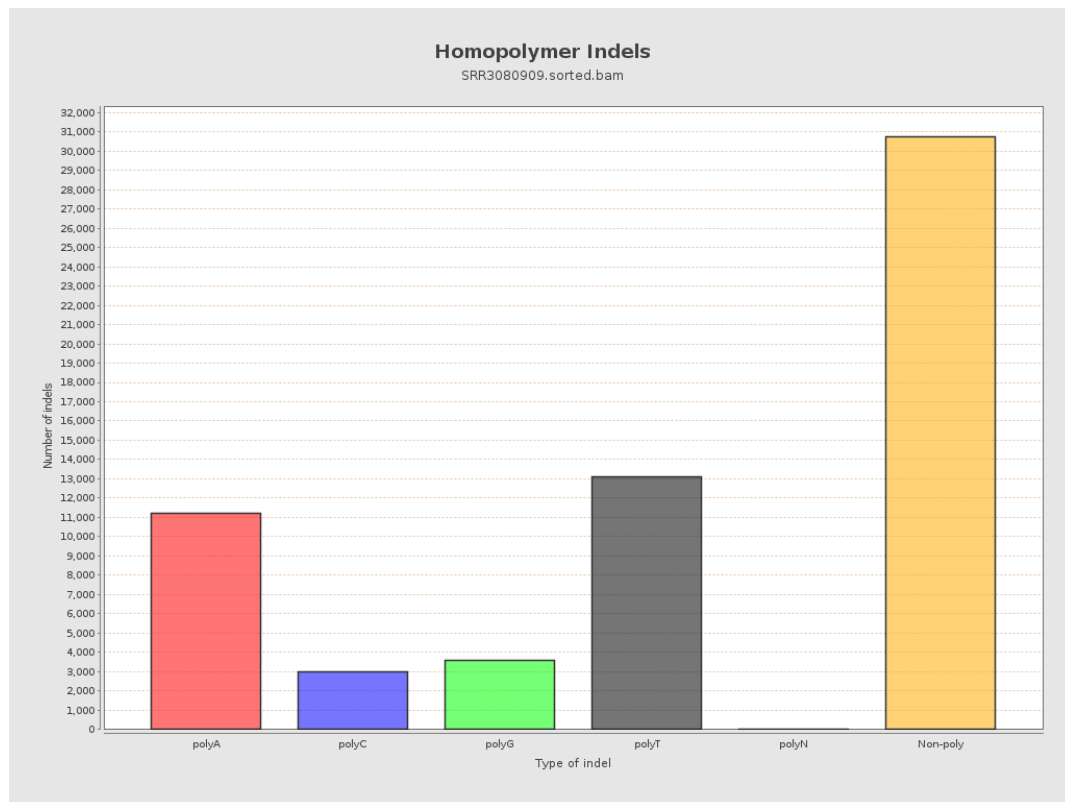
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

