

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:35:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818819.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_SRR1818819 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818819.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:35:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818819.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,612,290
Mapped reads	2,470,865 / 94.59%
Unmapped reads	141,425 / 5.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,202 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,238,730 / 47.42%
Duplication rate	41.39%
Clipped reads	2,475,899 / 94.78%

2.2. ACGT Content

Number/percentage of A's	49,931,161 / 29.72%
Number/percentage of C's	34,277,613 / 20.4%
Number/percentage of T's	46,818,494 / 27.87%
Number/percentage of G's	36,949,106 / 22%
Number/percentage of N's	10,219 / 0.01%
GC Percentage	42.4%

2.3. Coverage

Mean	0.0543

Standard Deviation	0.7023
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2.4. Mapping Quality

Mean Mapping Quality	47.77
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2.5. Mismatches and indels

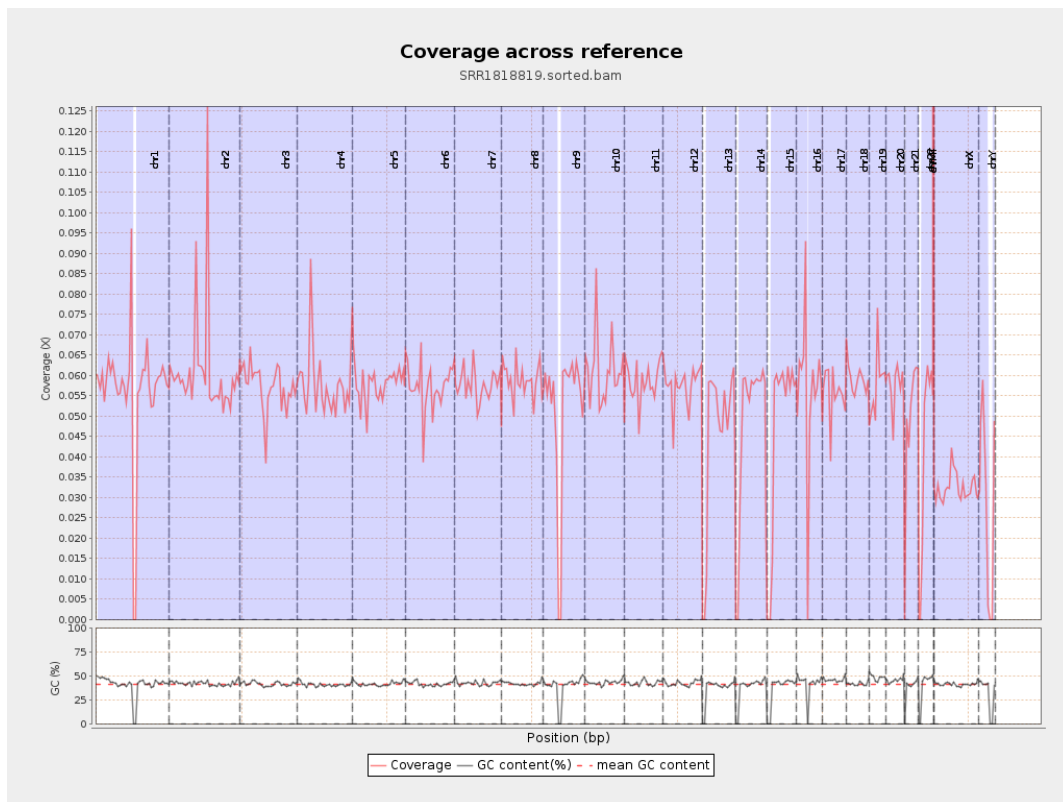
General error rate	0.53%
Mismatches	835,319
Insertions	21,827
Mapped reads with at least one insertion	0.87%
Deletions	41,555
Mapped reads with at least one deletion	1.67%
Homopolymer indels	41.33%

2.6. Chromosome stats

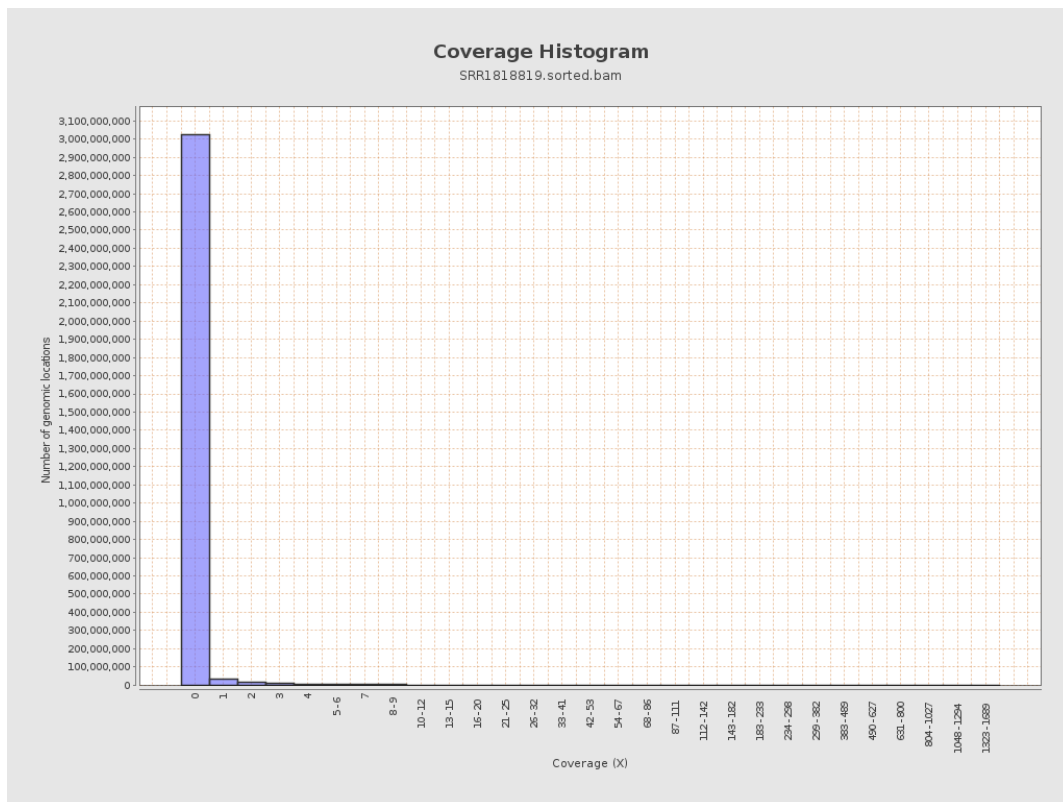
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14008746	0.0562	1.0169
chr2	243199373	14813459	0.0609	1.1885
chr3	198022430	11326869	0.0572	0.4811
chr4	191154276	11007213	0.0576	0.5914
chr5	180915260	10463462	0.0578	0.5064
chr6	171115067	9815212	0.0574	0.5401
chr7	159138663	9188489	0.0577	0.5901

chr8	146364022	8621842	0.0589	0.5486
chr9	141213431	7240178	0.0513	0.5312
chr10	135534747	8242291	0.0608	0.7958
chr11	135006516	7909011	0.0586	0.5459
chr12	133851895	7675139	0.0573	0.5206
chr13	115169878	5204206	0.0452	0.4196
chr14	107349540	5190702	0.0484	0.5198
chr15	102531392	4837051	0.0472	0.4419
chr16	90354753	5111479	0.0566	0.8174
chr17	81195210	4488882	0.0553	0.506
chr18	78077248	4612801	0.0591	0.7102
chr19	59128983	3437673	0.0581	0.8524
chr20	63025520	3617550	0.0574	0.5308
chr21	48129895	2375312	0.0494	0.4806
chr22	51304566	2068907	0.0403	0.451
chrMT	16571	88215	5.3235	5.9038
chrX	155270560	5054558	0.0326	0.4045
chrY	59373566	1655960	0.0279	1.3989

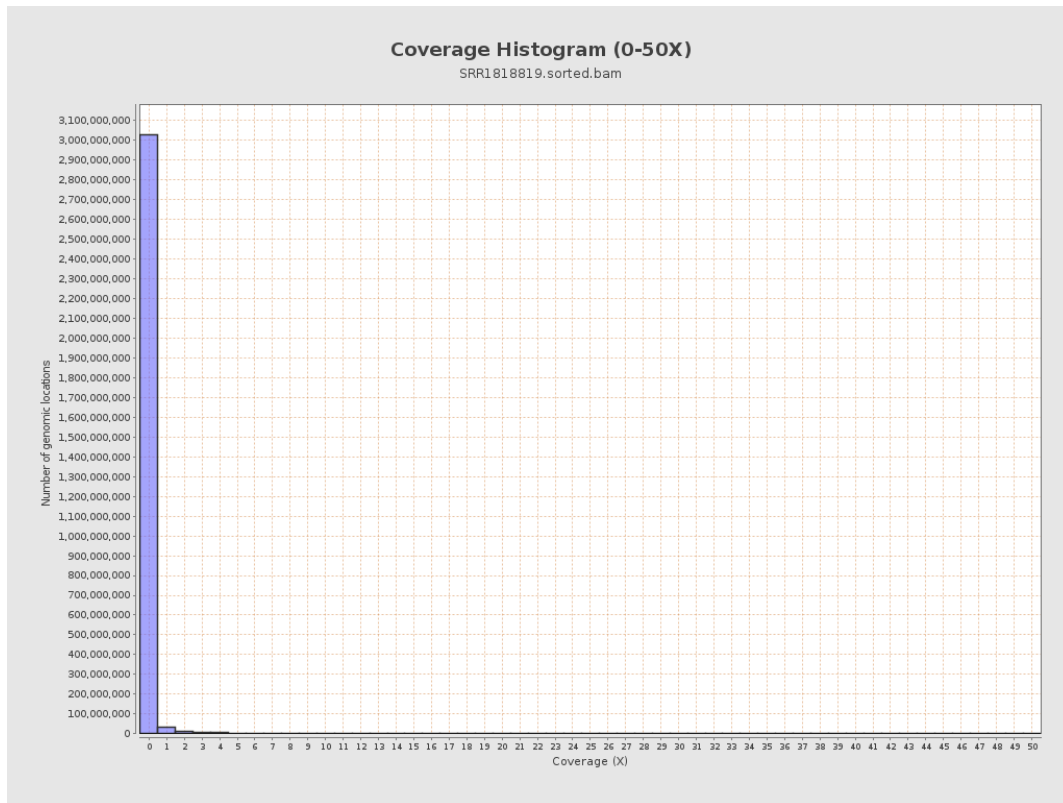
3. Results : Coverage across reference



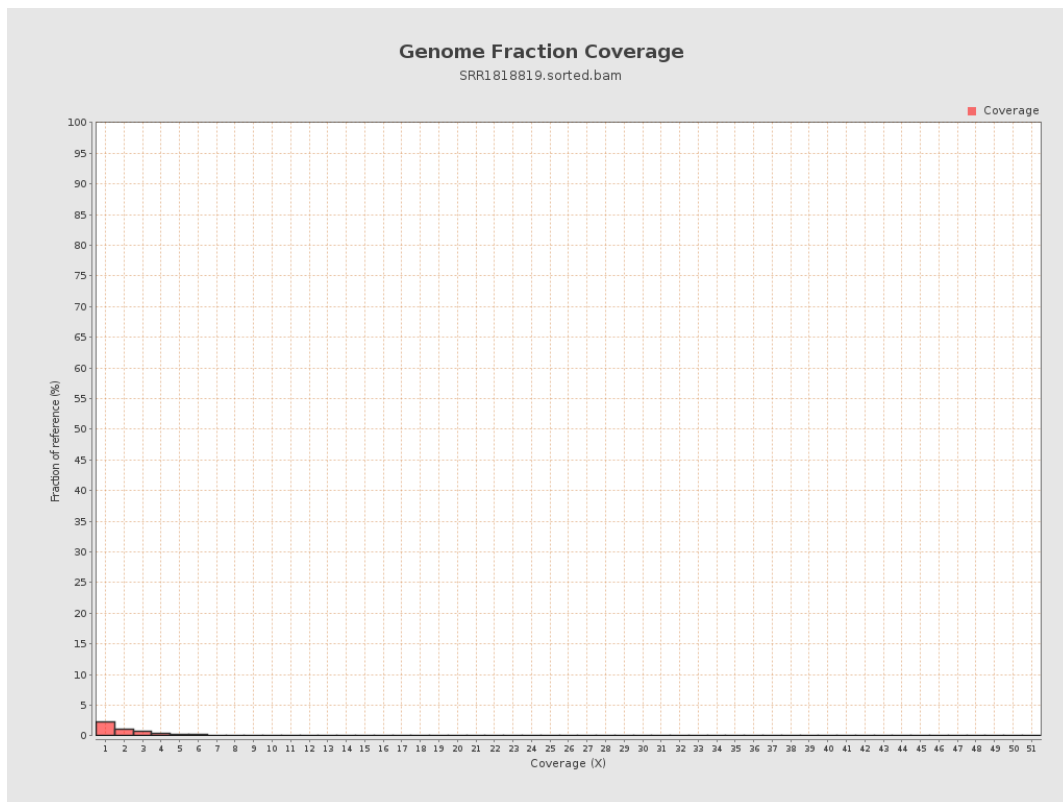
4. Results : Coverage Histogram



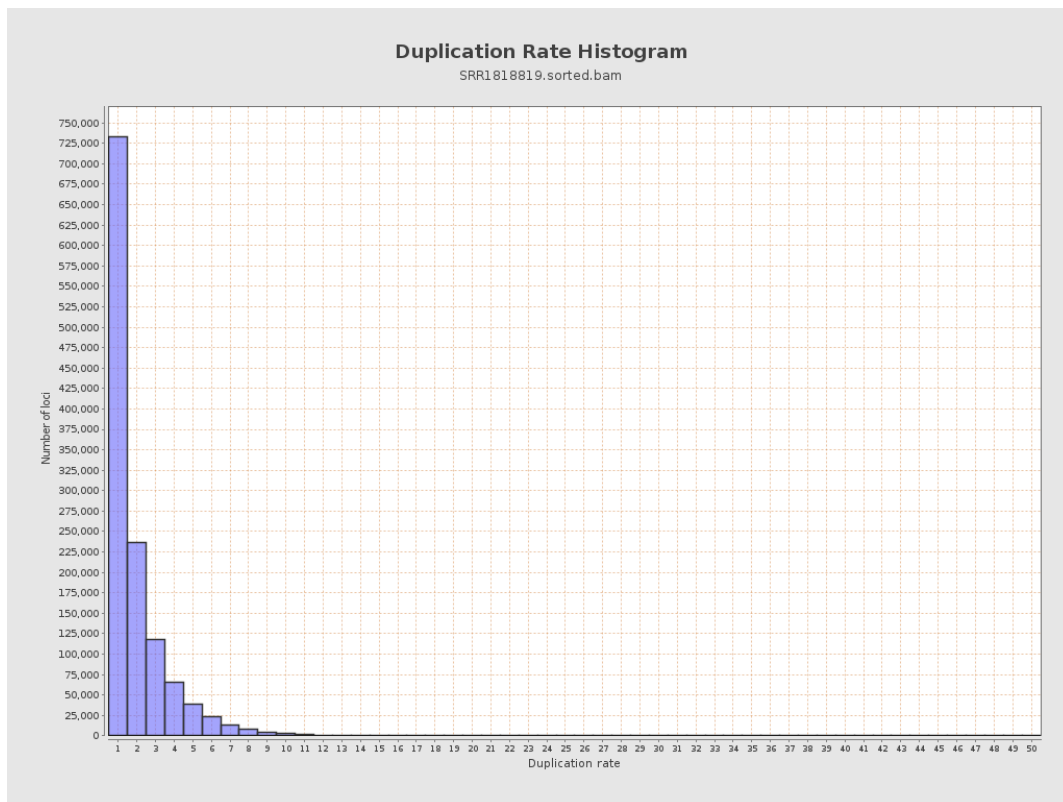
5. Results : Coverage Histogram (0-50X)



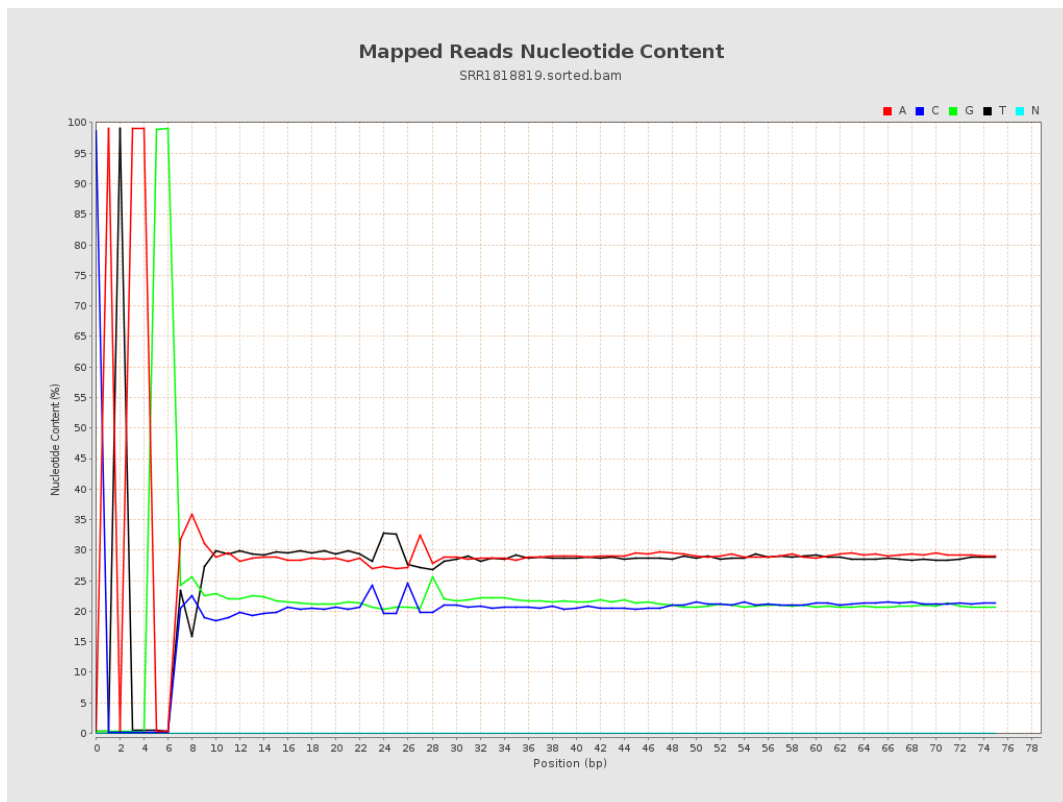
6. Results : Genome Fraction Coverage



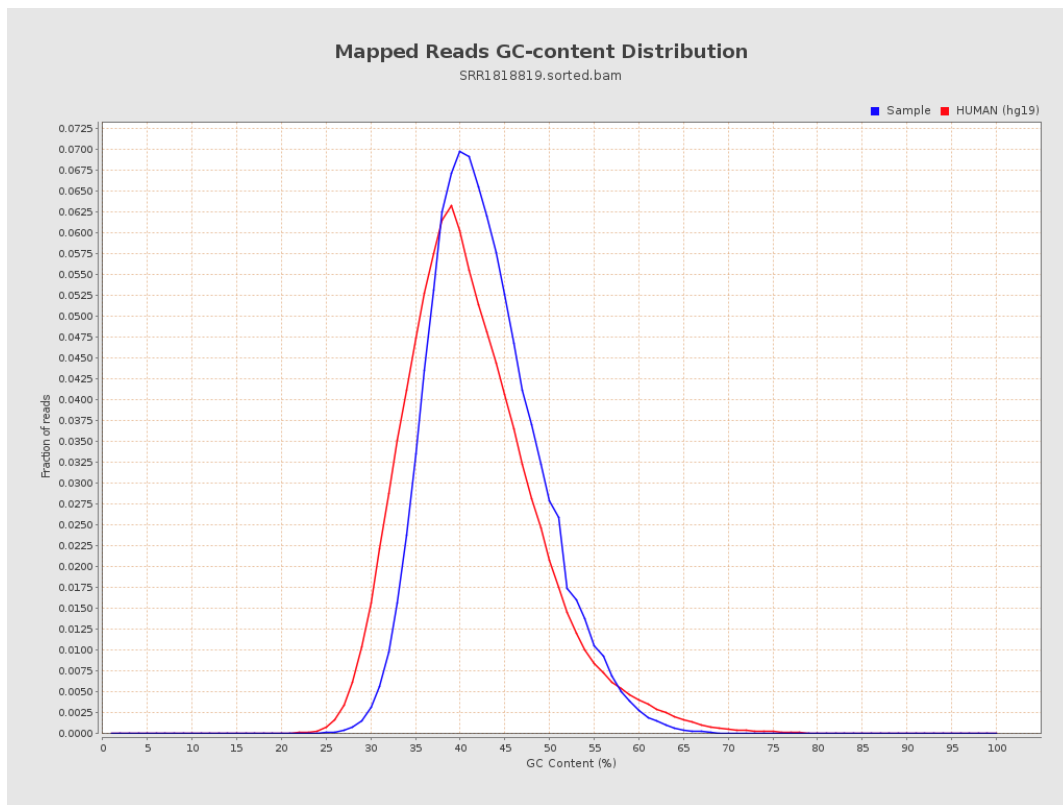
7. Results : Duplication Rate Histogram



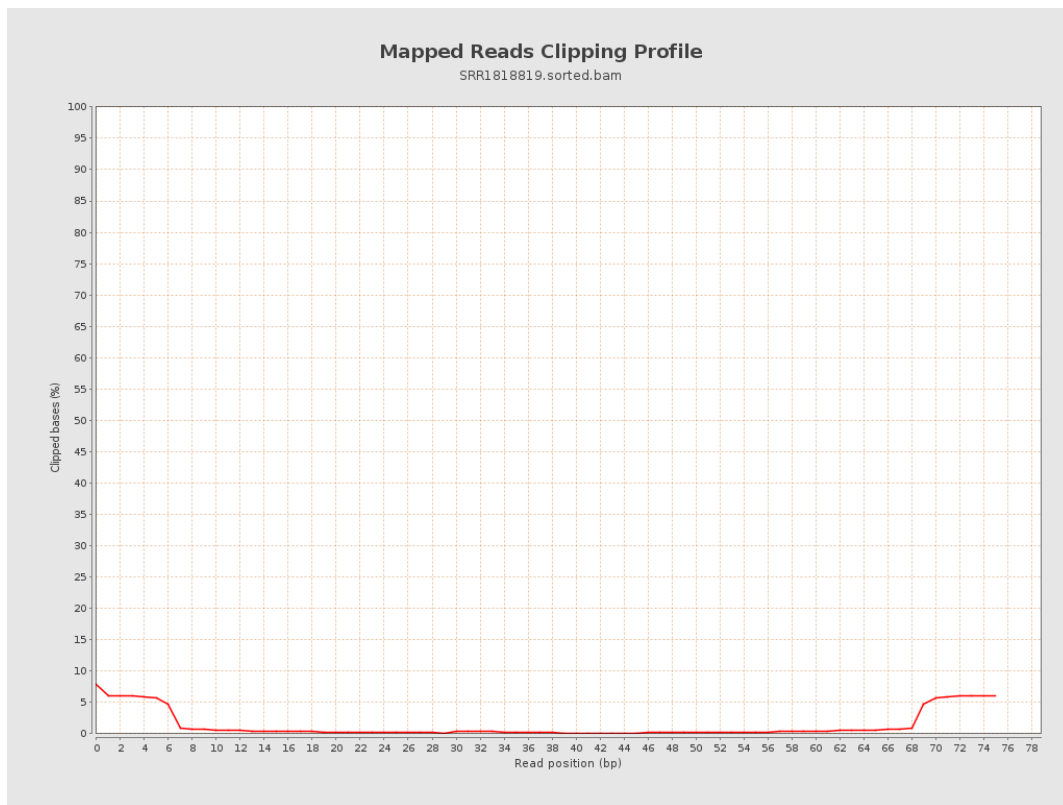
8. Results : Mapped Reads Nucleotide Content



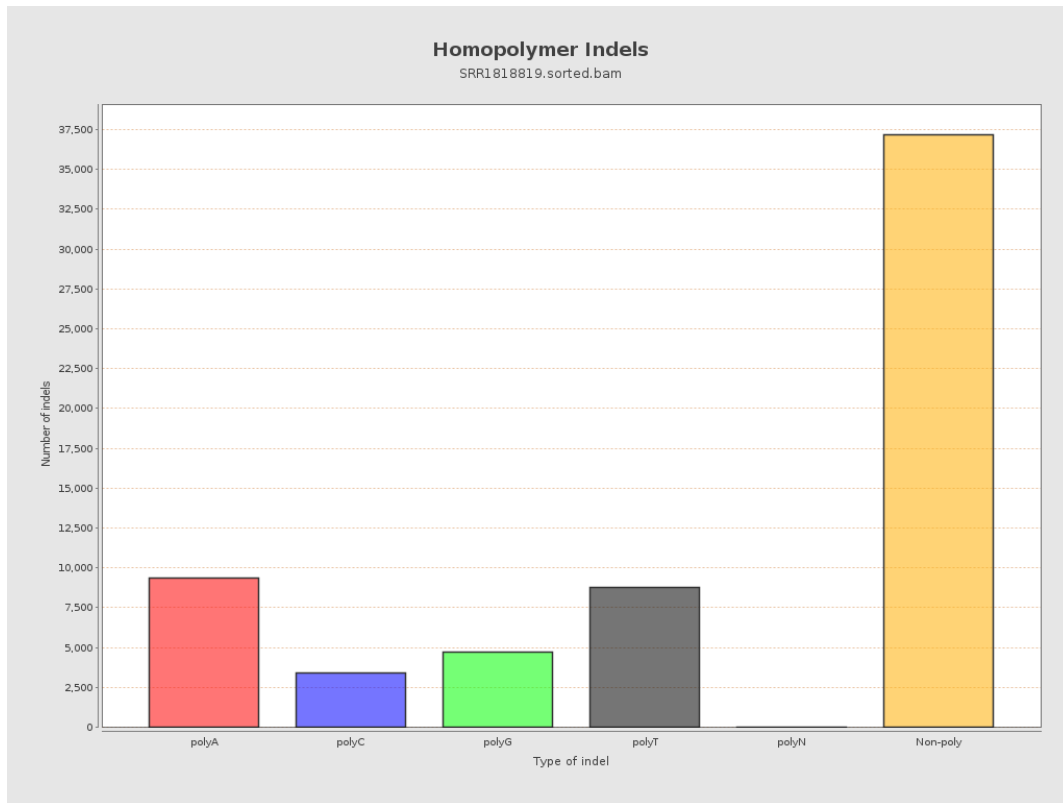
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

