

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:23:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708587.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_SRR1708587 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708587.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:23:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708587.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,561,491
Mapped reads	4,466,692 / 97.92%
Unmapped reads	94,799 / 2.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	112 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	43,919 / 0.96%
Duplication rate	0.98%
Clipped reads	60,378 / 1.32%

2.2. ACGT Content

Number/percentage of A's	69,031,167 / 30.99%
Number/percentage of C's	42,255,710 / 18.97%
Number/percentage of T's	68,684,721 / 30.83%
Number/percentage of G's	42,782,549 / 19.21%
Number/percentage of N's	7,570 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	0.072

Standard Deviation	0.281
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2.4. Mapping Quality

Mean Mapping Quality	46.62
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2.5. Mismatches and indels

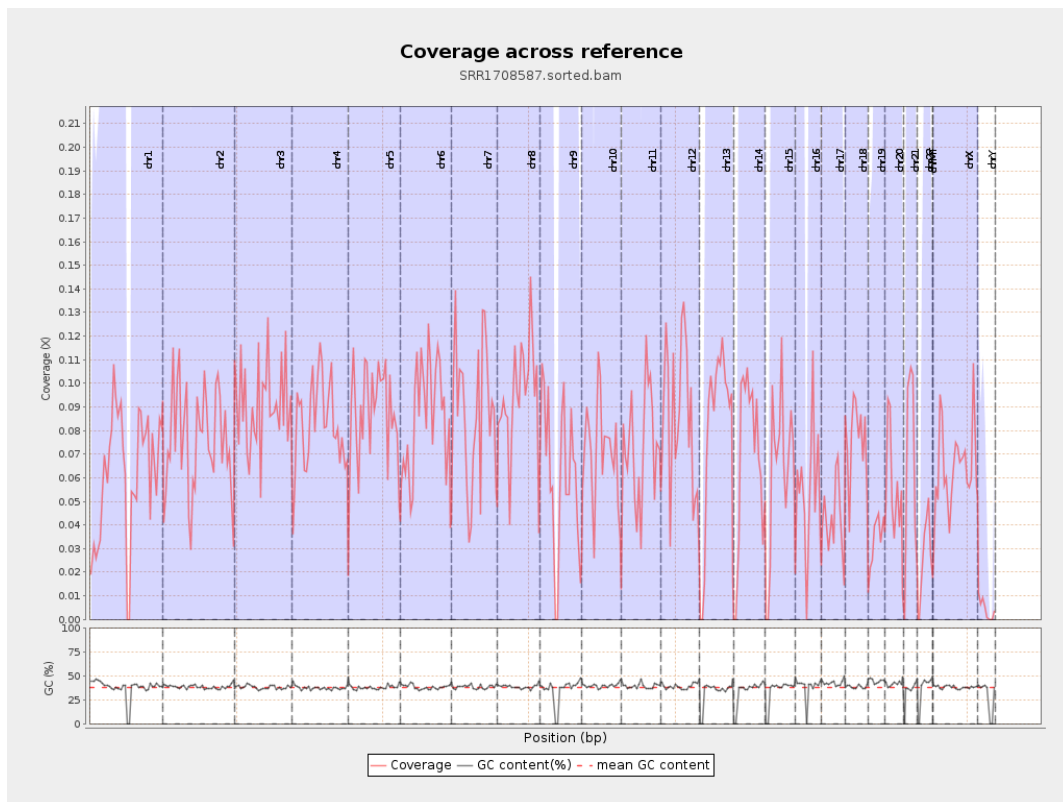
General error rate	0.16%
Mismatches	329,051
Insertions	13,919
Mapped reads with at least one insertion	0.31%
Deletions	11,529
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.04%

2.6. Chromosome stats

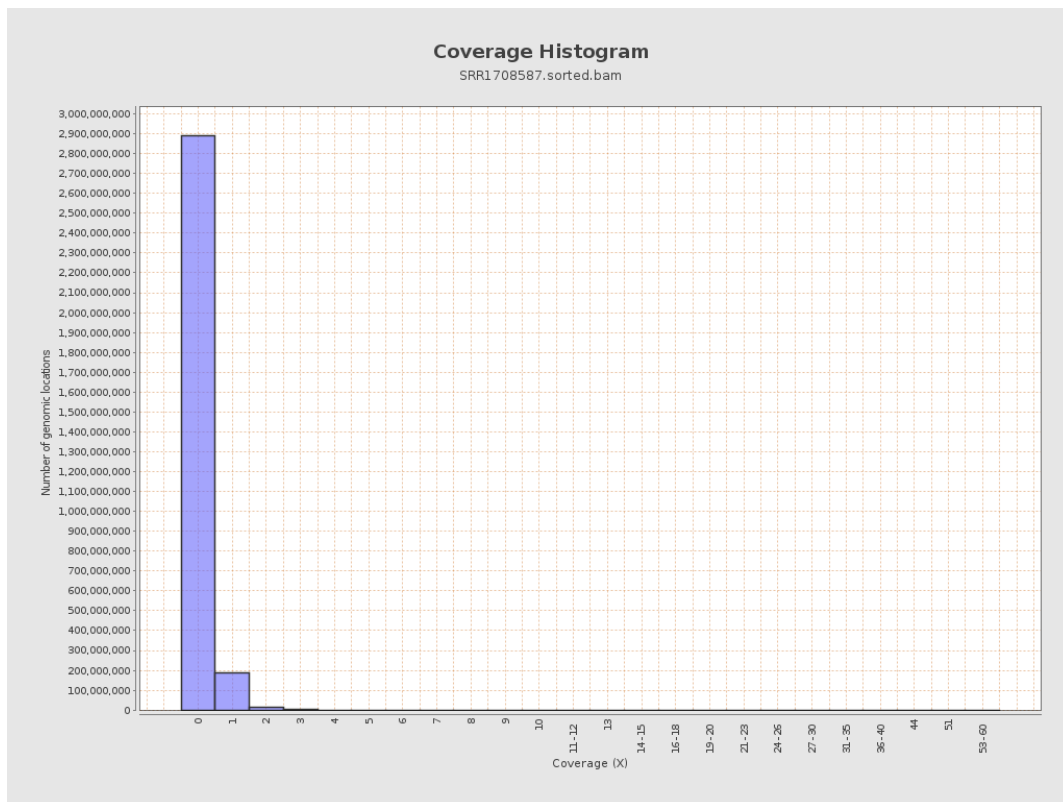
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15401212	0.0618	0.2615
chr2	243199373	18372064	0.0755	0.2867
chr3	198022430	18039789	0.0911	0.3147
chr4	191154276	15838979	0.0829	0.2998
chr5	180915260	15659705	0.0866	0.3072
chr6	171115067	14787032	0.0864	0.3063
chr7	159138663	13730366	0.0863	0.3084

chr8	146364022	13826686	0.0945	0.3206
chr9	141213431	8673285	0.0614	0.2599
chr10	135534747	9746622	0.0719	0.2789
chr11	135006516	9747232	0.0722	0.2815
chr12	133851895	11376006	0.085	0.3058
chr13	115169878	9276752	0.0805	0.2971
chr14	107349540	7428832	0.0692	0.2766
chr15	102531392	6393459	0.0624	0.2622
chr16	90354753	4787110	0.053	0.2401
chr17	81195210	3525797	0.0434	0.2168
chr18	78077248	5926234	0.0759	0.2867
chr19	59128983	2046613	0.0346	0.1924
chr20	63025520	3547398	0.0563	0.2487
chr21	48129895	3013700	0.0626	0.2657
chr22	51304566	1378115	0.0269	0.1705
chrMT	16571	300	0.0181	0.1333
chrX	155270560	10003220	0.0644	0.2645
chrY	59373566	254736	0.0043	0.0687

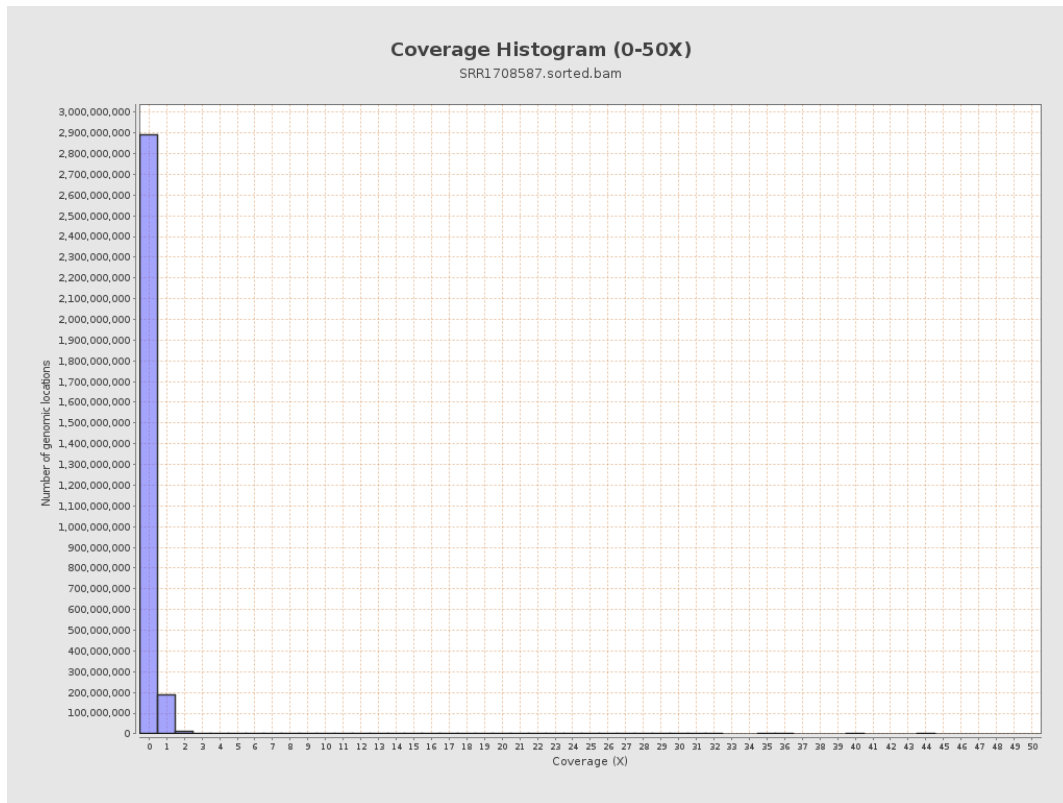
3. Results : Coverage across reference



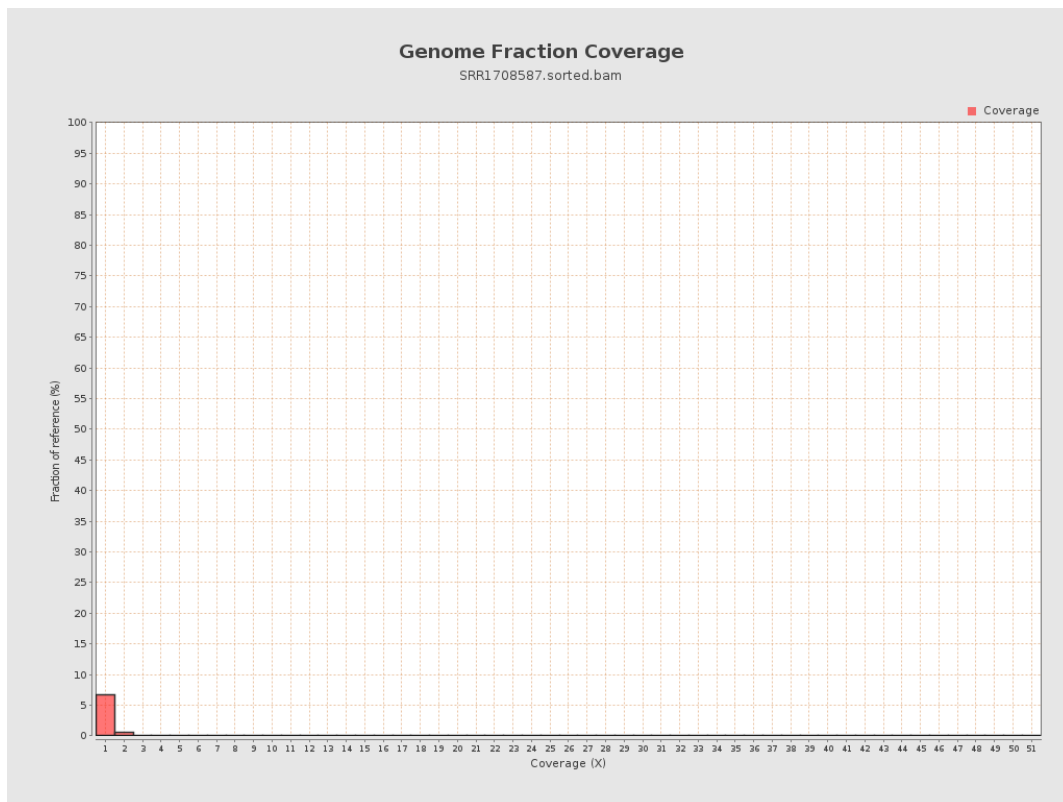
4. Results : Coverage Histogram



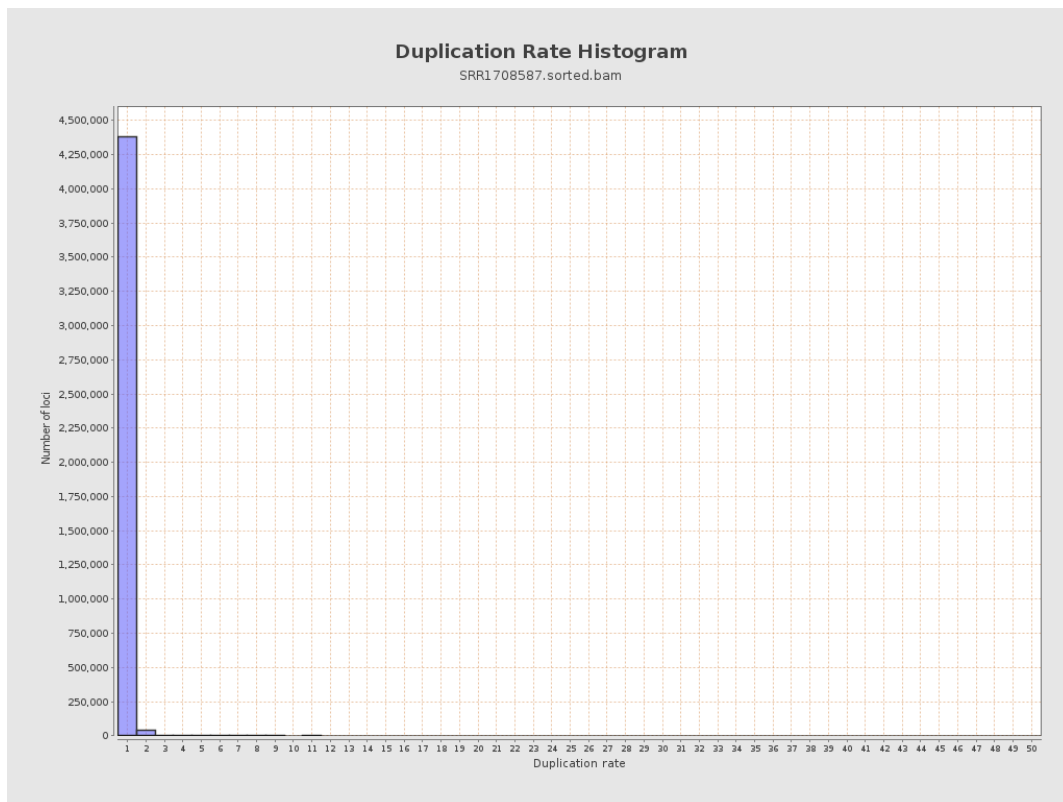
5. Results : Coverage Histogram (0-50X)



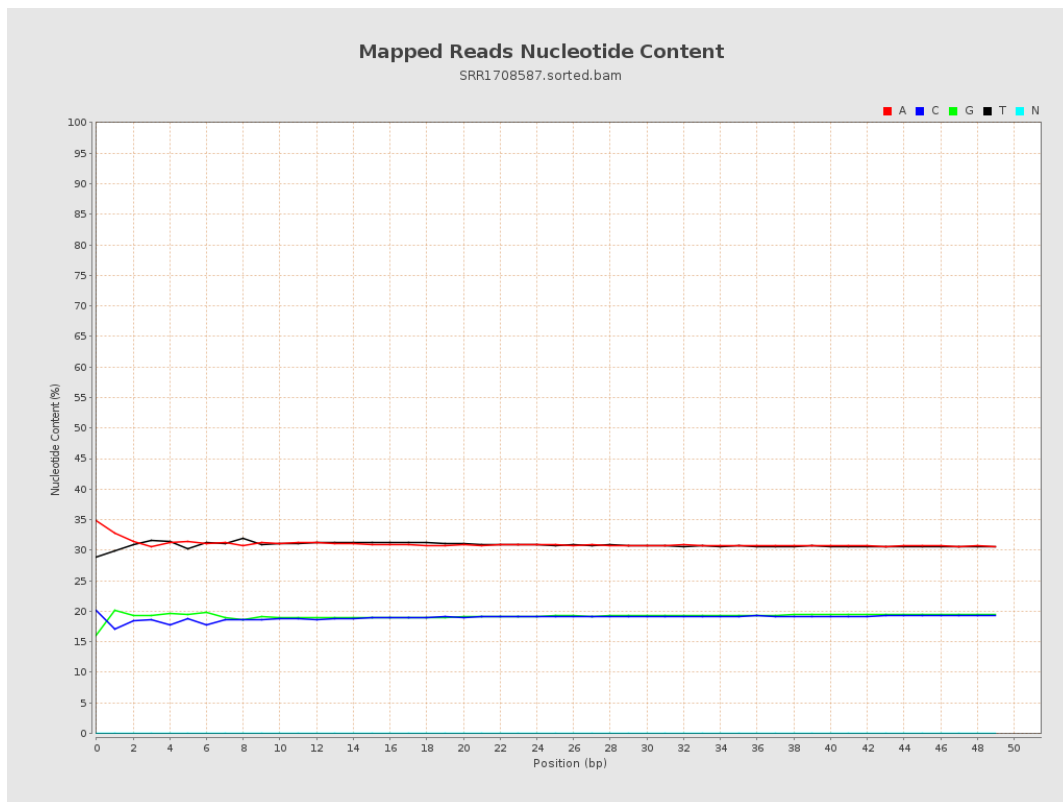
6. Results : Genome Fraction Coverage



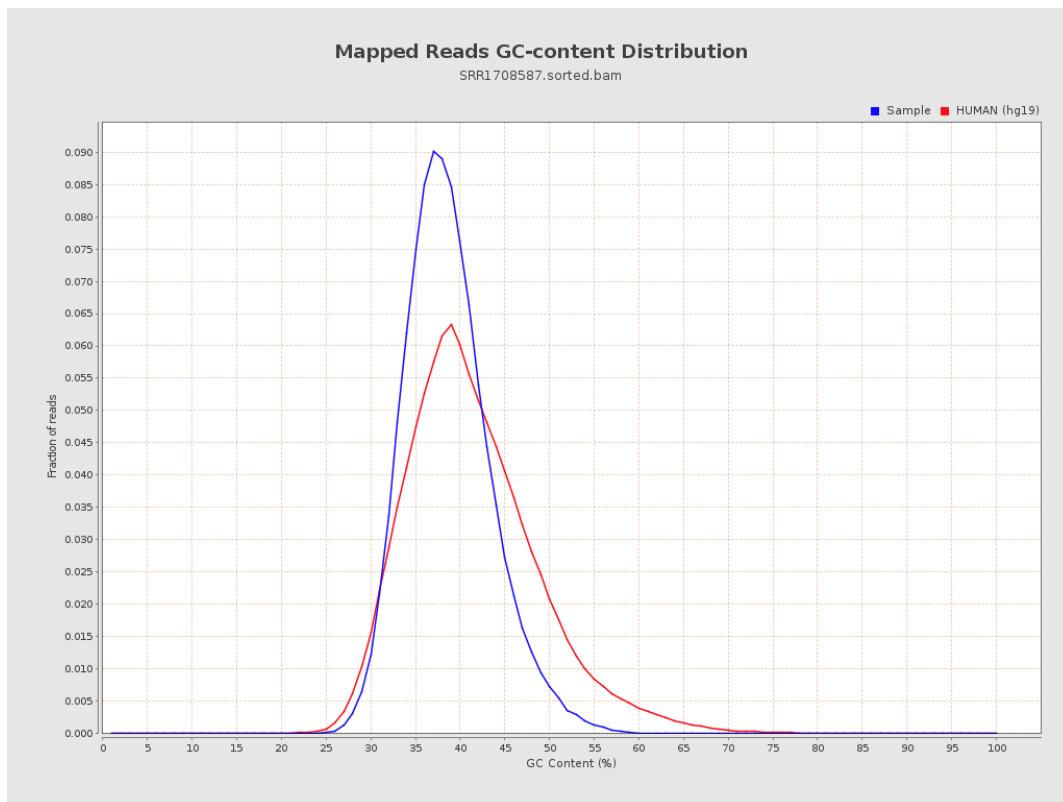
7. Results : Duplication Rate Histogram



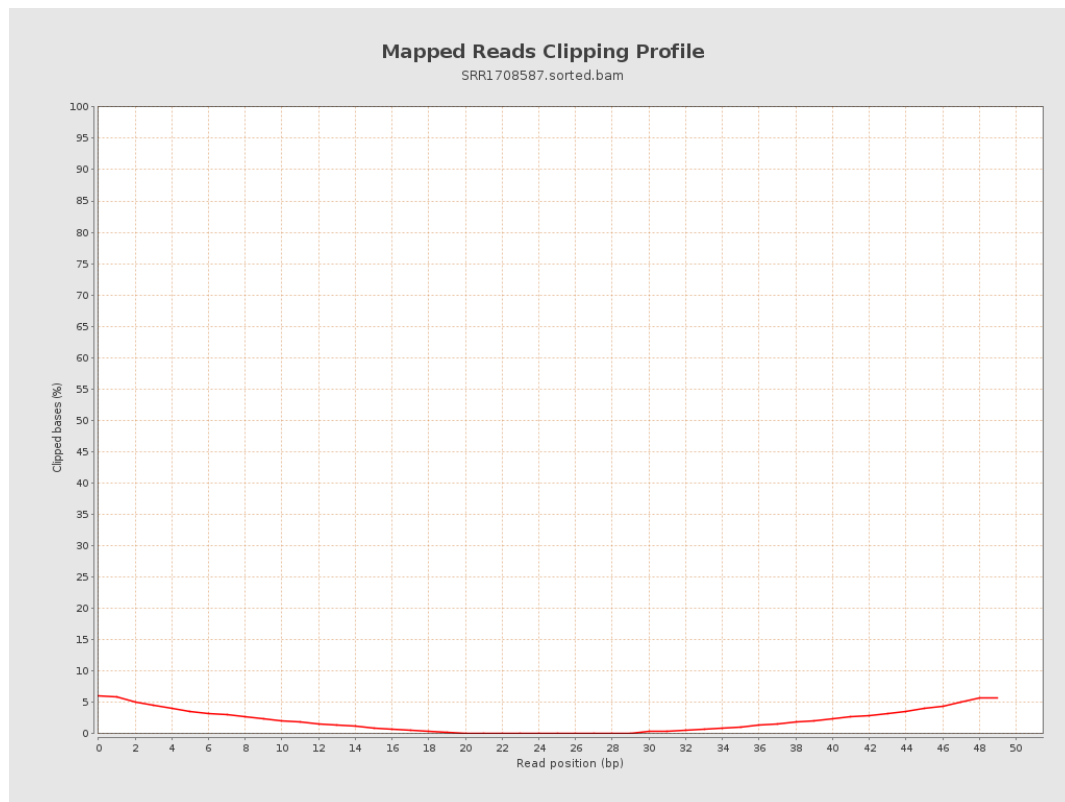
8. Results : Mapped Reads Nucleotide Content



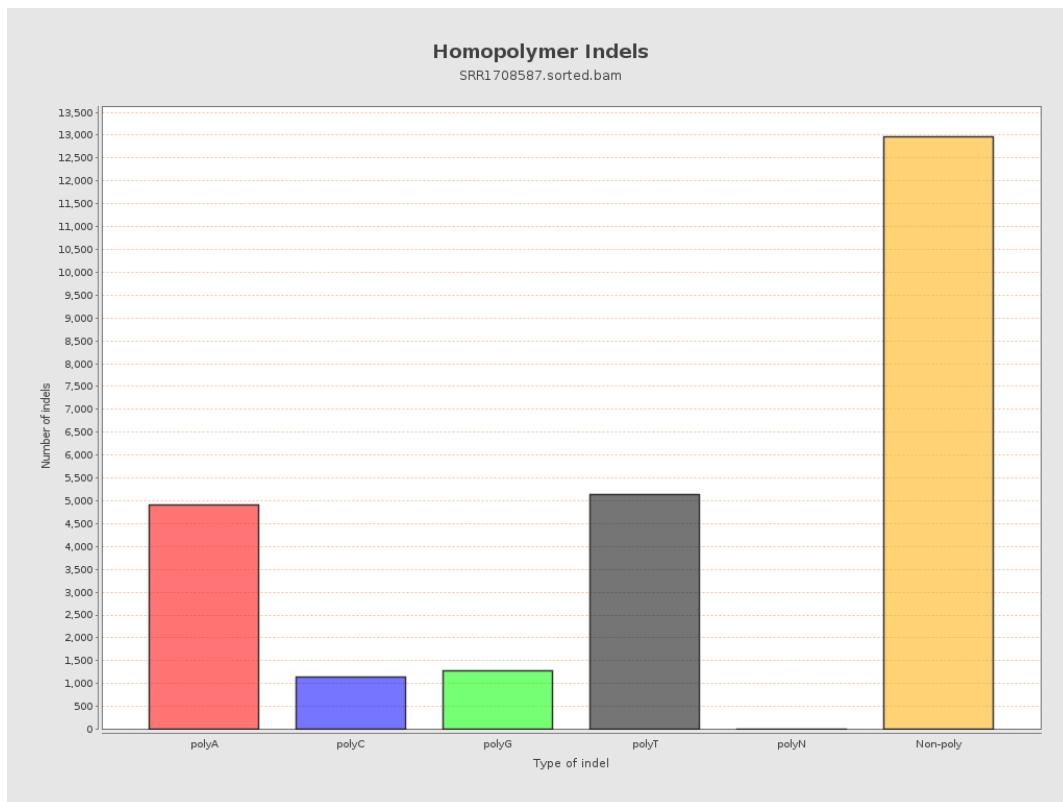
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

