

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:49:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818928.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_SRR1818928 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818928.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:49:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,444,156
Mapped reads	2,413,803 / 98.76%
Unmapped reads	30,353 / 1.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,936 / 1.31%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	1,185,652 / 48.51%
Duplication rate	41.28%
Clipped reads	2,437,890 / 99.74%

2.2. ACGT Content

Number/percentage of A's	64,253,224 / 28.74%
Number/percentage of C's	48,059,101 / 21.5%
Number/percentage of T's	62,687,841 / 28.04%
Number/percentage of G's	48,572,811 / 21.72%
Number/percentage of N's	9,258 / 0%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0723

Standard Deviation	0.7899
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2.4. Mapping Quality

Mean Mapping Quality	49.25
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2.5. Mismatches and indels

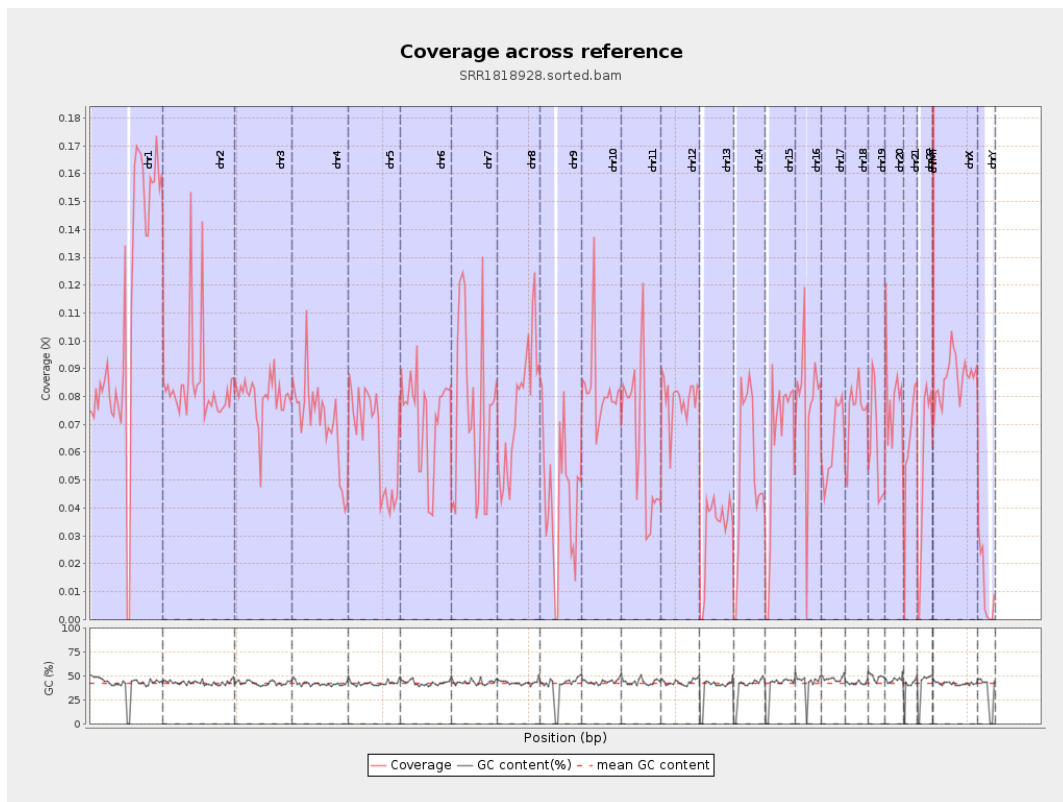
General error rate	0.65%
Mismatches	1,398,980
Insertions	26,165
Mapped reads with at least one insertion	1.05%
Deletions	68,007
Mapped reads with at least one deletion	2.75%
Homopolymer indels	43.54%

2.6. Chromosome stats

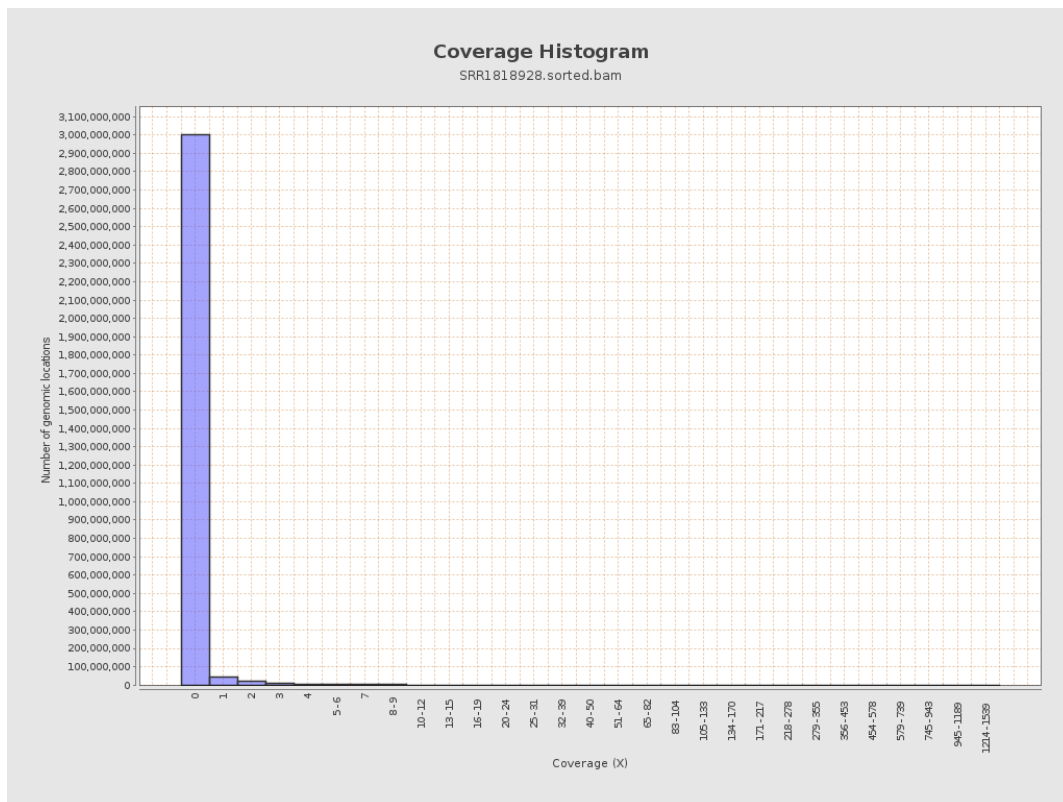
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27371094	0.1098	1.3826
chr2	243199373	20526444	0.0844	1.1558
chr3	198022430	15779775	0.0797	0.564
chr4	191154276	13629710	0.0713	0.581
chr5	180915260	11793825	0.0652	0.5224
chr6	171115067	12435122	0.0727	0.5882
chr7	159138663	11941914	0.075	0.7163

chr8	146364022	11230508	0.0767	0.6467
chr9	141213431	6066009	0.043	0.7273
chr10	135534747	11112104	0.082	0.9129
chr11	135006516	8579094	0.0635	0.5707
chr12	133851895	10637398	0.0795	0.5772
chr13	115169878	3706073	0.0322	0.3499
chr14	107349540	5831564	0.0543	0.5029
chr15	102531392	6365577	0.0621	0.5088
chr16	90354753	6997994	0.0775	0.8978
chr17	81195210	5168227	0.0637	0.5559
chr18	78077248	5835123	0.0747	1.0034
chr19	59128983	3658962	0.0619	1.1273
chr20	63025520	5012221	0.0795	0.6096
chr21	48129895	3081030	0.064	0.5406
chr22	51304566	2818503	0.0549	0.5049
chrMT	16571	16429	0.9914	2.0342
chrX	155270560	13455091	0.0867	0.699
chrY	59373566	656415	0.0111	0.6879

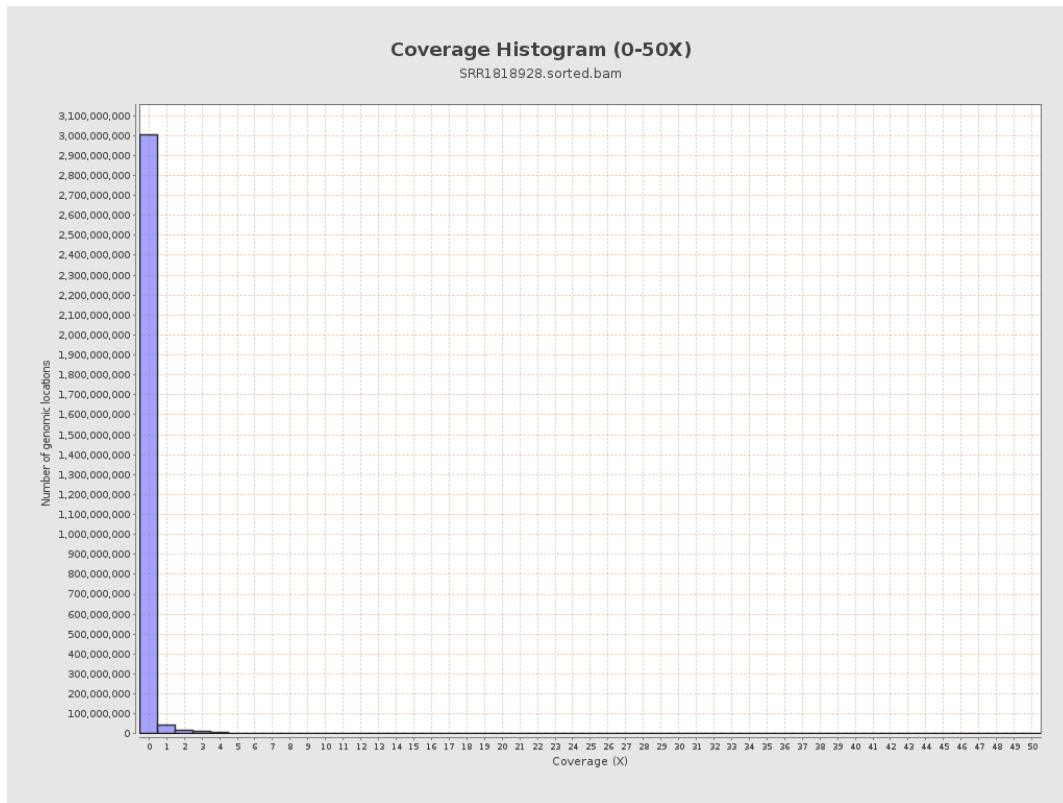
3. Results : Coverage across reference



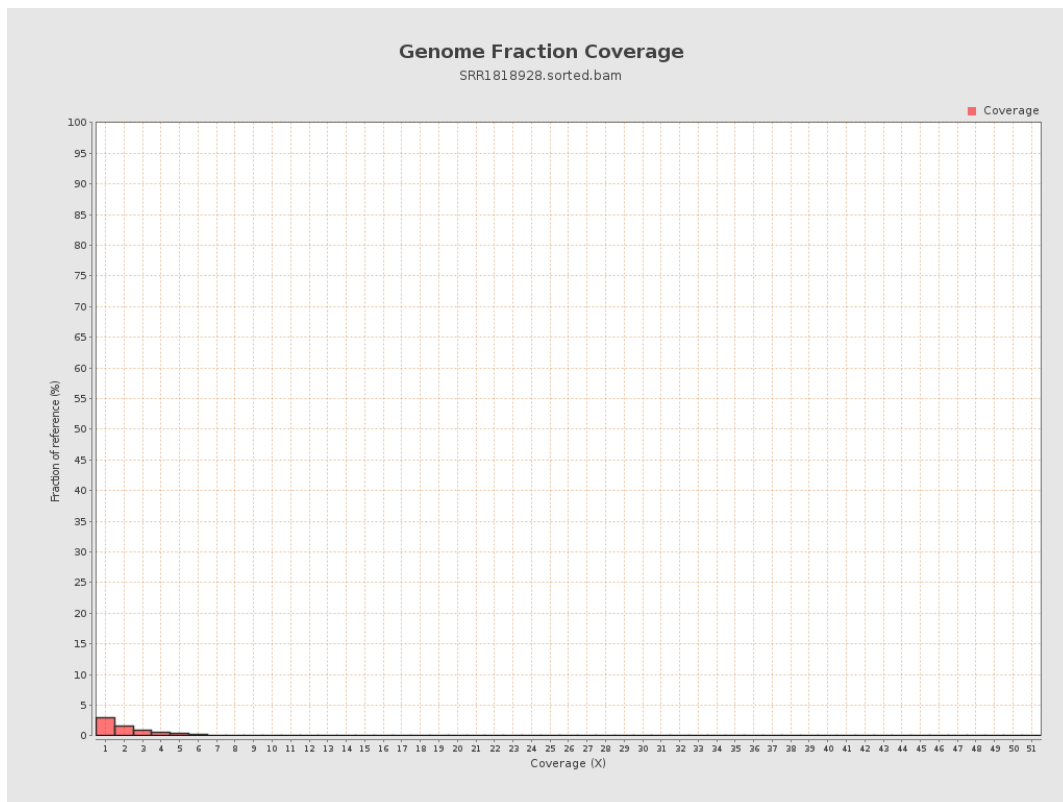
4. Results : Coverage Histogram



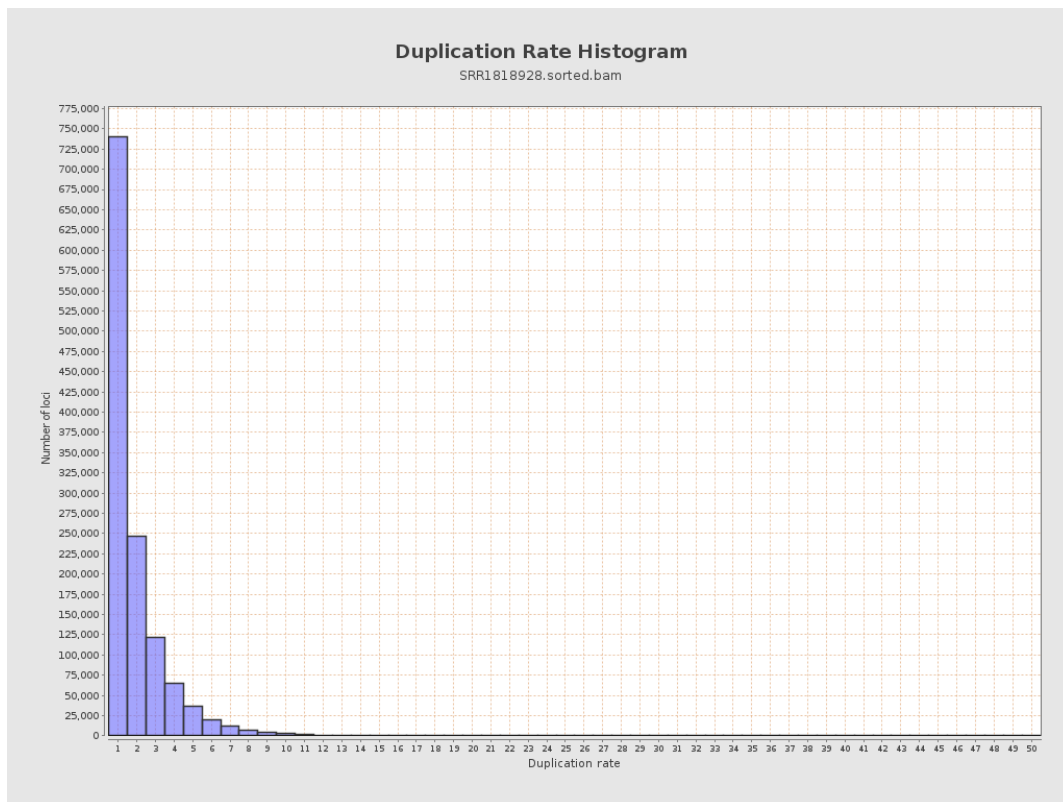
5. Results : Coverage Histogram (0-50X)



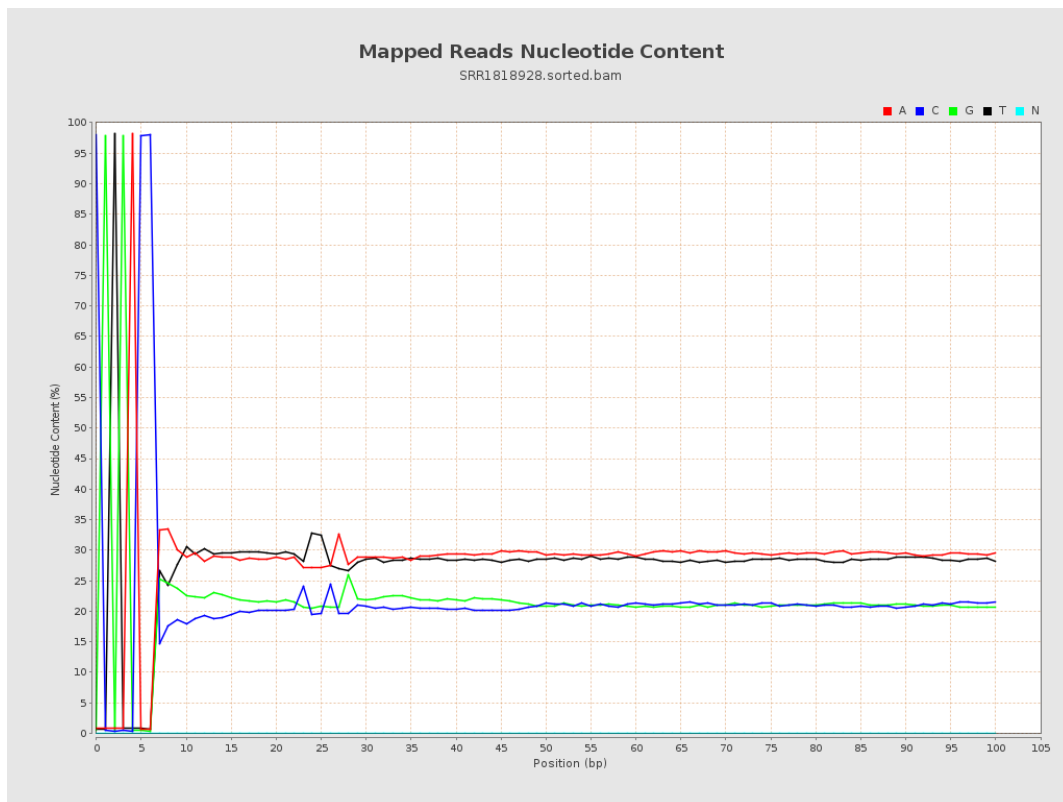
6. Results : Genome Fraction Coverage



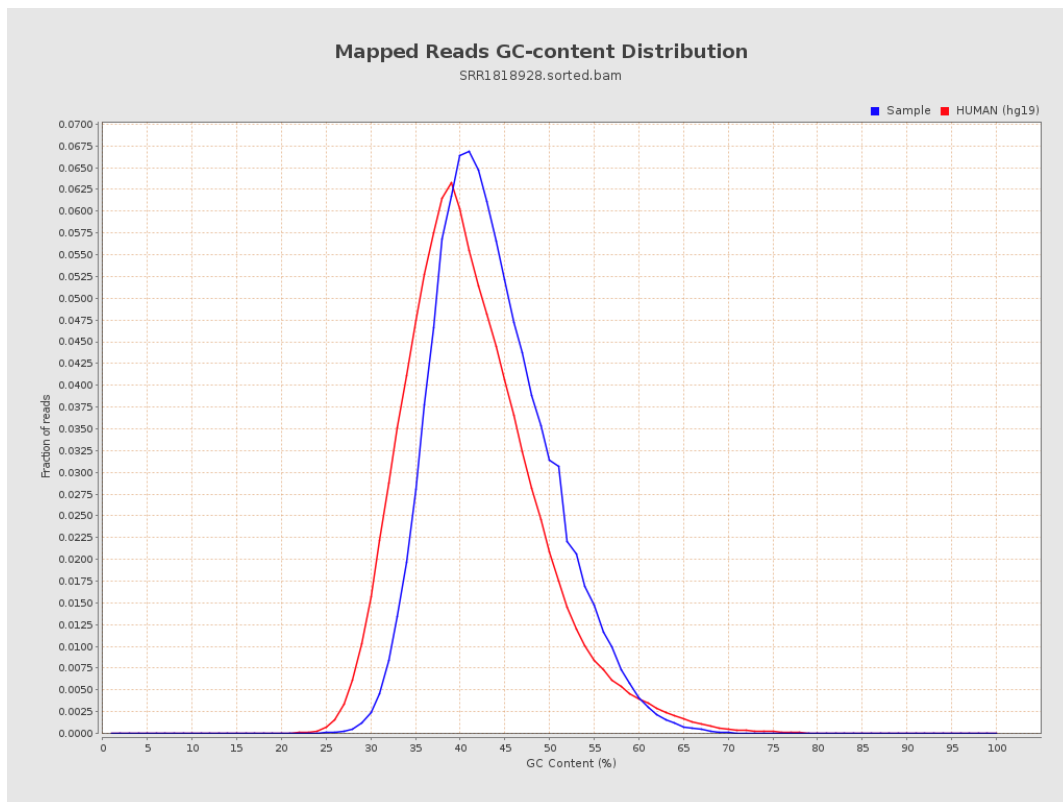
7. Results : Duplication Rate Histogram



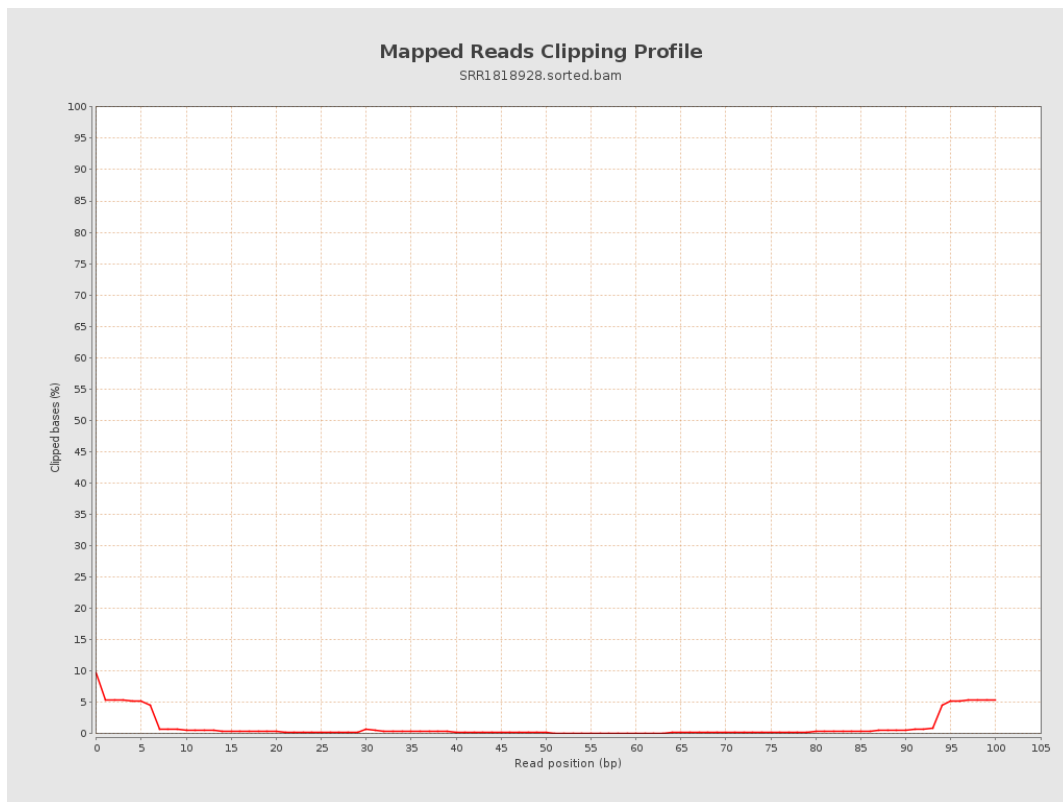
8. Results : Mapped Reads Nucleotide Content



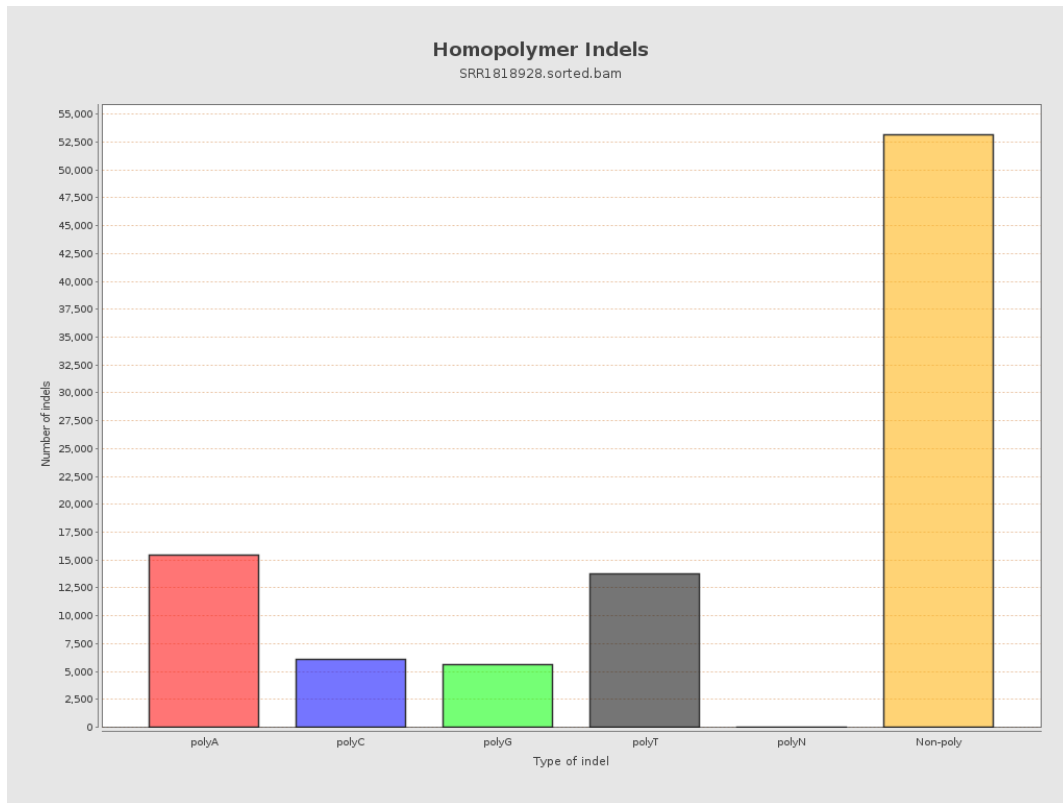
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

