

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:25:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818823.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_SRR1818823 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818823.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:25:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818823.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,600,064
Mapped reads	1,559,067 / 97.44%
Unmapped reads	40,997 / 2.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,259 / 0.83%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	699,835 / 43.74%
Duplication rate	37.95%
Clipped reads	1,558,569 / 97.41%

2.2. ACGT Content

Number/percentage of A's	29,756,269 / 28.14%
Number/percentage of C's	22,755,298 / 21.52%
Number/percentage of T's	30,420,818 / 28.76%
Number/percentage of G's	22,819,015 / 21.58%
Number/percentage of N's	6,196 / 0.01%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0342

Standard Deviation	0.4602
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2.4. Mapping Quality

Mean Mapping Quality	47.61
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2.5. Mismatches and indels

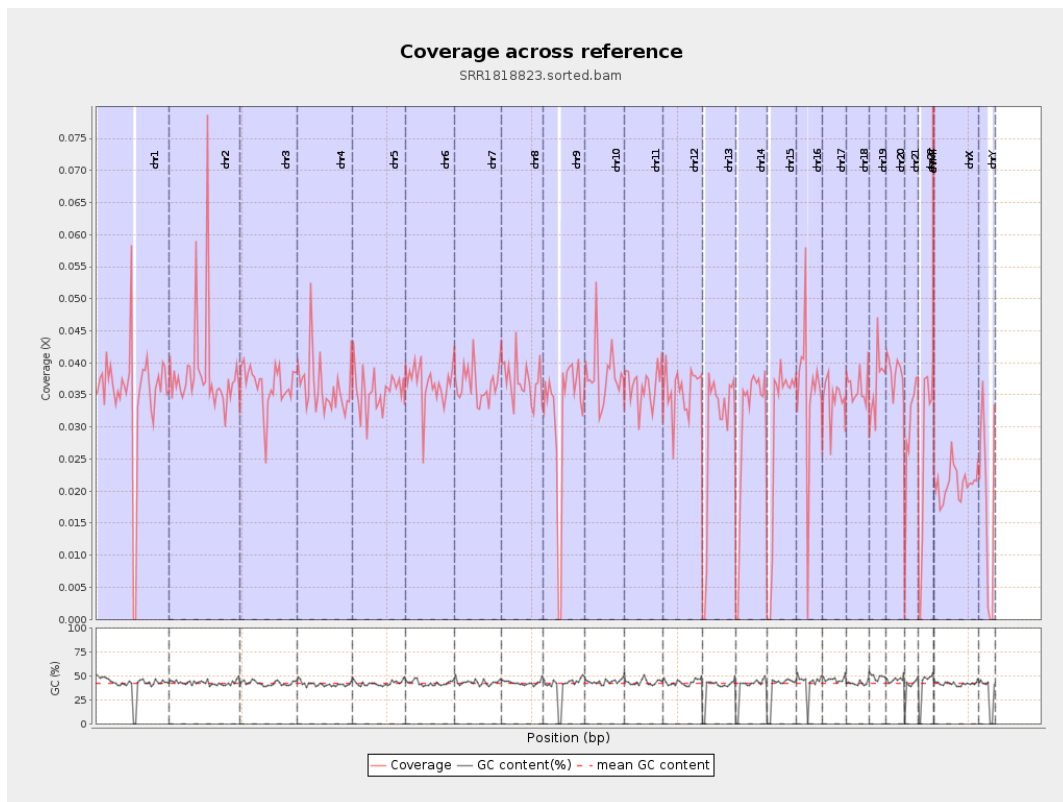
General error rate	0.54%
Mismatches	548,508
Insertions	13,194
Mapped reads with at least one insertion	0.83%
Deletions	27,350
Mapped reads with at least one deletion	1.74%
Homopolymer indels	38.96%

2.6. Chromosome stats

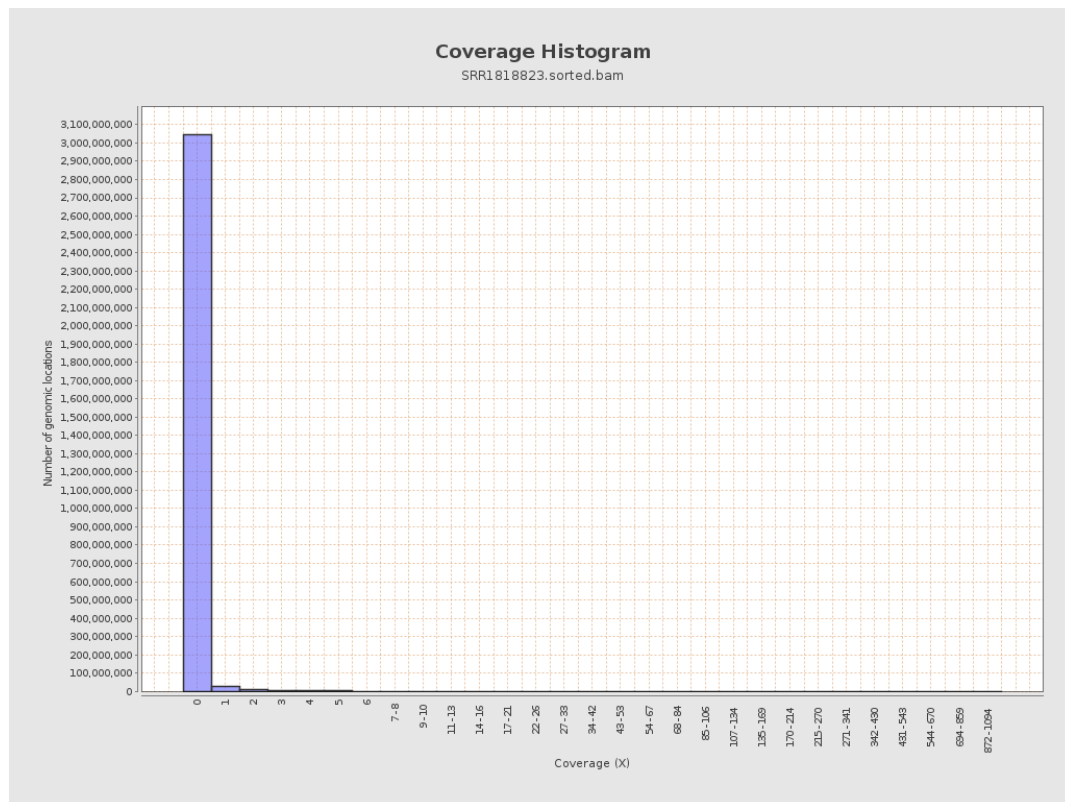
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8731723	0.035	0.6122
chr2	243199373	9387264	0.0386	0.7817
chr3	198022430	7216453	0.0364	0.3438
chr4	191154276	6915318	0.0362	0.4054
chr5	180915260	6433865	0.0356	0.3537
chr6	171115067	6295403	0.0368	0.3775
chr7	159138663	5825572	0.0366	0.3974

chr8	146364022	5431220	0.0371	0.3796
chr9	141213431	4523141	0.032	0.3765
chr10	135534747	5139335	0.0379	0.5017
chr11	135006516	4910556	0.0364	0.389
chr12	133851895	4781634	0.0357	0.365
chr13	115169878	3345278	0.029	0.3057
chr14	107349540	3233433	0.0301	0.3675
chr15	102531392	3040589	0.0297	0.3136
chr16	90354753	3224822	0.0357	0.5288
chr17	81195210	2783400	0.0343	0.3534
chr18	78077248	2822354	0.0361	0.4692
chr19	59128983	2175458	0.0368	0.521
chr20	63025520	2420543	0.0384	0.3776
chr21	48129895	1424636	0.0296	0.3302
chr22	51304566	1285872	0.0251	0.3068
chrMT	16571	82351	4.9696	5.1684
chrX	155270560	3302434	0.0213	0.287
chrY	59373566	1069699	0.018	0.7826

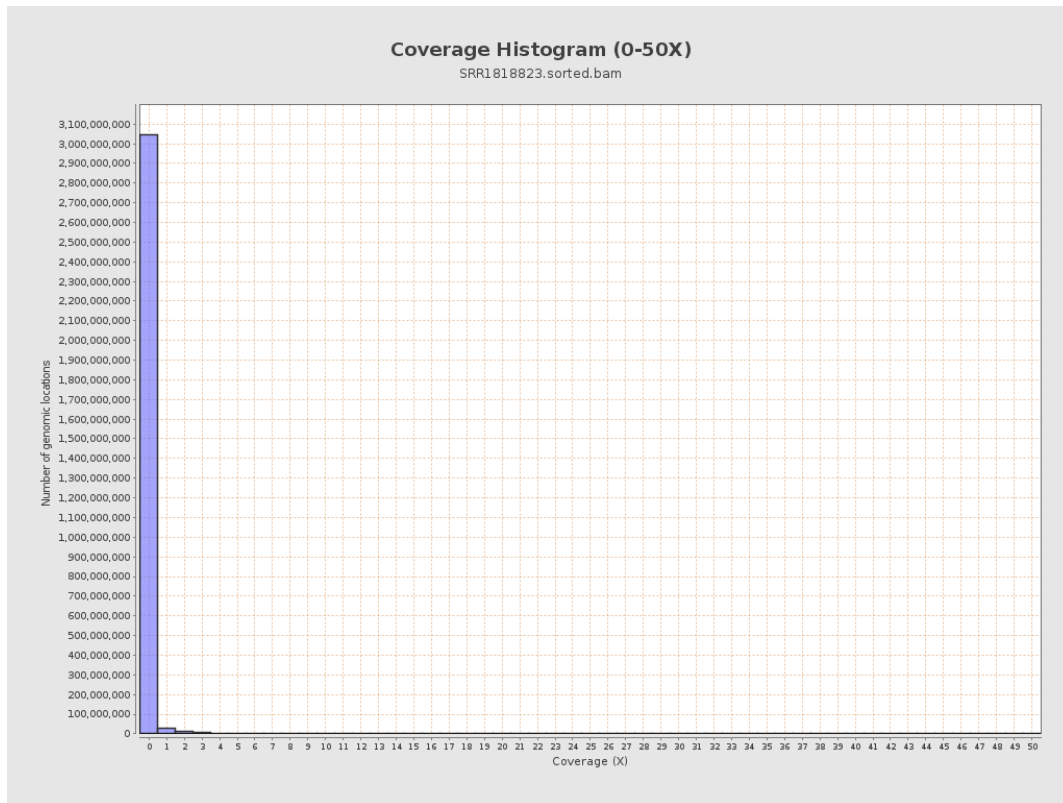
3. Results : Coverage across reference



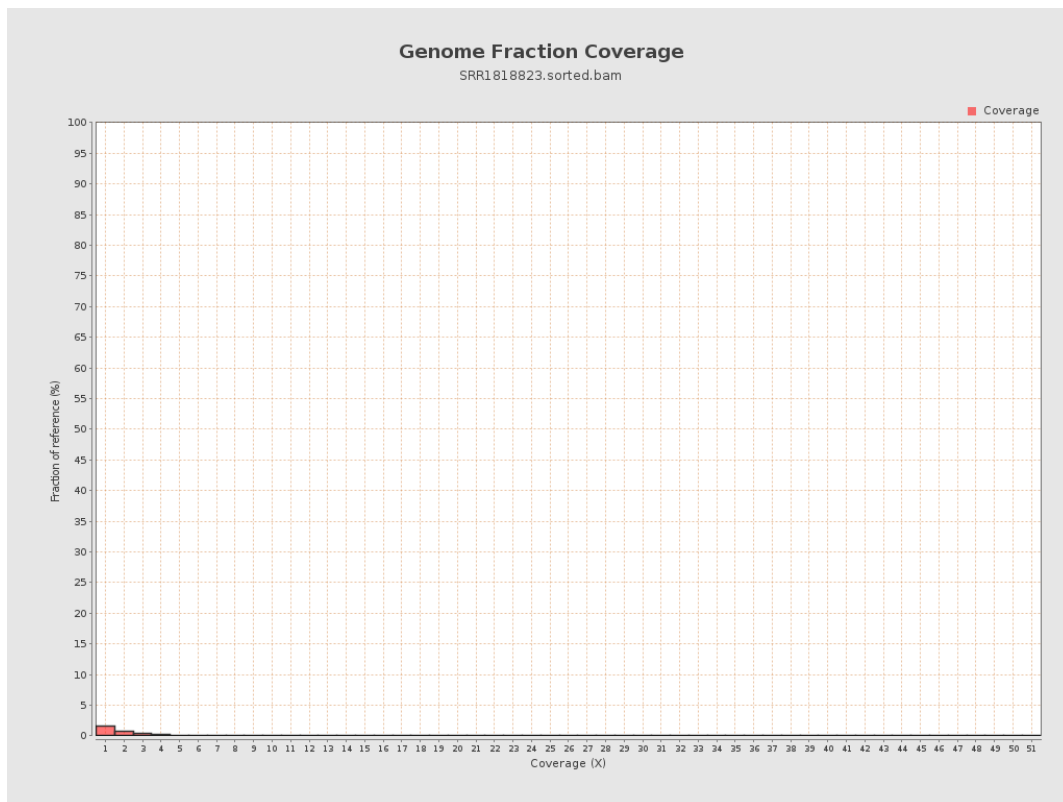
4. Results : Coverage Histogram



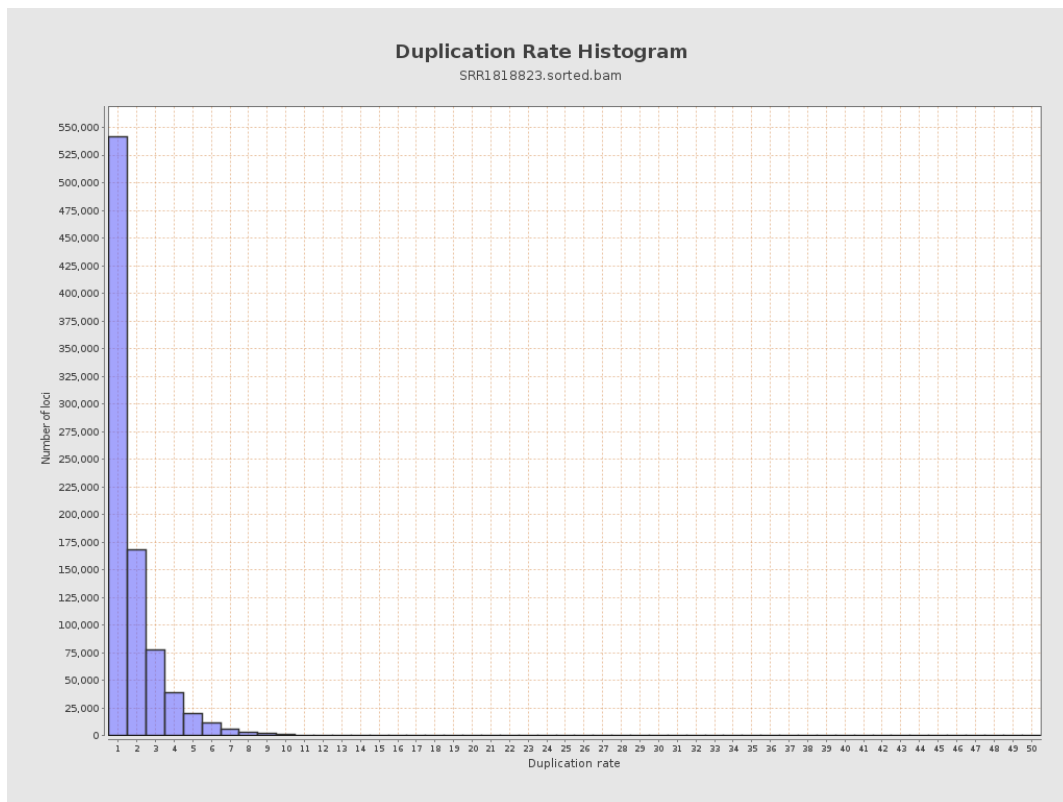
5. Results : Coverage Histogram (0-50X)



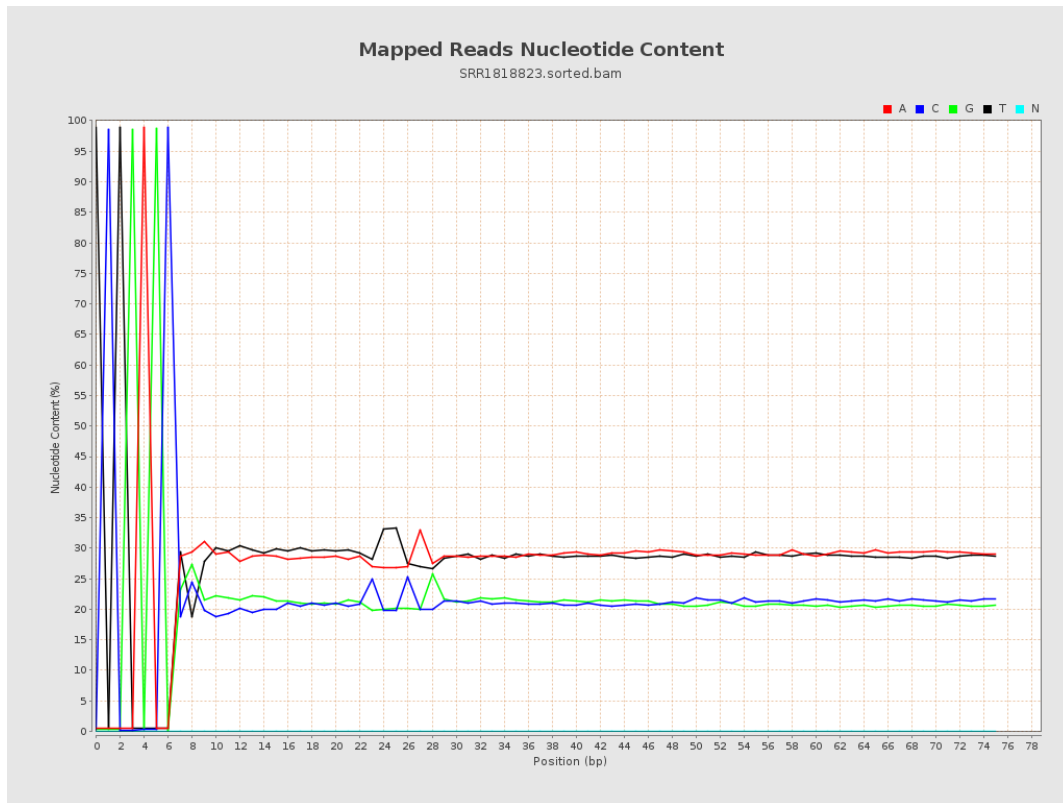
6. Results : Genome Fraction Coverage



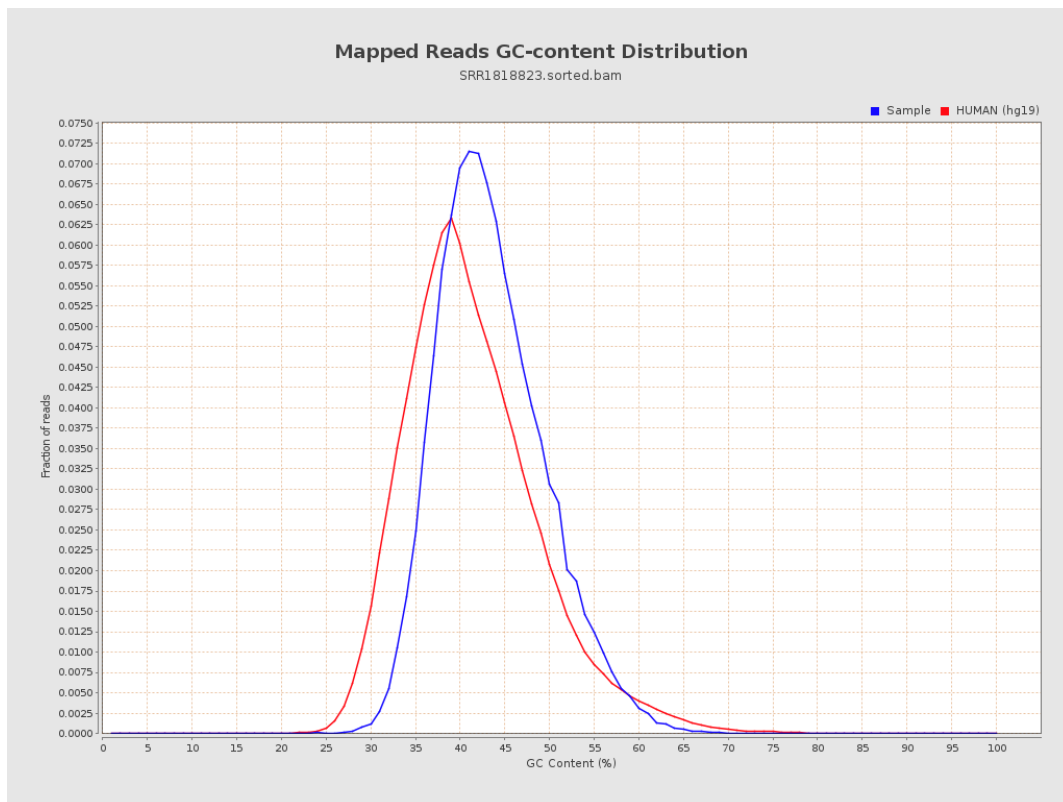
7. Results : Duplication Rate Histogram



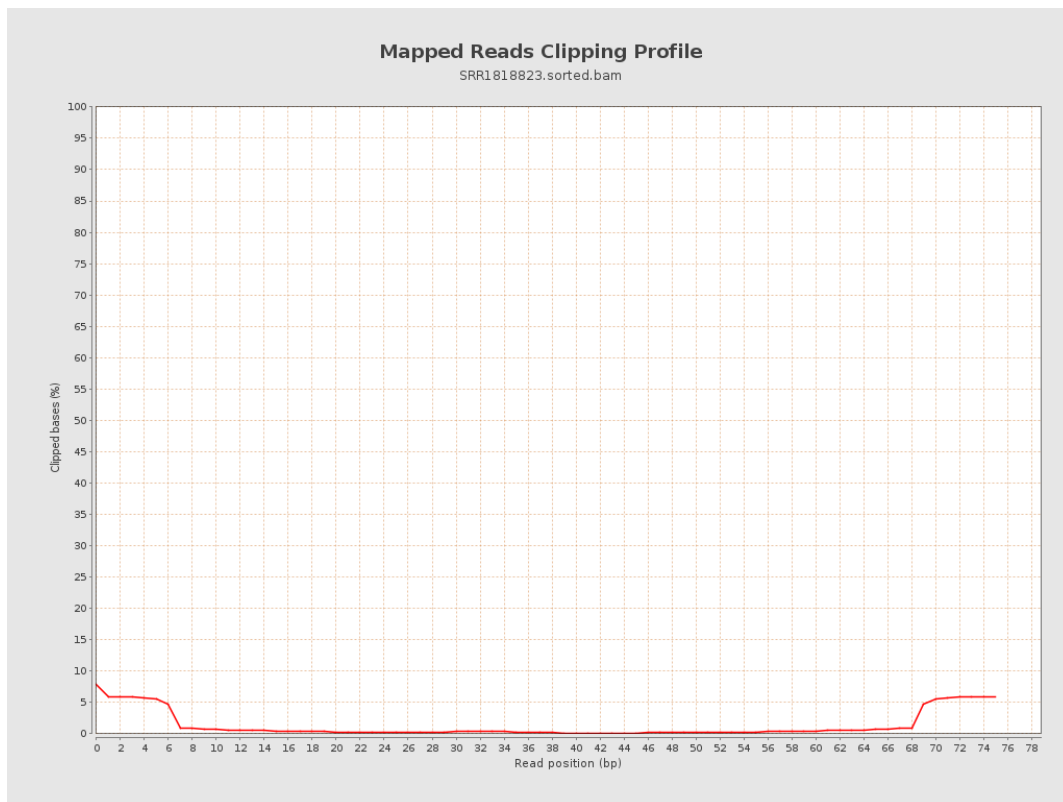
8. Results : Mapped Reads Nucleotide Content



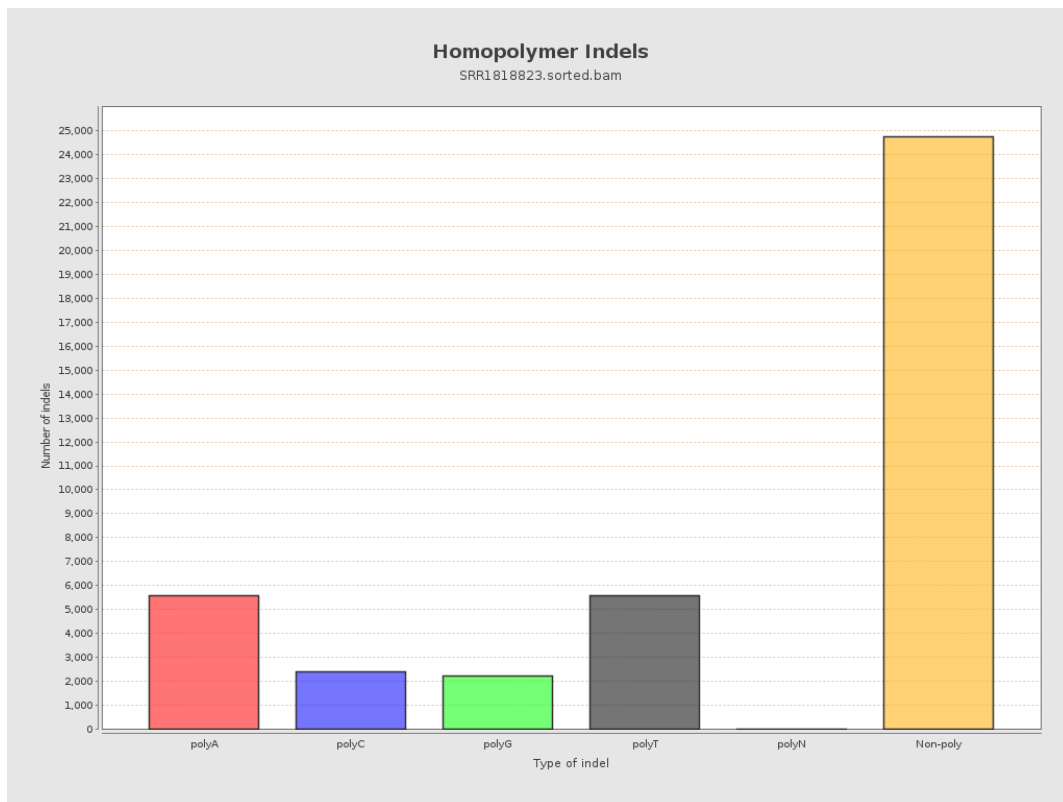
9. Results : Mapped Reads GC-content Distribution



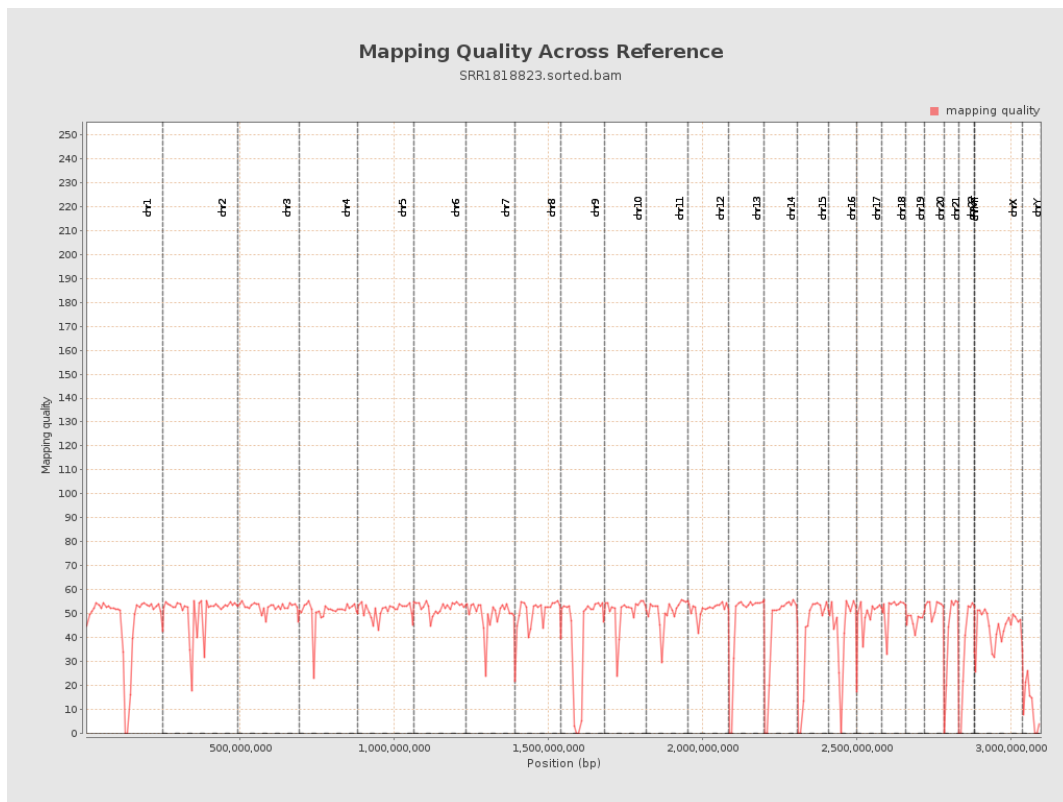
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

