

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:44:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818965.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_SRR1818965 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818965.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:44:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818965.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,585,537
Mapped reads	1,560,364 / 98.41%
Unmapped reads	25,173 / 1.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,231 / 1.65%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	614,438 / 38.75%
Duplication rate	33.68%
Clipped reads	1,575,086 / 99.34%

2.2. ACGT Content

Number/percentage of A's	42,423,222 / 29.4%
Number/percentage of C's	29,991,411 / 20.78%
Number/percentage of T's	40,280,677 / 27.91%
Number/percentage of G's	31,600,959 / 21.9%
Number/percentage of N's	6,922 / 0%
GC Percentage	42.68%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.559
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2.4. Mapping Quality

Mean Mapping Quality	49.23
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2.5. Mismatches and indels

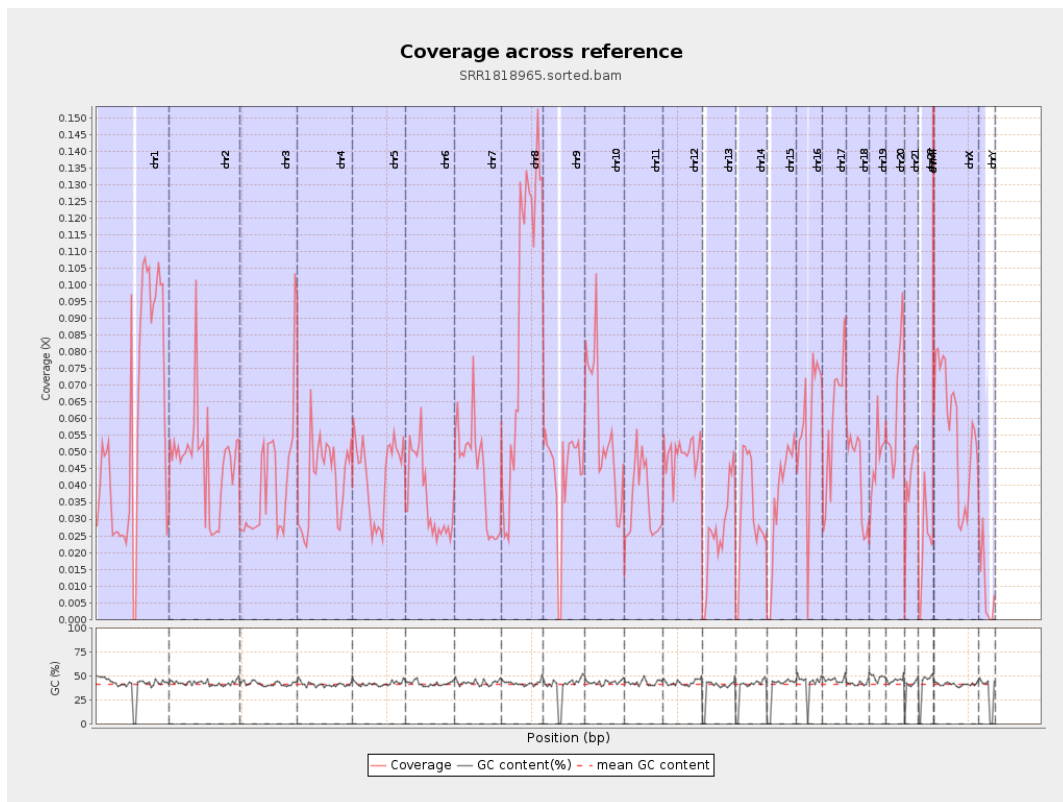
General error rate	0.66%
Mismatches	903,534
Insertions	22,679
Mapped reads with at least one insertion	1.42%
Deletions	45,995
Mapped reads with at least one deletion	2.88%
Homopolymer indels	41.82%

2.6. Chromosome stats

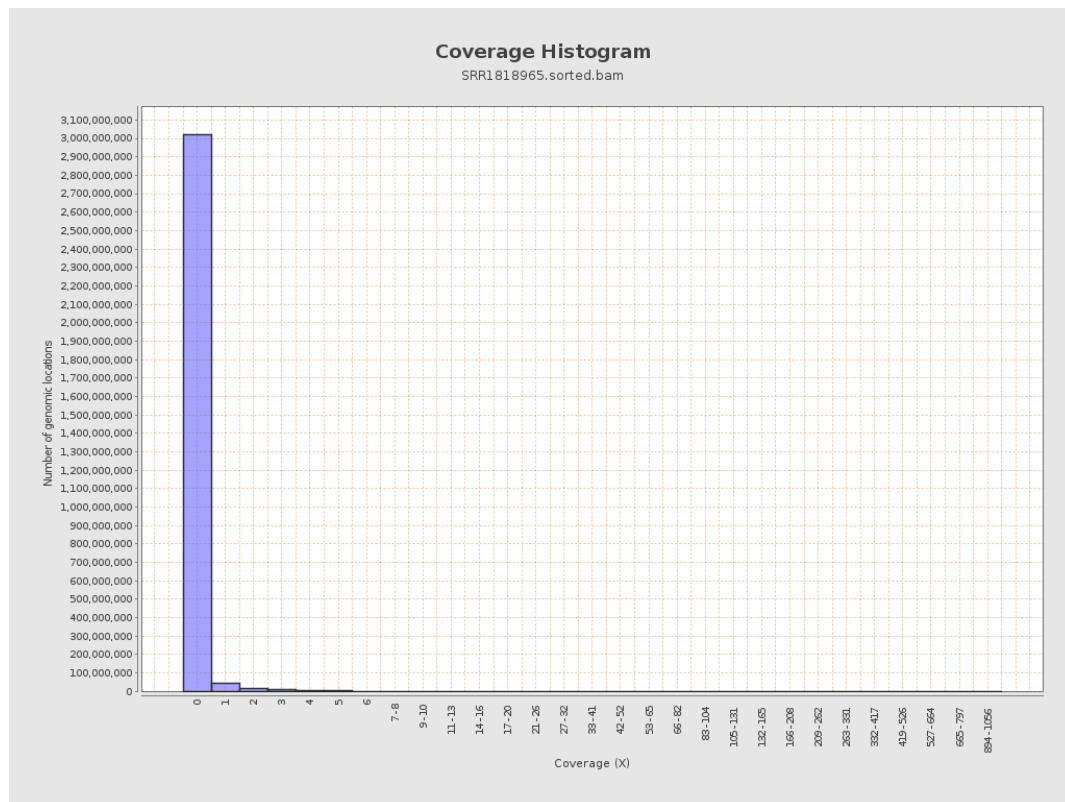
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14369214	0.0576	1.0355
chr2	243199373	11532761	0.0474	0.7472
chr3	198022430	7949807	0.0401	0.3325
chr4	191154276	8002603	0.0419	0.3895
chr5	180915260	7867470	0.0435	0.3565
chr6	171115067	6167011	0.036	0.3629
chr7	159138663	6986495	0.0439	0.6646

chr8	146364022	13470365	0.092	0.5564
chr9	141213431	6120395	0.0433	0.4714
chr10	135534747	7642525	0.0564	0.6554
chr11	135006516	4703649	0.0348	0.3519
chr12	133851895	6648079	0.0497	0.383
chr13	115169878	3017970	0.0262	0.2703
chr14	107349540	3366423	0.0314	0.3149
chr15	102531392	3703452	0.0361	0.3165
chr16	90354753	5334610	0.059	0.5922
chr17	81195210	4863048	0.0599	0.4435
chr18	78077248	3390037	0.0434	0.567
chr19	59128983	2837957	0.048	0.9599
chr20	63025520	4046468	0.0642	0.4454
chr21	48129895	1972432	0.041	0.3771
chr22	51304566	1086460	0.0212	0.264
chrMT	16571	13227	0.7982	1.4902
chrX	155270560	8755245	0.0564	0.4512
chrY	59373566	541348	0.0091	0.4958

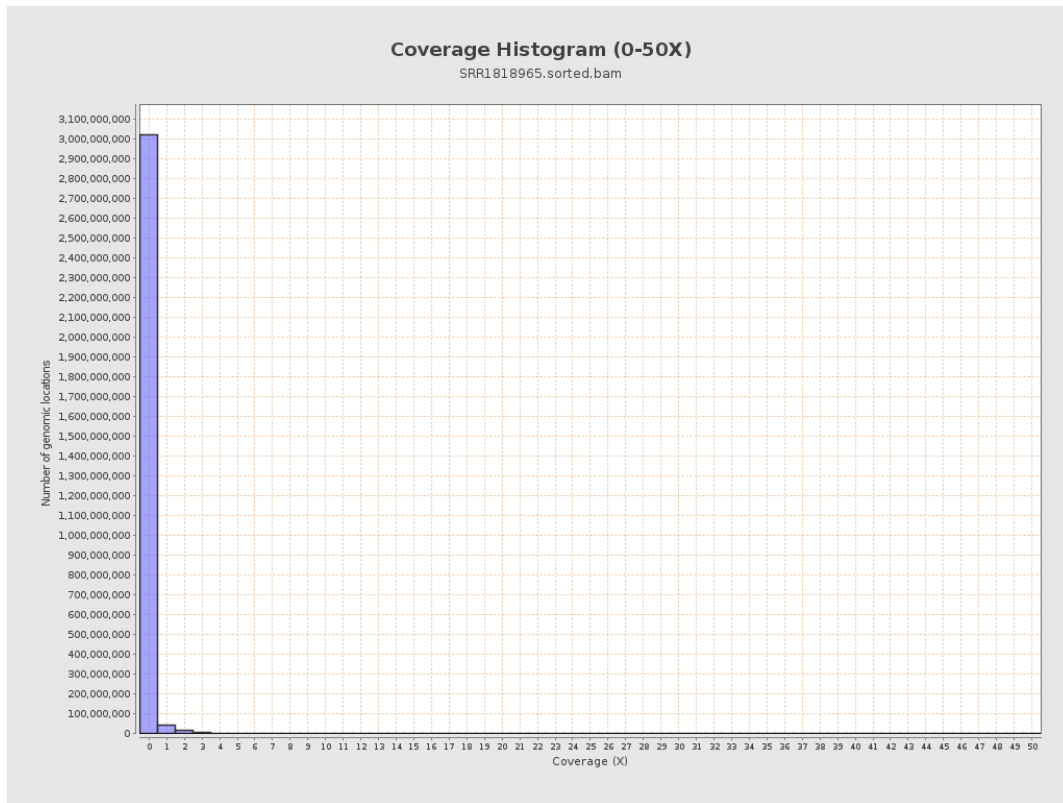
3. Results : Coverage across reference



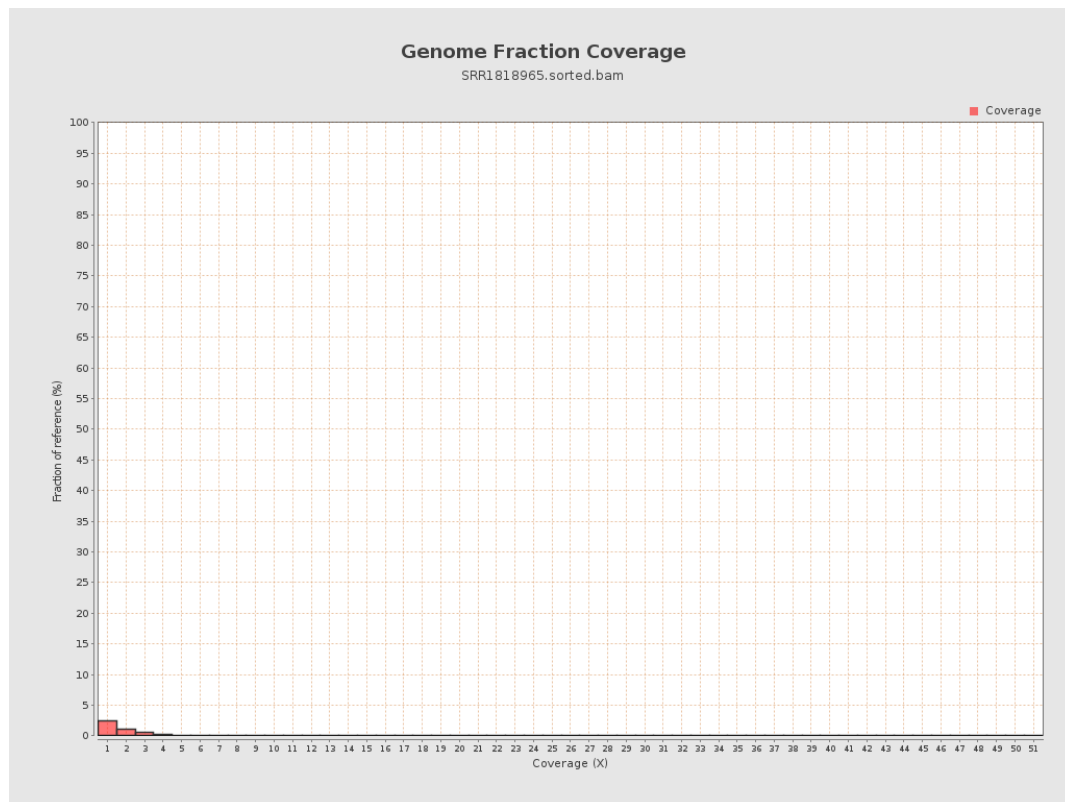
4. Results : Coverage Histogram



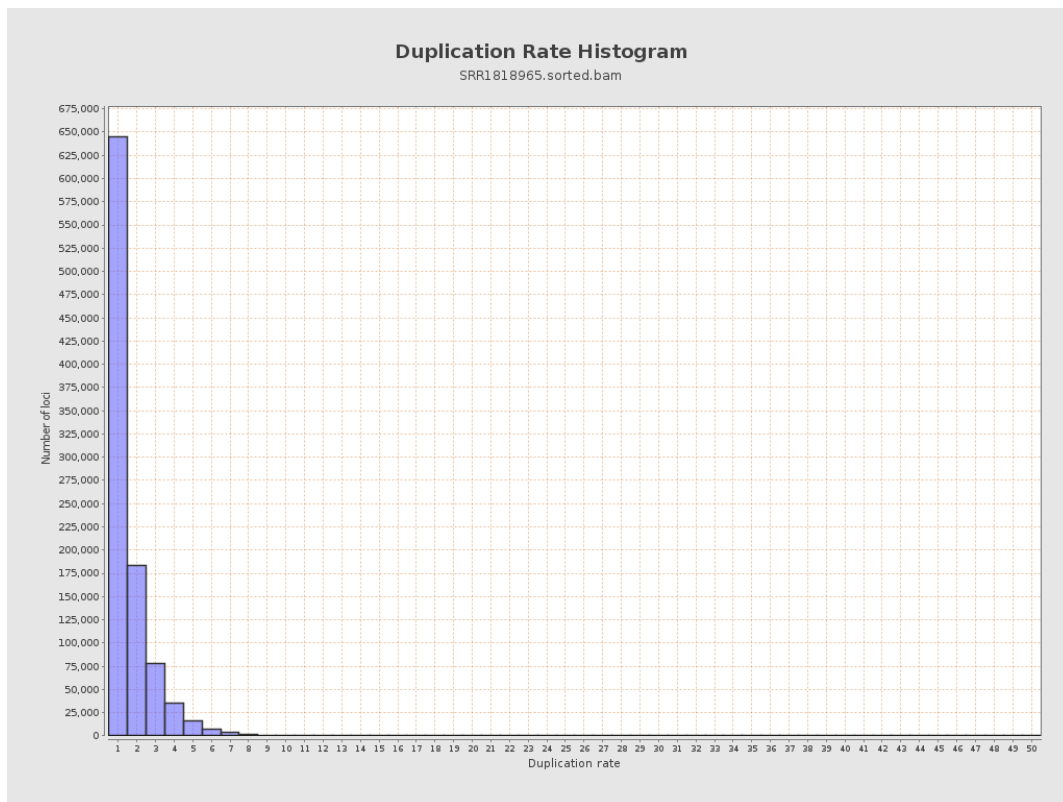
5. Results : Coverage Histogram (0-50X)



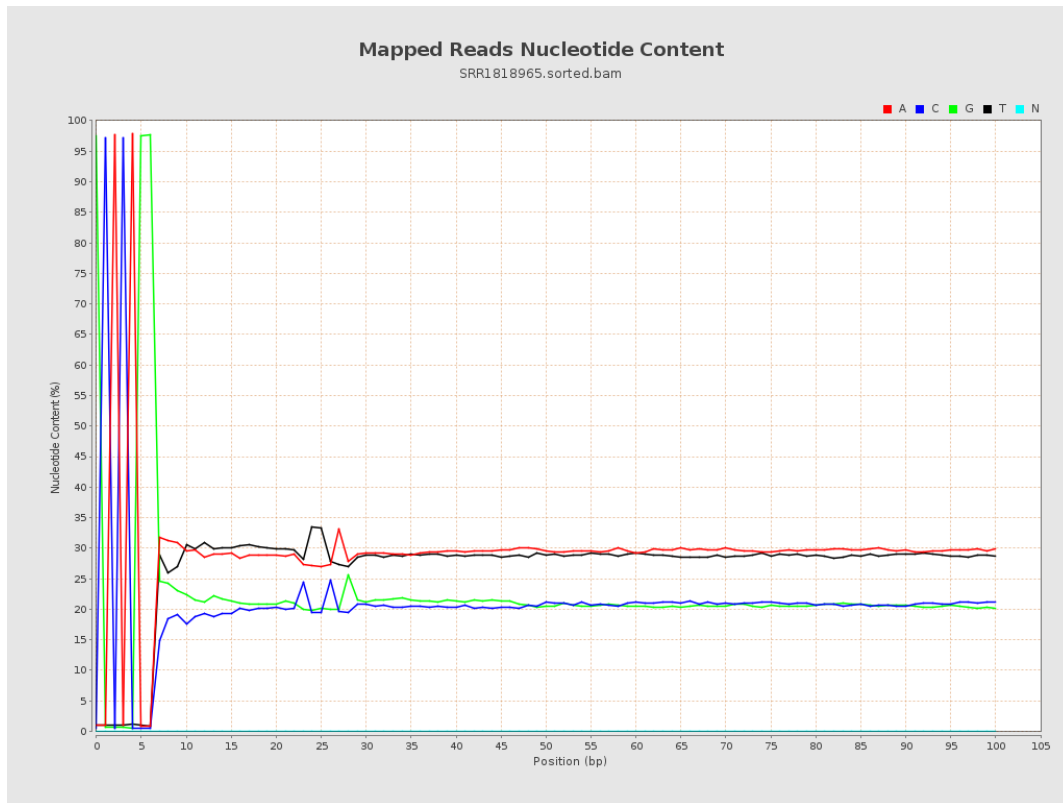
6. Results : Genome Fraction Coverage



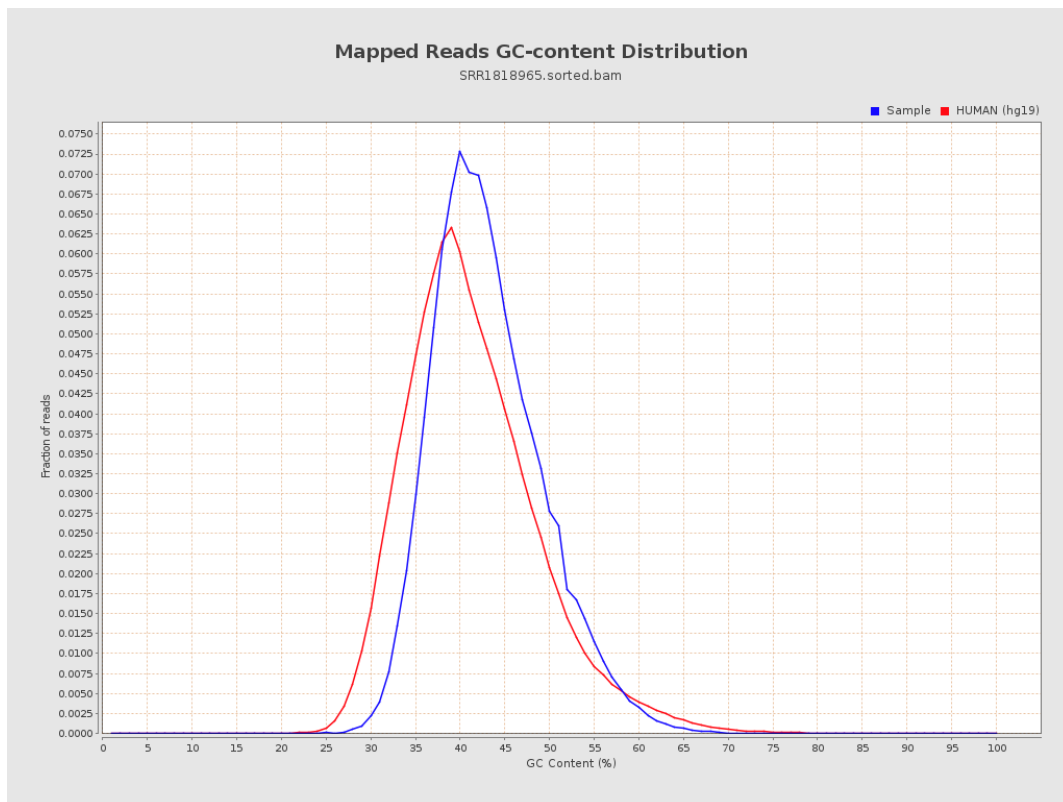
7. Results : Duplication Rate Histogram



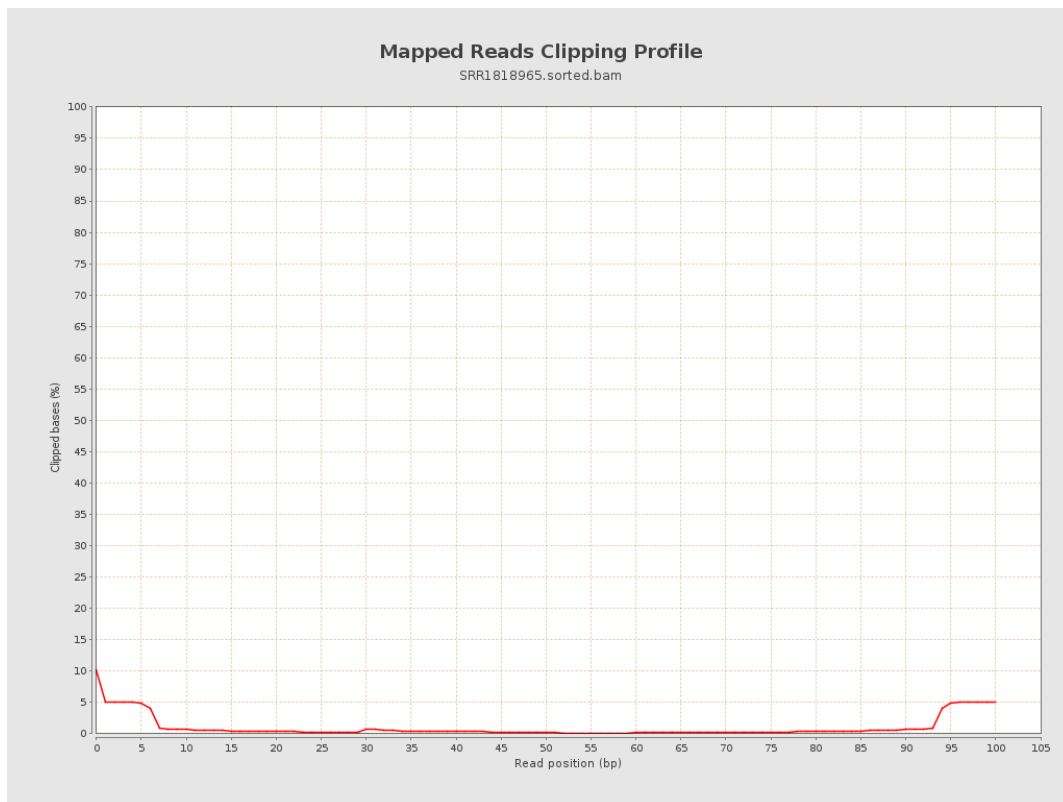
8. Results : Mapped Reads Nucleotide Content



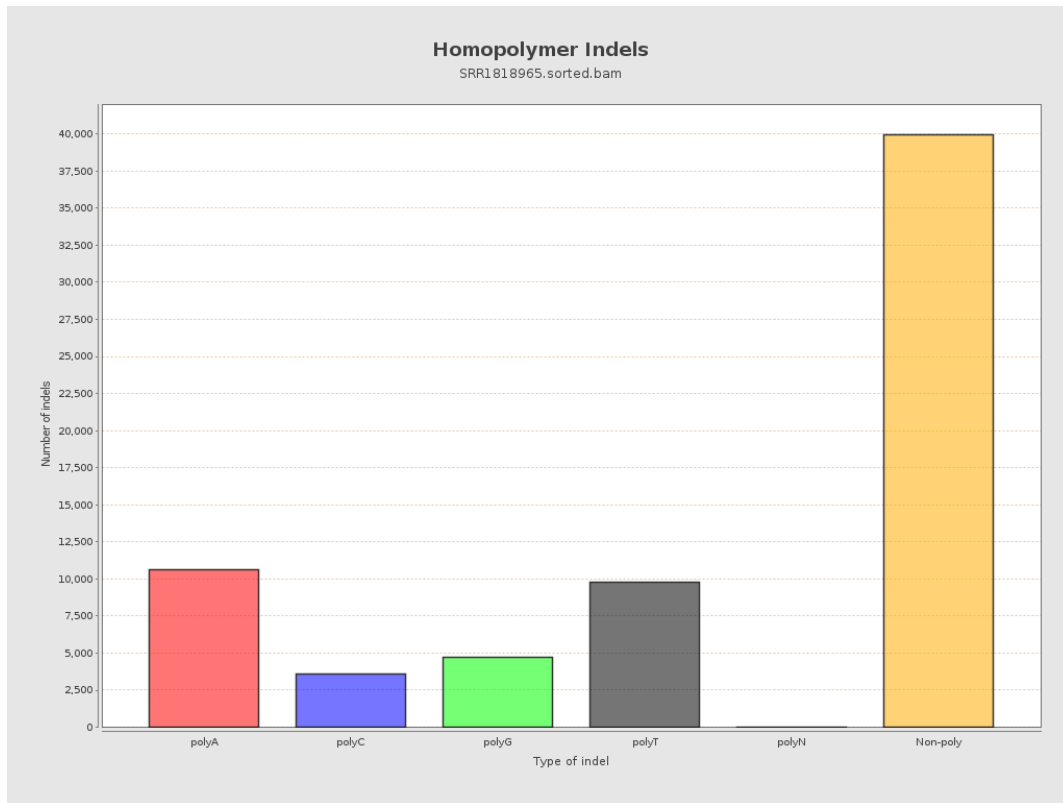
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

