

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:11:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818861.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_SRR1818861 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818861.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:11:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,003,130
Mapped reads	981,603 / 97.85%
Unmapped reads	21,527 / 2.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,356 / 1.63%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	173,347 / 17.28%
Duplication rate	14.89%
Clipped reads	994,680 / 99.16%

2.2. ACGT Content

Number/percentage of A's	25,401,381 / 28.01%
Number/percentage of C's	18,627,239 / 20.54%
Number/percentage of T's	26,494,637 / 29.21%
Number/percentage of G's	20,171,184 / 22.24%
Number/percentage of N's	1,300 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.3931
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2.4. Mapping Quality

Mean Mapping Quality	49.38
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2.5. Mismatches and indels

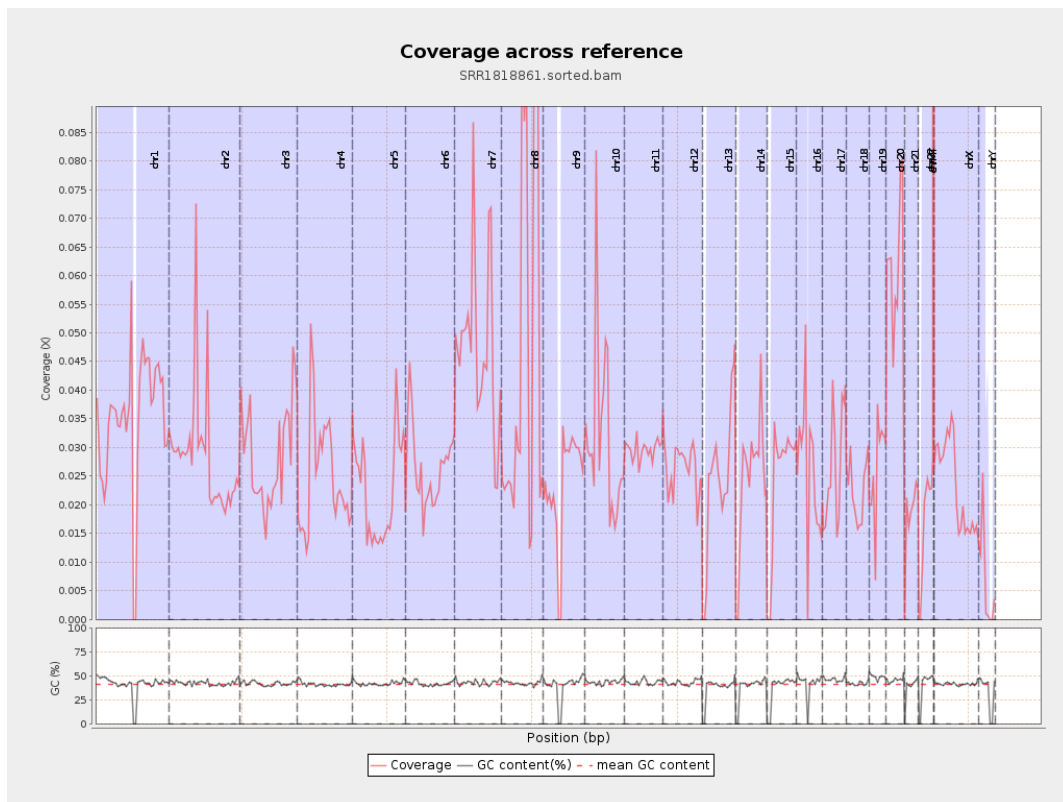
General error rate	0.66%
Mismatches	564,312
Insertions	11,819
Mapped reads with at least one insertion	1.16%
Deletions	30,139
Mapped reads with at least one deletion	3%
Homopolymer indels	42.43%

2.6. Chromosome stats

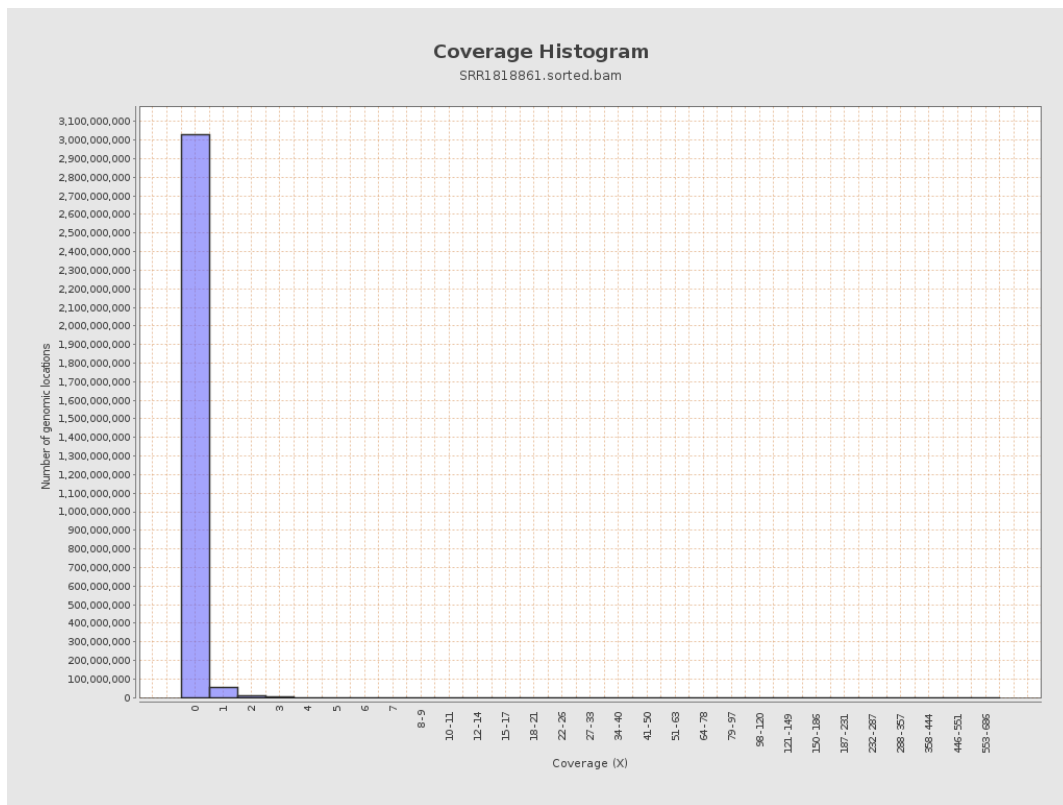
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8675755	0.0348	0.6048
chr2	243199373	6948469	0.0286	0.576
chr3	198022430	5663224	0.0286	0.2108
chr4	191154276	4673799	0.0245	0.2619
chr5	180915260	4055900	0.0224	0.1949
chr6	171115067	4504156	0.0263	0.2173
chr7	159138663	7654250	0.0481	0.7785

chr8	146364022	7944000	0.0543	0.3529
chr9	141213431	3328081	0.0236	0.3044
chr10	135534747	4280047	0.0316	0.5297
chr11	135006516	3998495	0.0296	0.2573
chr12	133851895	3548491	0.0265	0.2057
chr13	115169878	2775172	0.0241	0.1947
chr14	107349540	2630052	0.0245	0.2072
chr15	102531392	2504154	0.0244	0.1926
chr16	90354753	2305499	0.0255	0.3963
chr17	81195210	2186416	0.0269	0.2392
chr18	78077248	1755213	0.0225	0.359
chr19	59128983	1556438	0.0263	0.4751
chr20	63025520	3869705	0.0614	0.3277
chr21	48129895	892920	0.0186	0.2119
chr22	51304566	826364	0.0161	0.1683
chrMT	16571	145149	8.7592	6.5057
chrX	155270560	3646247	0.0235	0.2152
chrY	59373566	386529	0.0065	0.4939

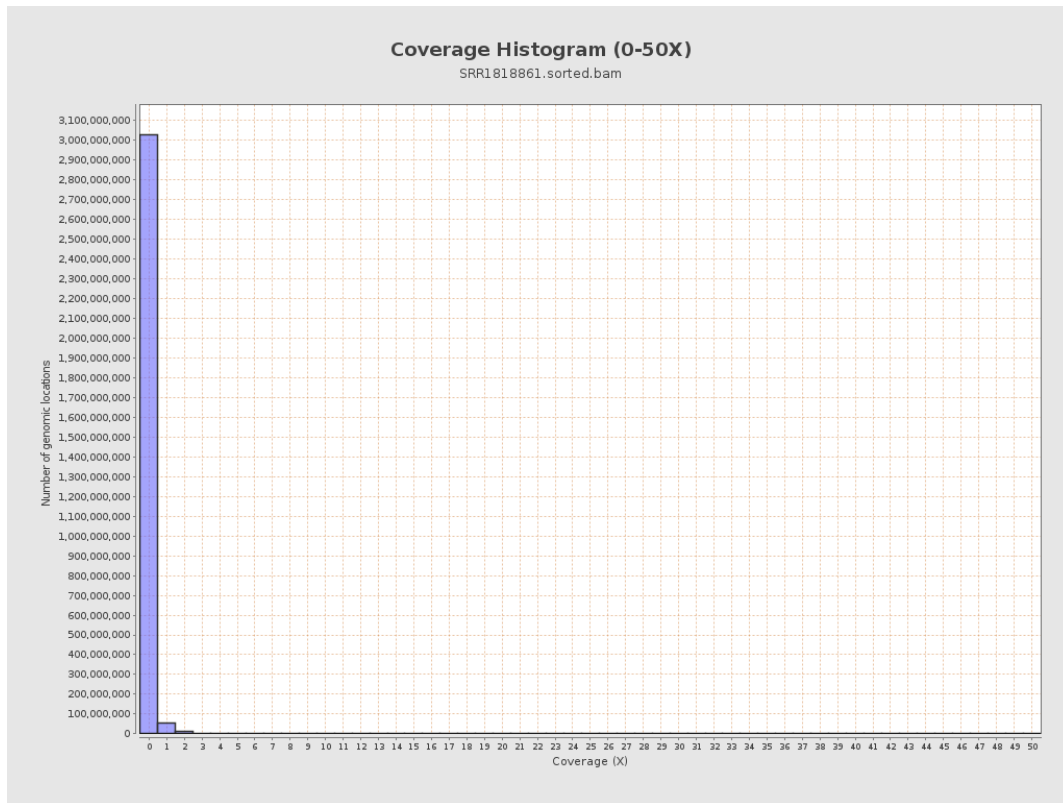
3. Results : Coverage across reference



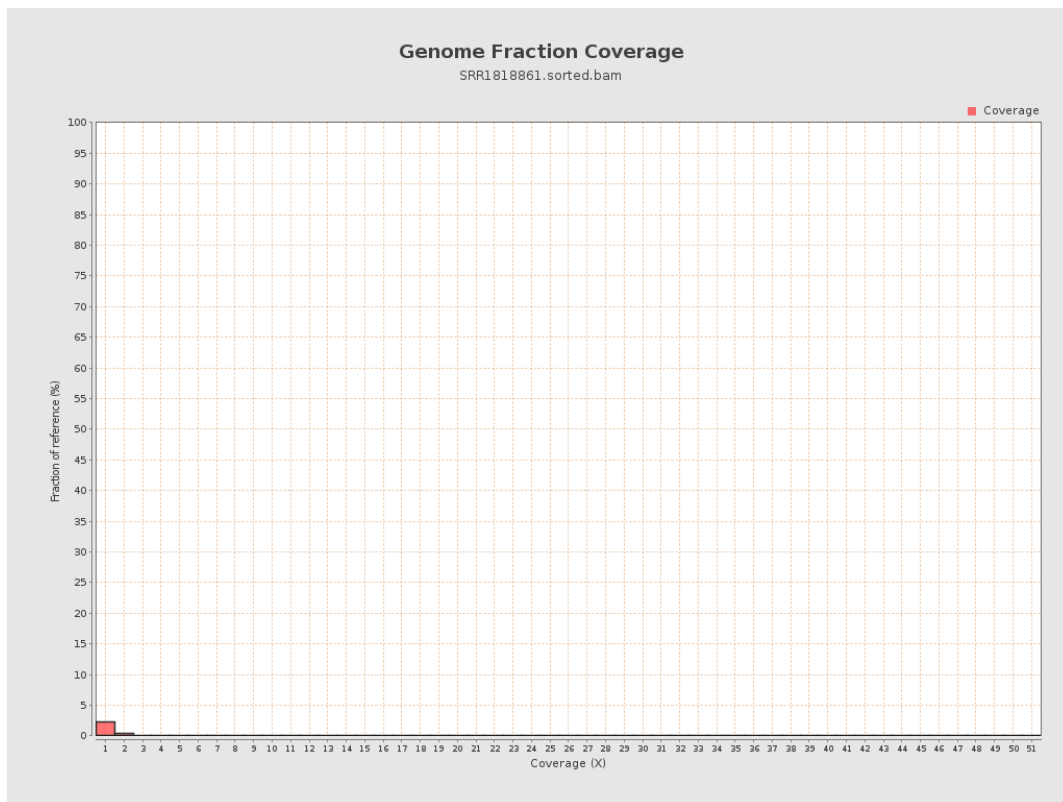
4. Results : Coverage Histogram



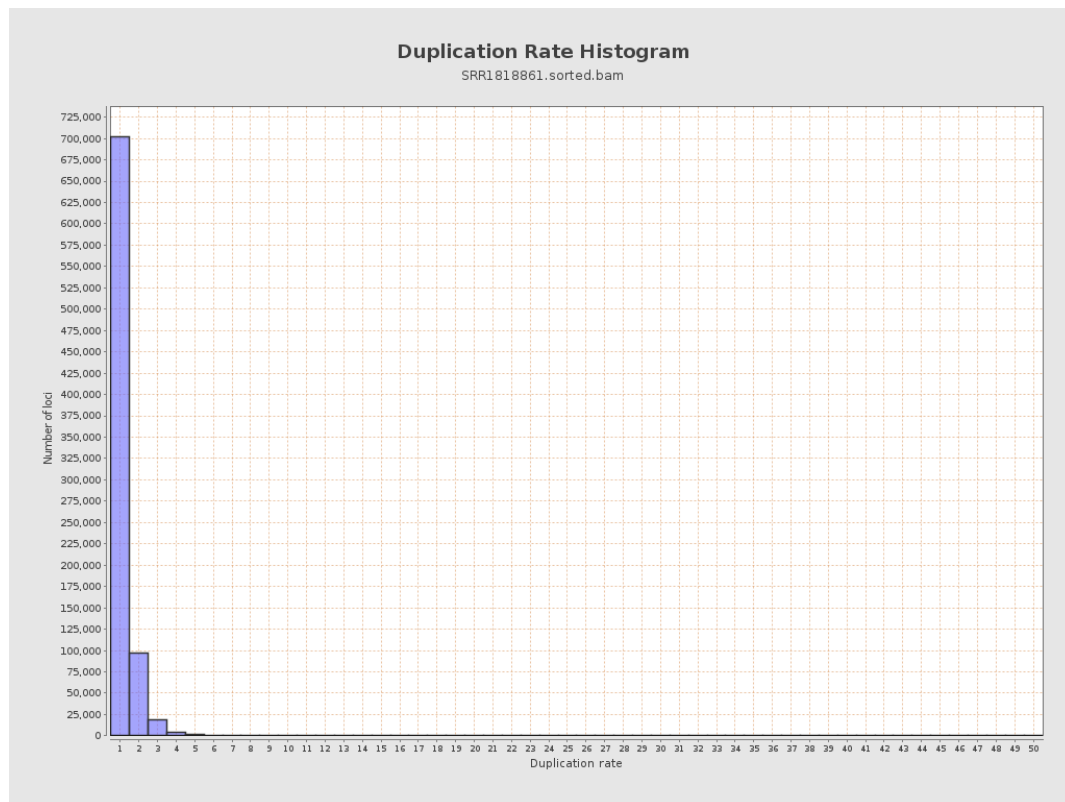
5. Results : Coverage Histogram (0-50X)



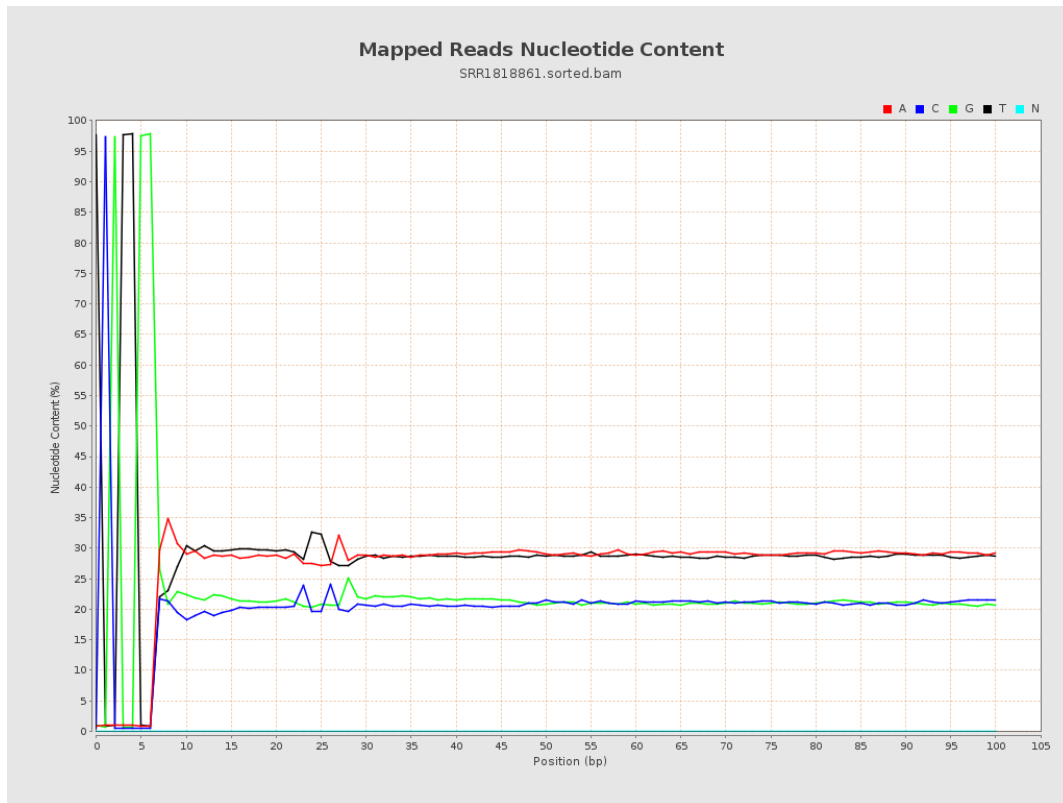
6. Results : Genome Fraction Coverage



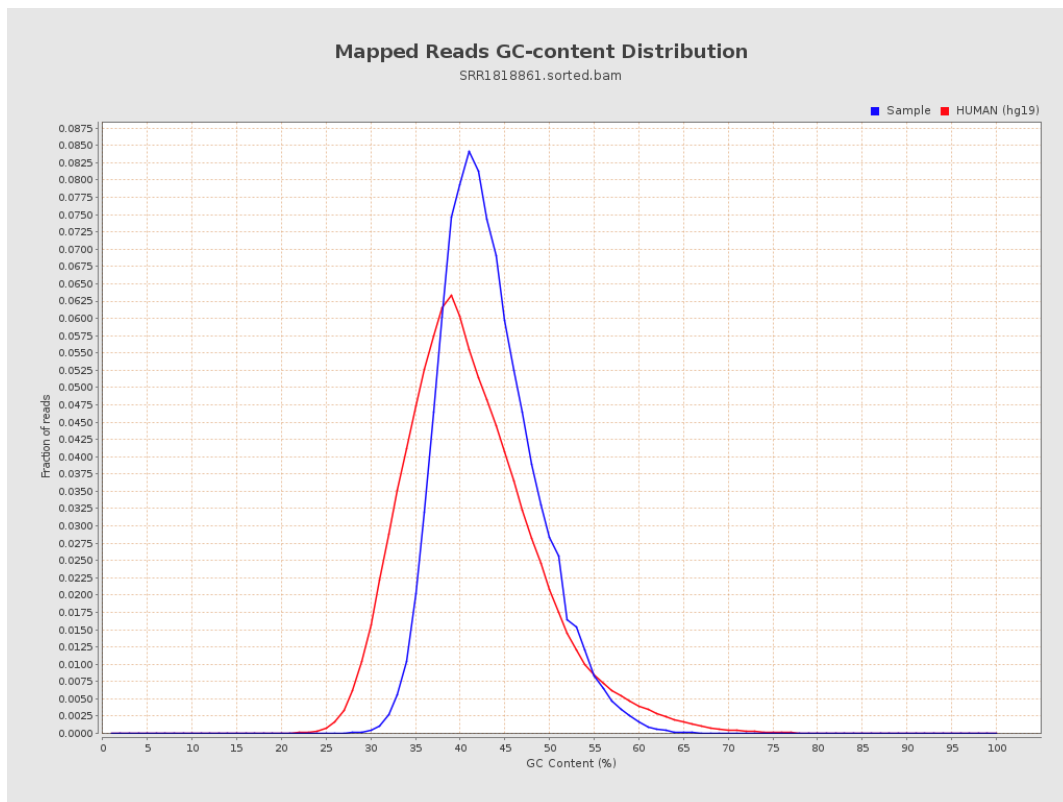
7. Results : Duplication Rate Histogram



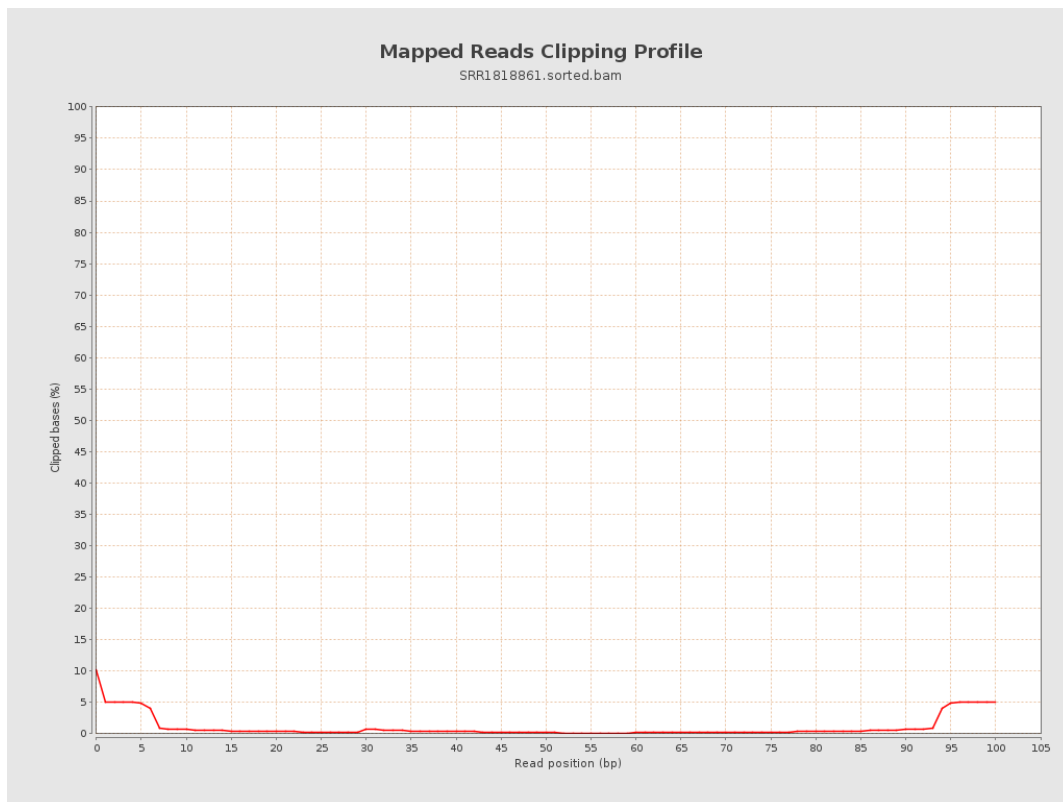
8. Results : Mapped Reads Nucleotide Content



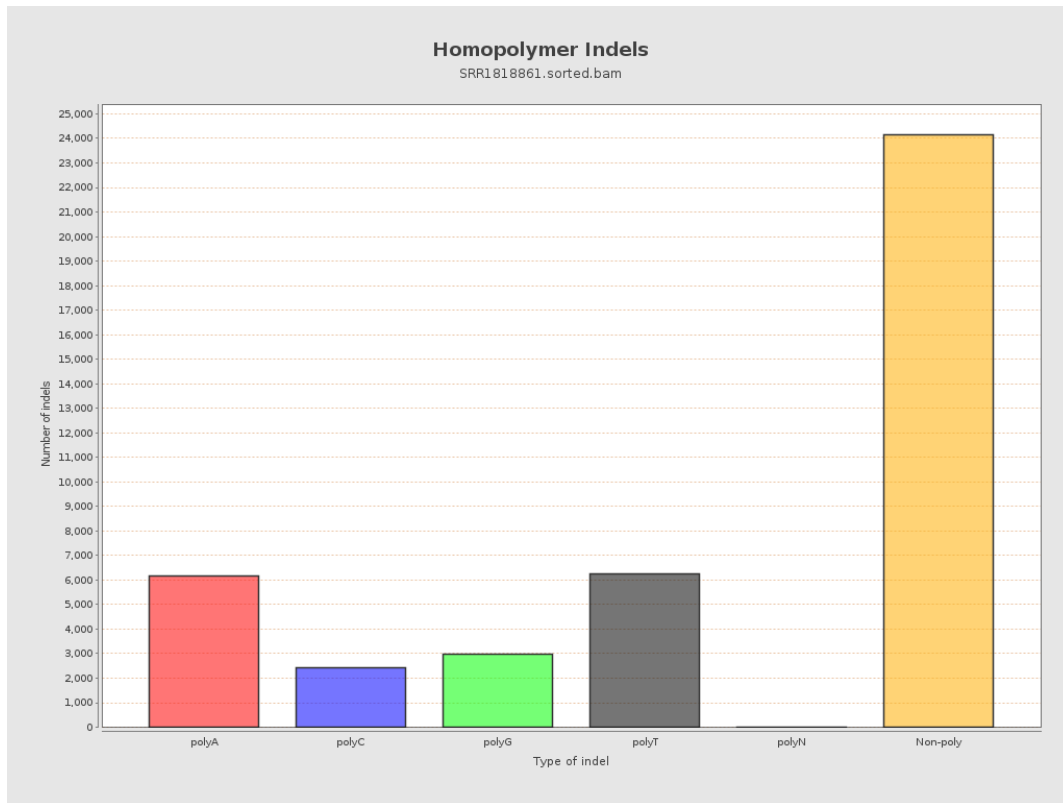
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

