

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:09:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008759.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_SRR6008759 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008759.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:09:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008759.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,001,197
Mapped reads	1,788,372 / 89.37%
Unmapped reads	212,825 / 10.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,853 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	109,288 / 5.46%
Duplication rate	4.66%
Clipped reads	805,408 / 40.25%

2.2. ACGT Content

Number/percentage of A's	32,225,808 / 27.19%
Number/percentage of C's	22,800,910 / 19.24%
Number/percentage of T's	36,635,348 / 30.91%
Number/percentage of G's	26,697,456 / 22.52%
Number/percentage of N's	169,061 / 0.14%
GC Percentage	41.76%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.4094
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2.4. Mapping Quality

Mean Mapping Quality	45.74
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2.5. Mismatches and indels

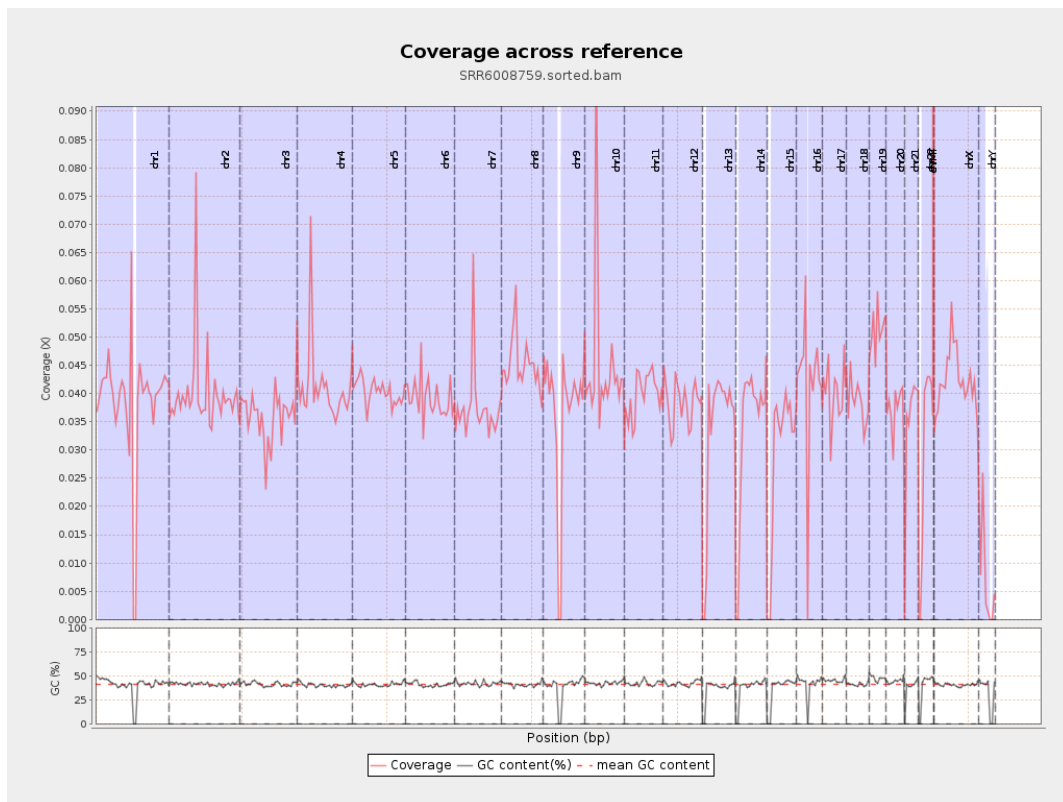
General error rate	0.88%
Mismatches	1,022,138
Insertions	9,019
Mapped reads with at least one insertion	0.5%
Deletions	34,149
Mapped reads with at least one deletion	1.89%
Homopolymer indels	44.63%

2.6. Chromosome stats

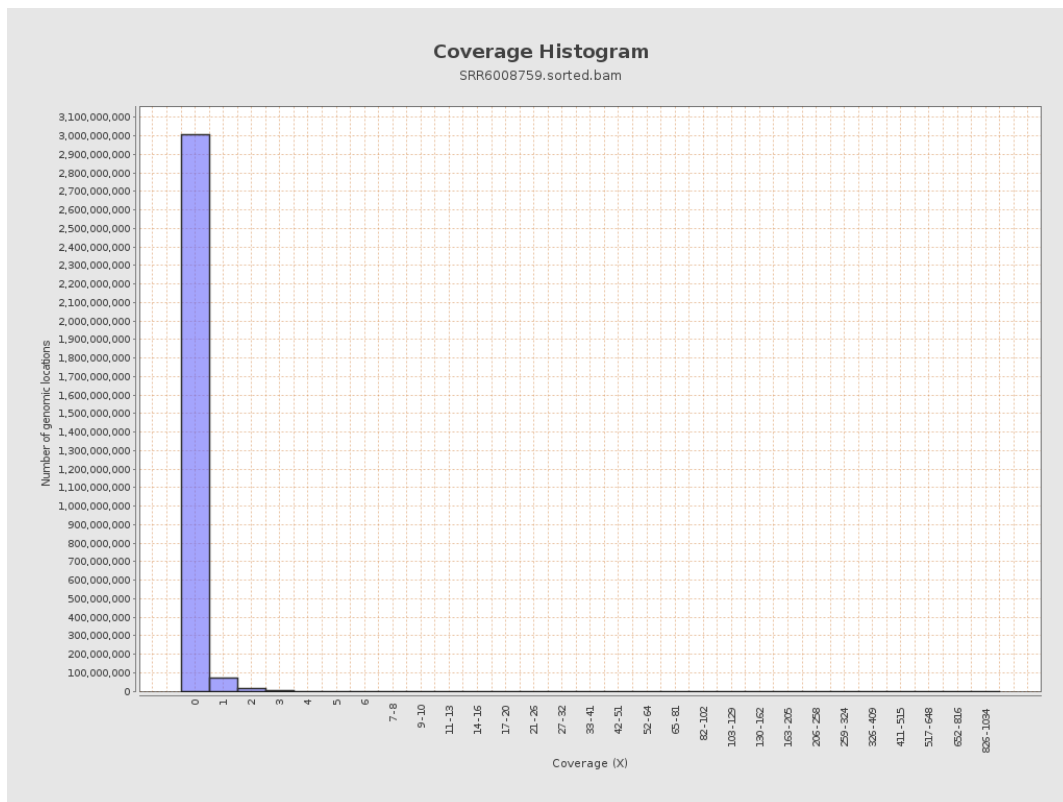
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9610563	0.0386	0.7464
chr2	243199373	9741872	0.0401	0.4578
chr3	198022430	7102370	0.0359	0.2502
chr4	191154276	7801837	0.0408	0.2848
chr5	180915260	7296078	0.0403	0.2514
chr6	171115067	6689418	0.0391	0.2715
chr7	159138663	5958361	0.0374	0.4393

chr8	146364022	6595484	0.0451	0.659
chr9	141213431	5106766	0.0362	0.3434
chr10	135534747	6029247	0.0445	0.5355
chr11	135006516	5377699	0.0398	0.3397
chr12	133851895	5155844	0.0385	0.2499
chr13	115169878	3795959	0.033	0.2264
chr14	107349540	3584456	0.0334	0.258
chr15	102531392	3004279	0.0293	0.2131
chr16	90354753	3786566	0.0419	0.3272
chr17	81195210	3256870	0.0401	0.2771
chr18	78077248	3004731	0.0385	0.5643
chr19	59128983	3032322	0.0513	0.5418
chr20	63025520	2341333	0.0371	0.2504
chr21	48129895	1682525	0.035	0.2603
chr22	51304566	1475721	0.0288	0.21
chrMT	16571	189576	11.4402	6.6639
chrX	155270560	6559239	0.0422	0.2752
chrY	59373566	410420	0.0069	0.2353

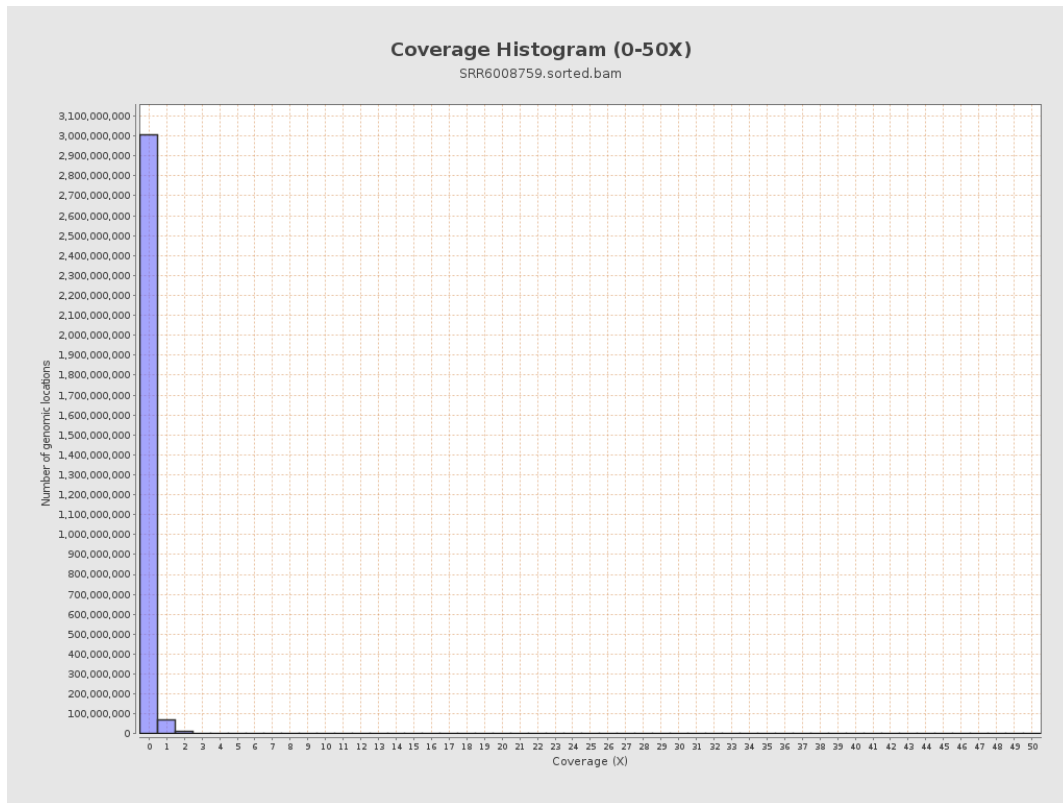
3. Results : Coverage across reference



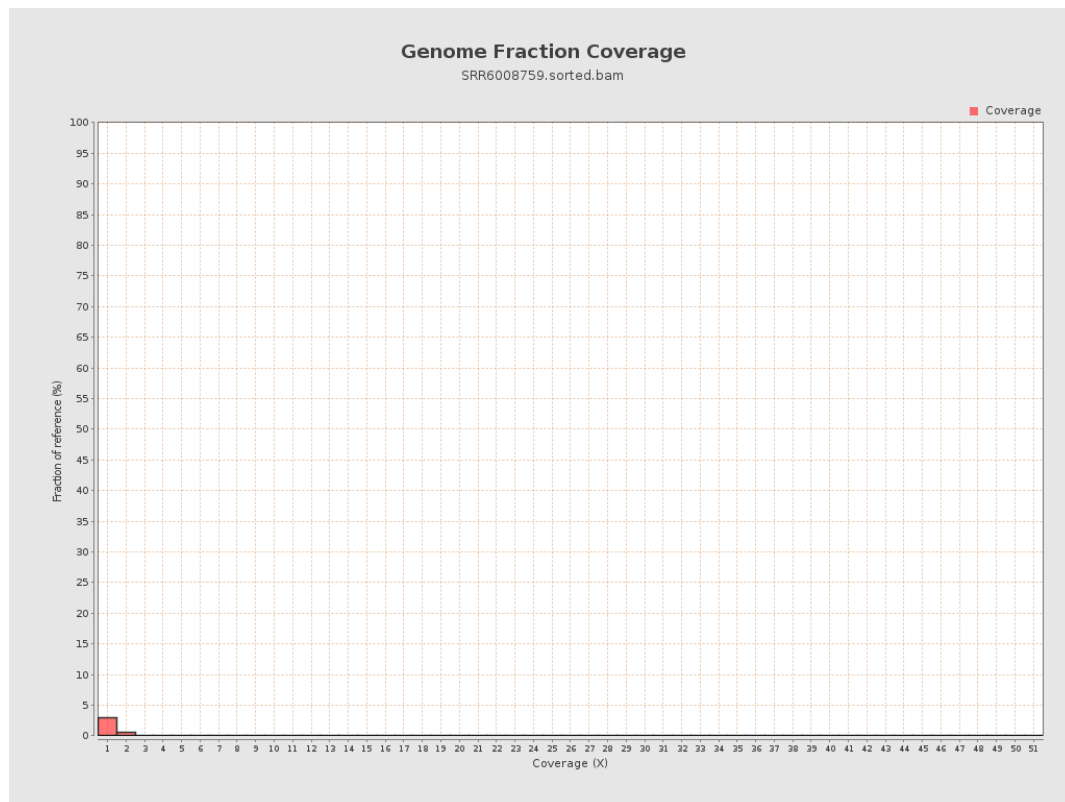
4. Results : Coverage Histogram



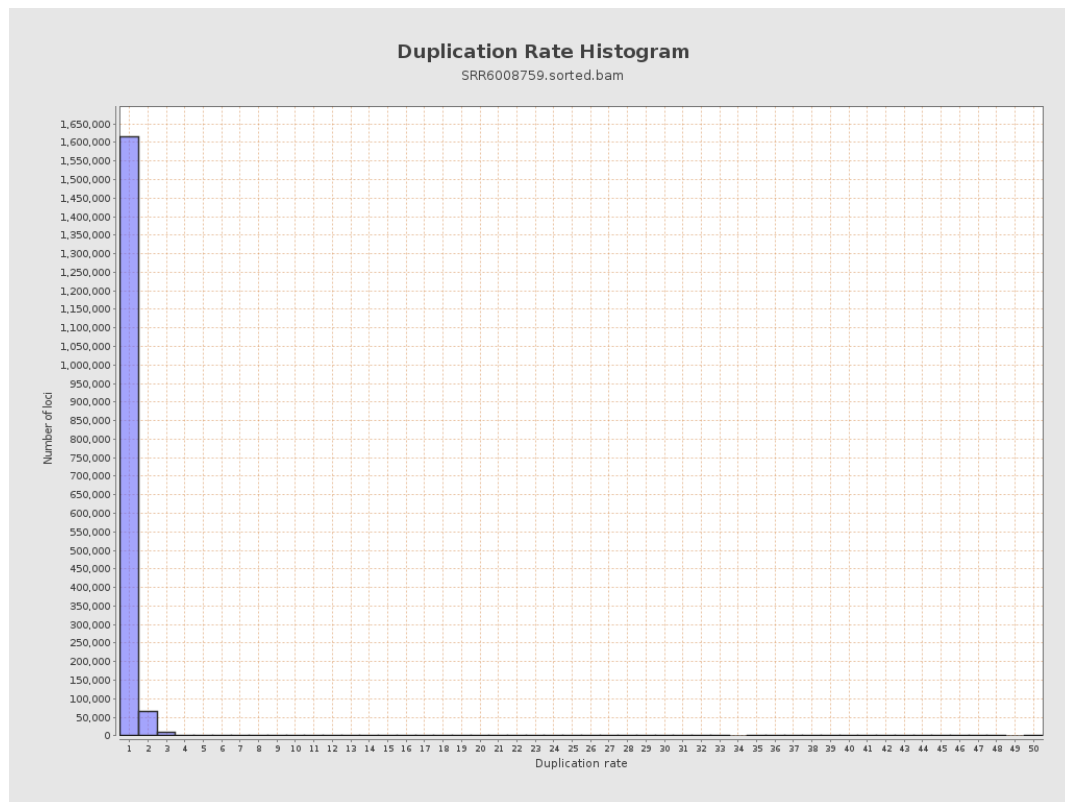
5. Results : Coverage Histogram (0-50X)



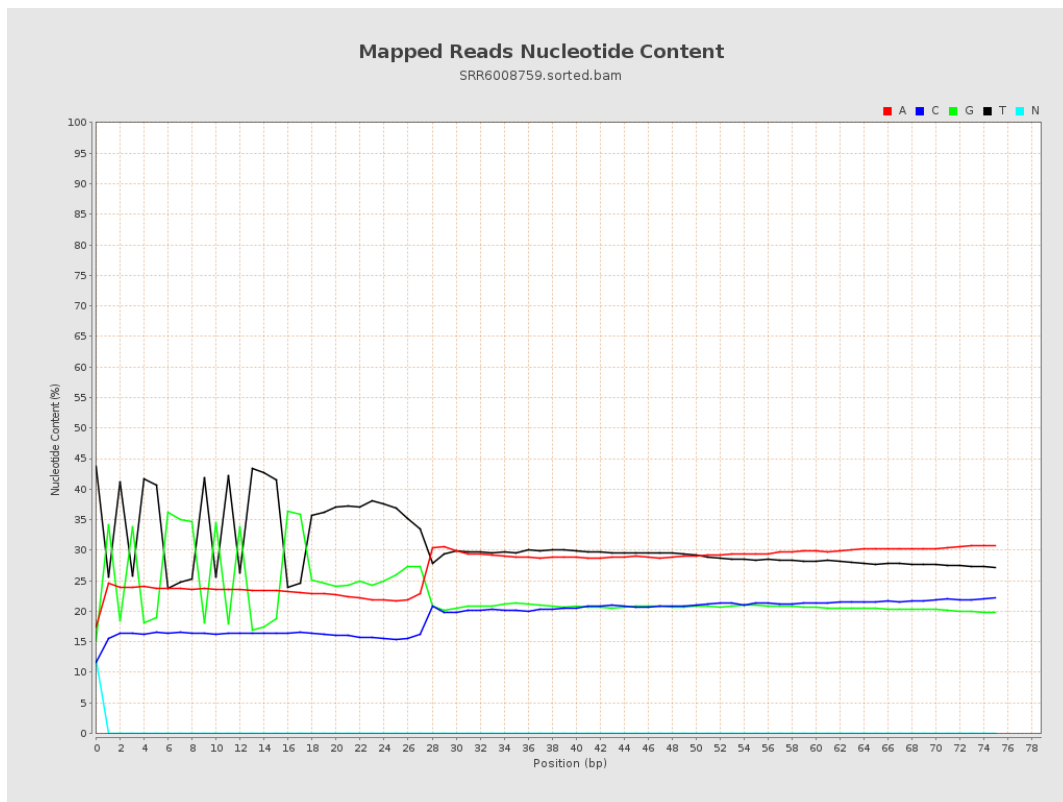
6. Results : Genome Fraction Coverage



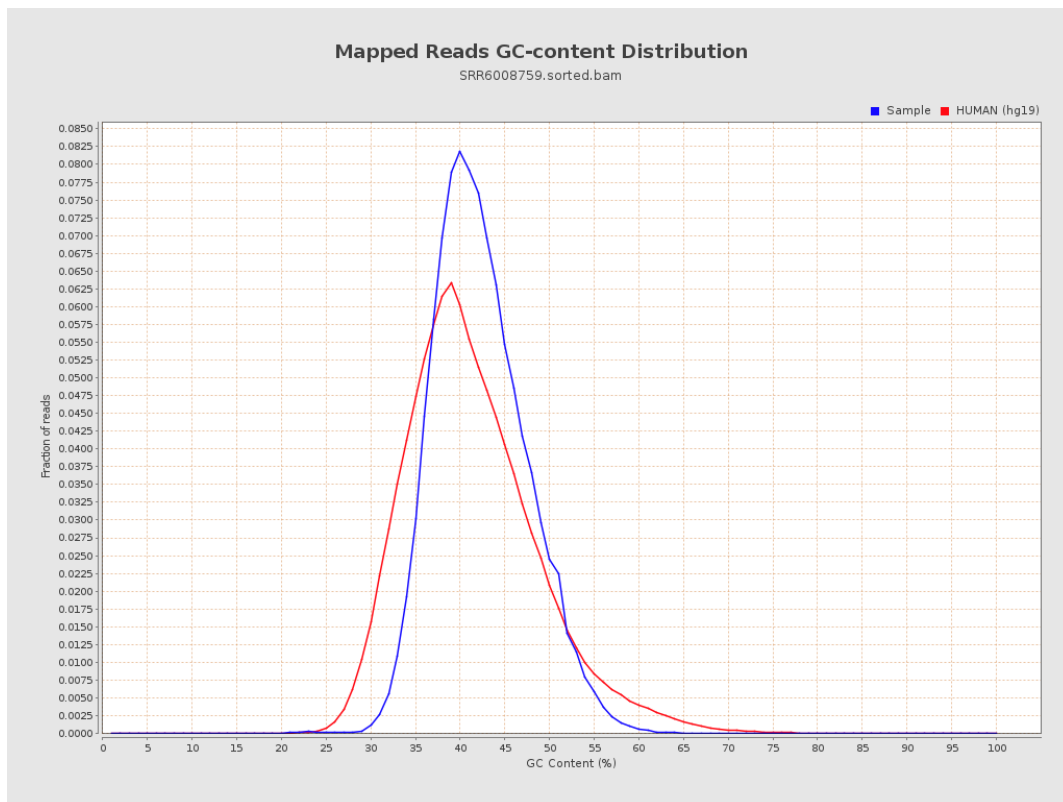
7. Results : Duplication Rate Histogram



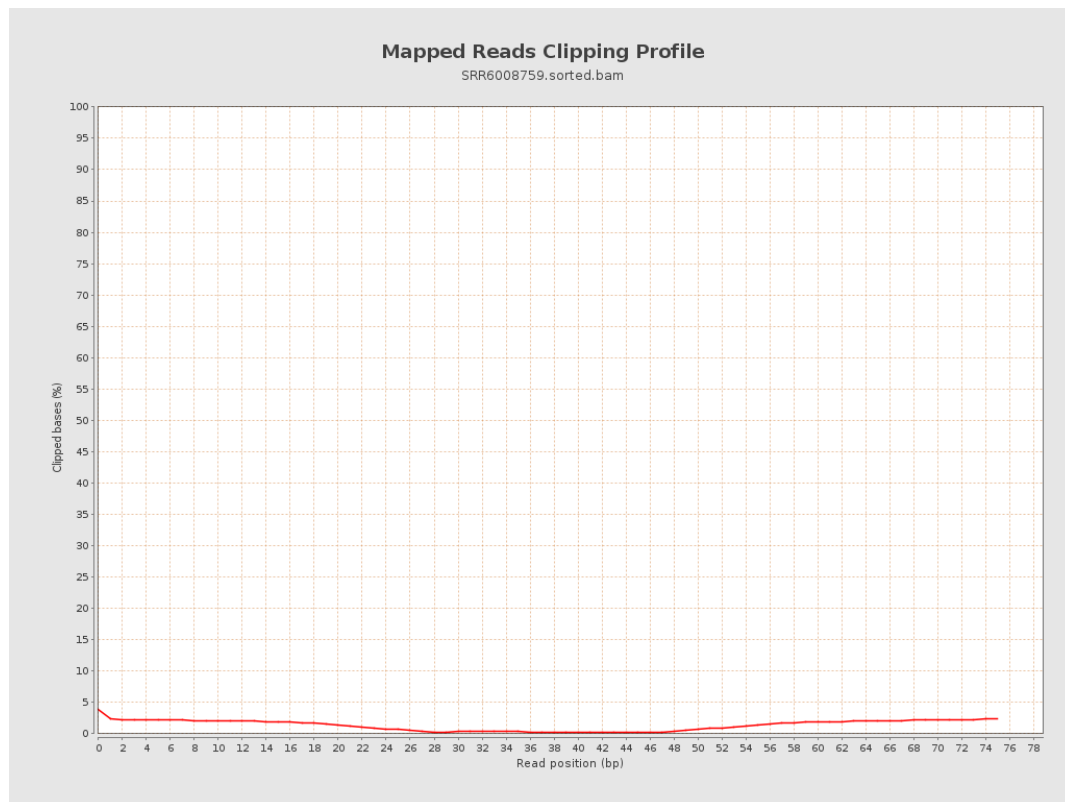
8. Results : Mapped Reads Nucleotide Content



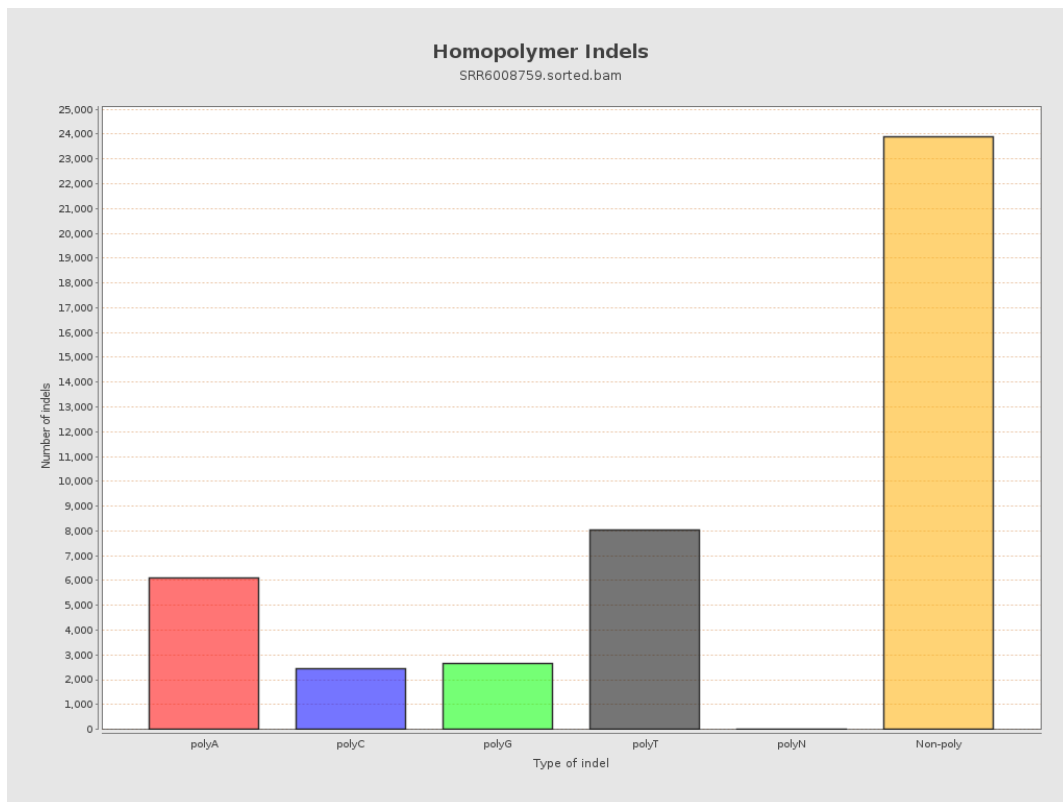
9. Results : Mapped Reads GC-content Distribution



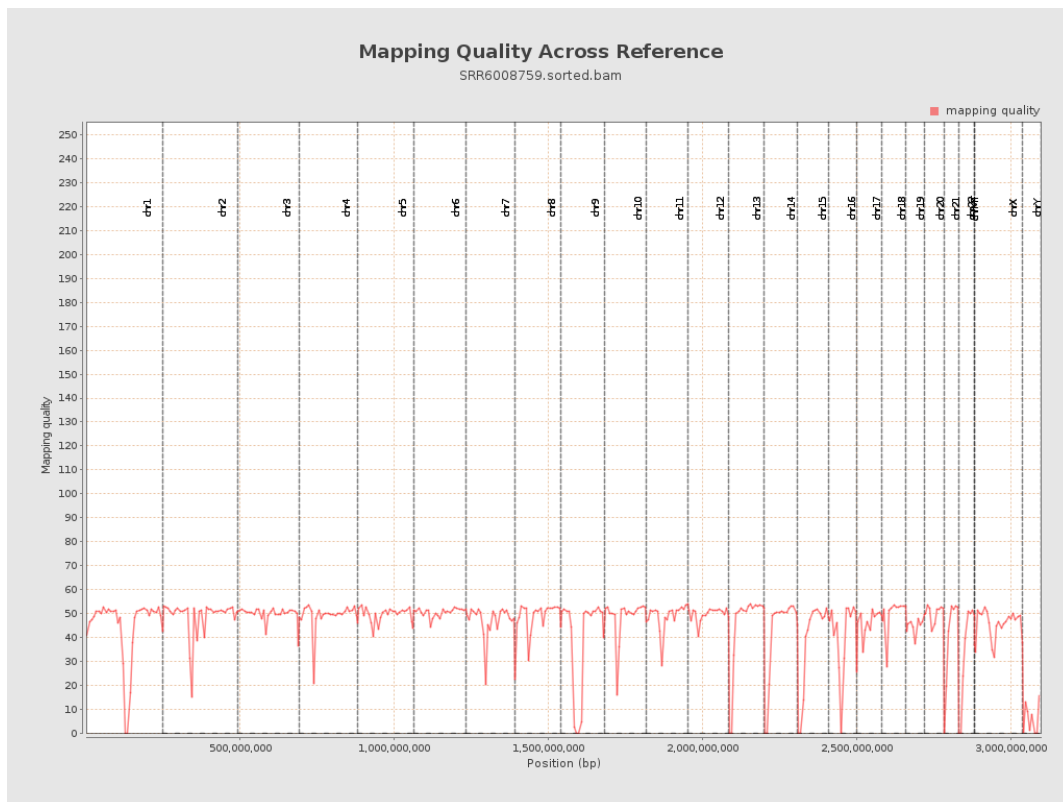
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

