

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:08:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR23117306.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_SRR23117306 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR23117306.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:08:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR23117306.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,236,235
Mapped reads	7,611,162 / 92.41%
Unmapped reads	625,073 / 7.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	82,573 / 1%
Read min/max/mean length	25 / 389 / 262.71
Duplicated reads (estimated)	4,323,078 / 52.49%
Duplication rate	35.3%
Clipped reads	7,693,690 / 93.41%

2.2. ACGT Content

Number/percentage of A's	545,239,017 / 28.34%
Number/percentage of C's	407,863,821 / 21.2%
Number/percentage of T's	551,984,863 / 28.69%
Number/percentage of G's	418,710,468 / 21.76%
Number/percentage of N's	0 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.6227

Standard Deviation	9.3782
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2.4. Mapping Quality

Mean Mapping Quality	51.99
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2.5. Mismatches and indels

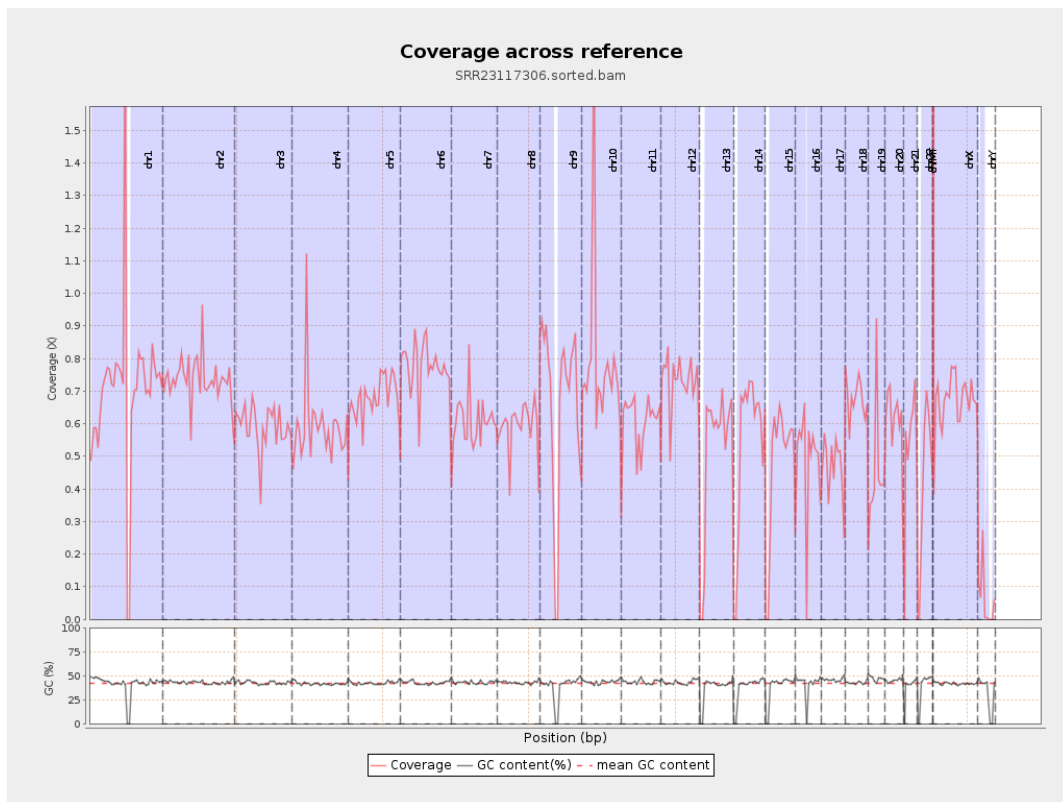
General error rate	1.18%
Mismatches	13,440,782
Insertions	7,923,304
Mapped reads with at least one insertion	47.21%
Deletions	3,099,982
Mapped reads with at least one deletion	27.02%
Homopolymer indels	31.18%

2.6. Chromosome stats

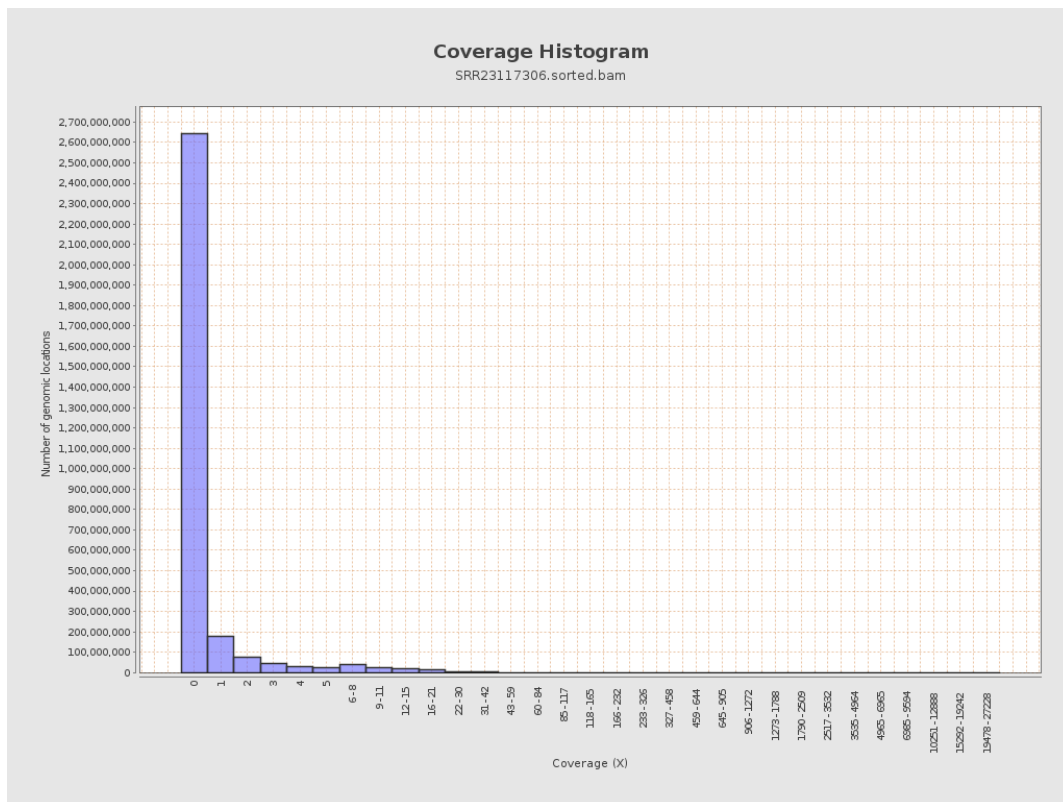
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	176160665	0.7068	27.2262
chr2	243199373	179001709	0.736	5.0325
chr3	198022430	116794421	0.5898	2.3585
chr4	191154276	113597241	0.5943	4.986
chr5	180915260	122469044	0.6769	2.6465
chr6	171115067	132617633	0.775	2.981
chr7	159138663	96430769	0.606	8.0943

chr8	146364022	86550065	0.5913	2.4101
chr9	141213431	94319162	0.6679	3.5015
chr10	135534747	106018331	0.7822	15.398
chr11	135006516	82106551	0.6082	2.5281
chr12	133851895	98464111	0.7356	2.8761
chr13	115169878	59553246	0.5171	2.3383
chr14	107349540	58871421	0.5484	2.3859
chr15	102531392	48324866	0.4713	2.1491
chr16	90354753	43085065	0.4768	3.8921
chr17	81195210	38557926	0.4749	2.2459
chr18	78077248	52599412	0.6737	3.9123
chr19	59128983	27091521	0.4582	16.4126
chr20	63025520	39224608	0.6224	4.4347
chr21	48129895	25682222	0.5336	4.7181
chr22	51304566	21839123	0.4257	2.1469
chrMT	16571	436704	26.3535	82.3369
chrX	155270560	104225241	0.6712	2.8376
chrY	59373566	3762544	0.0634	4.1228

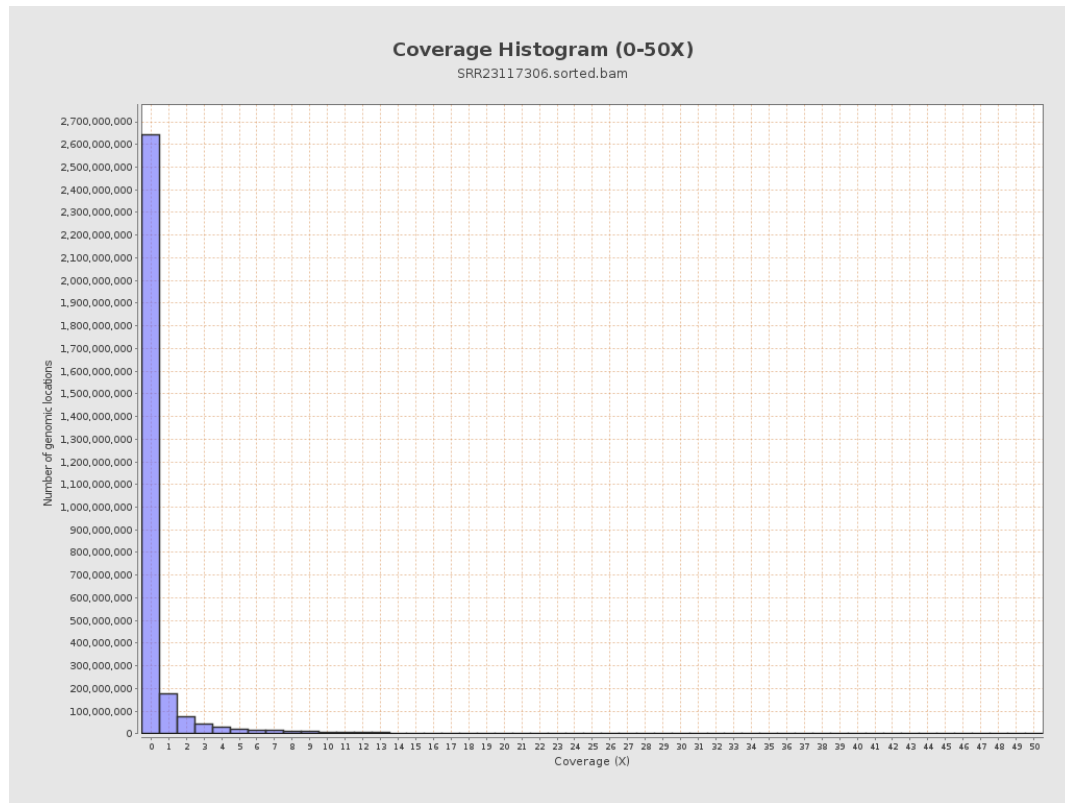
3. Results : Coverage across reference



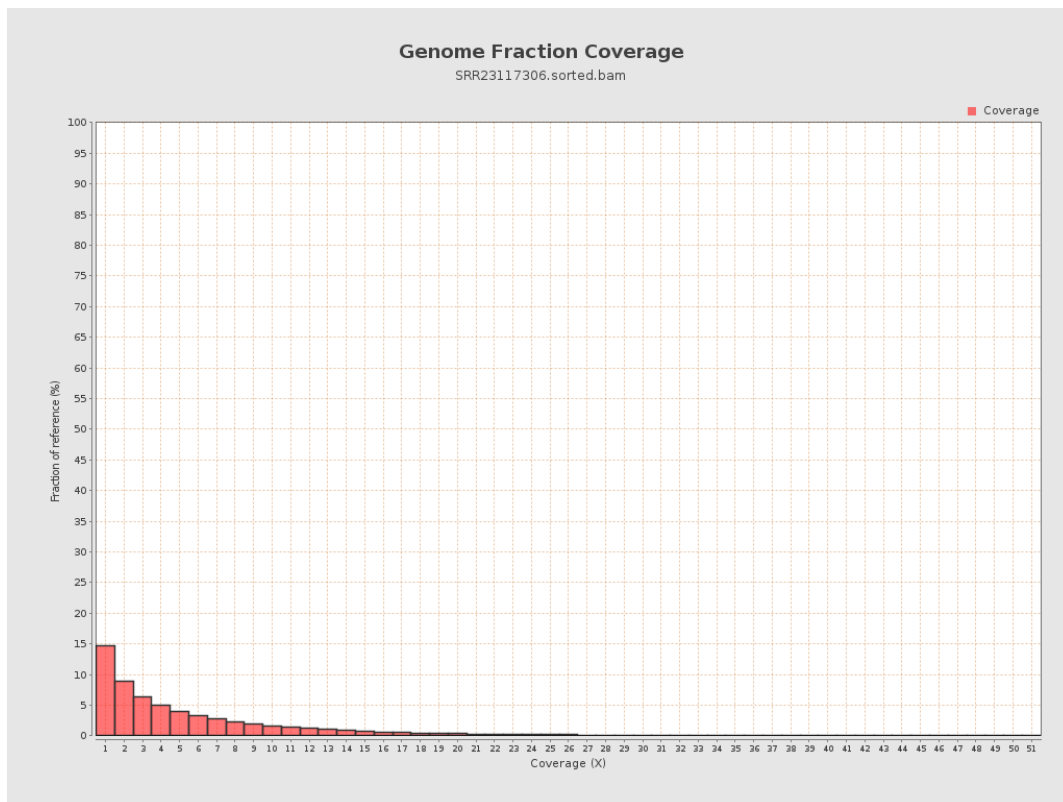
4. Results : Coverage Histogram



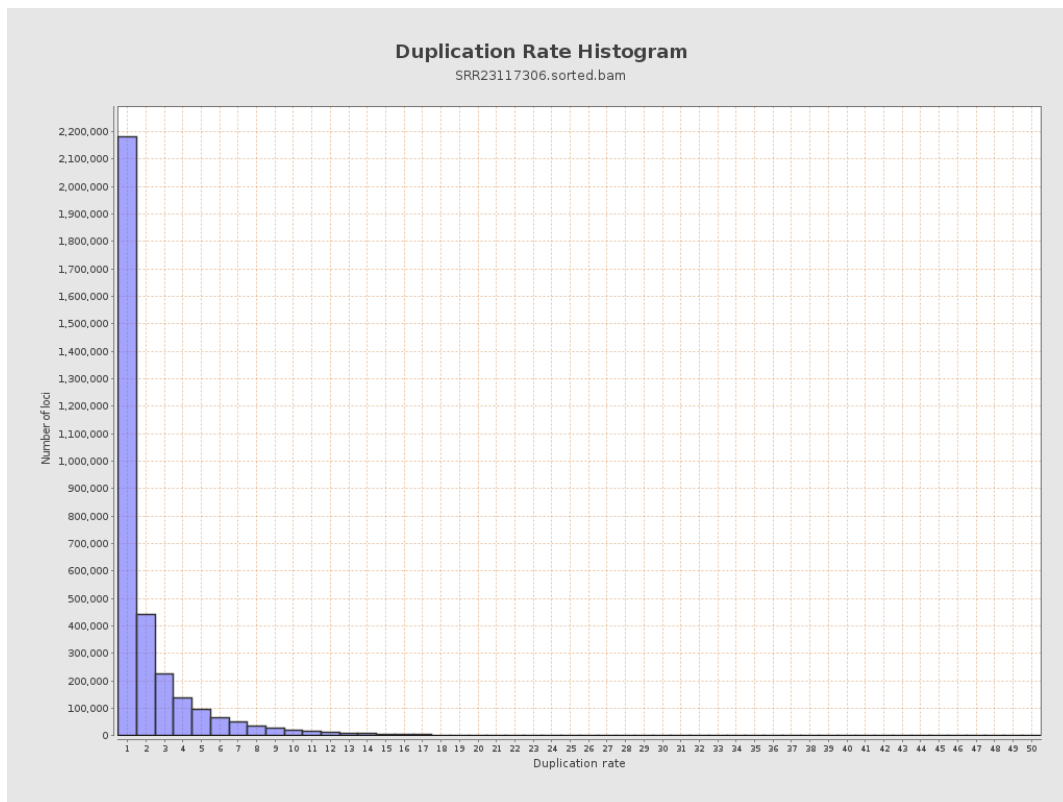
5. Results : Coverage Histogram (0-50X)



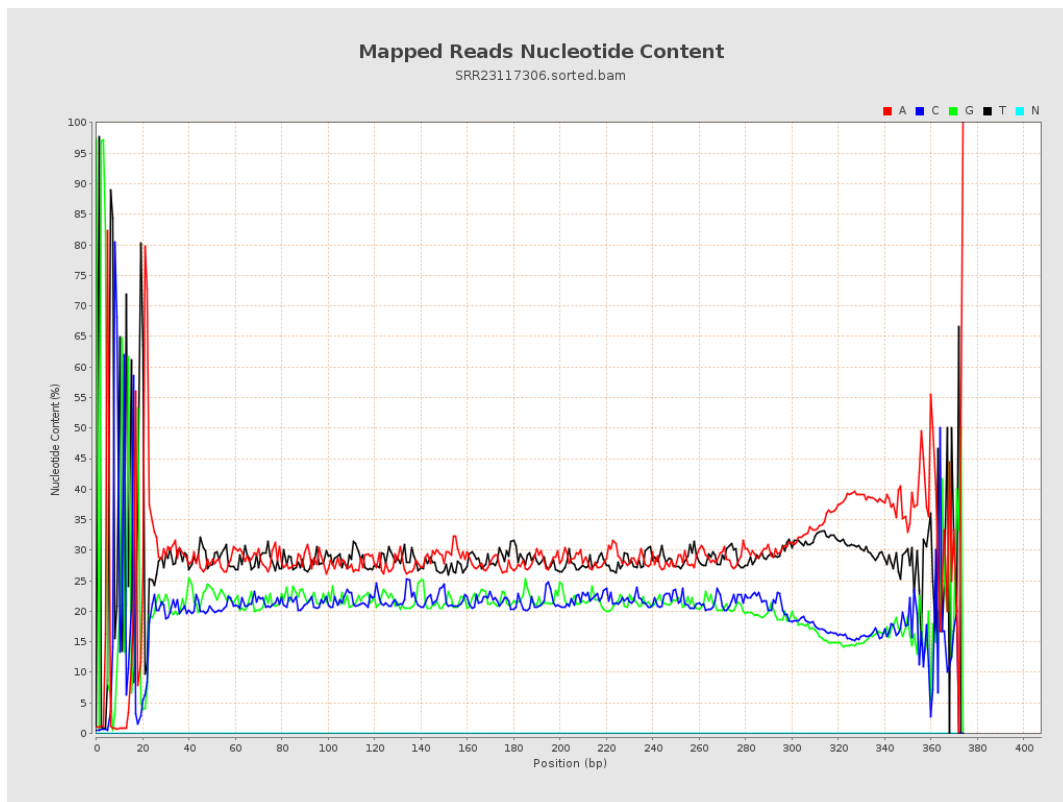
6. Results : Genome Fraction Coverage



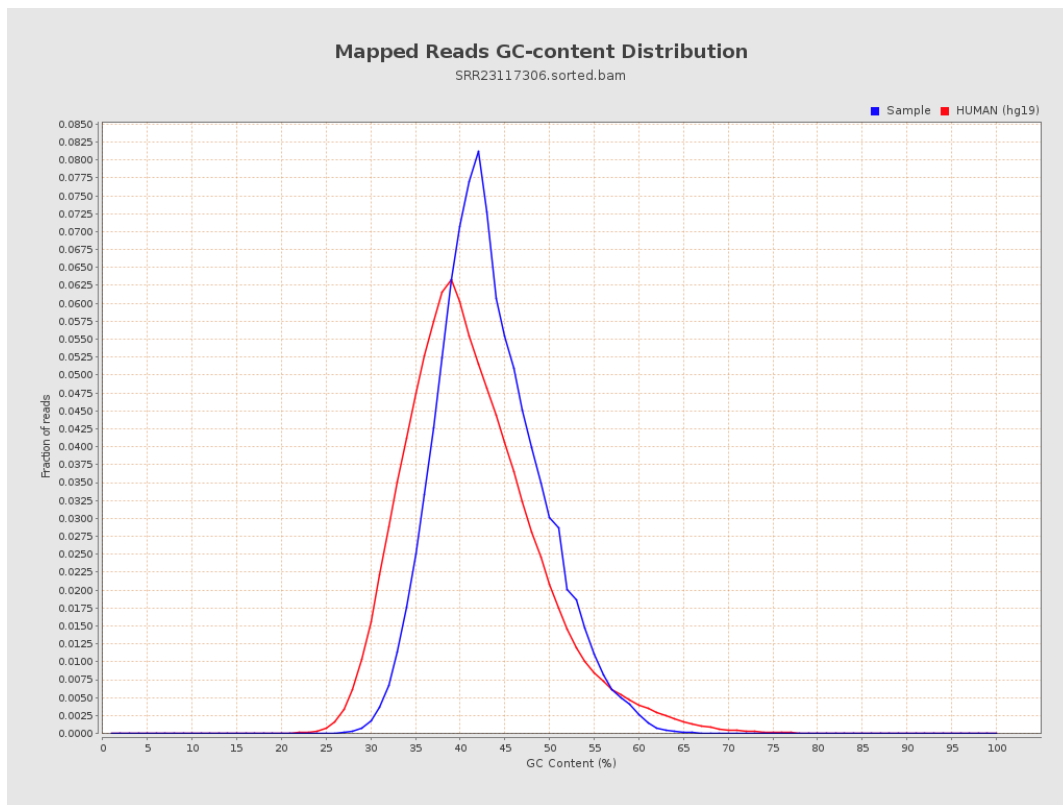
7. Results : Duplication Rate Histogram



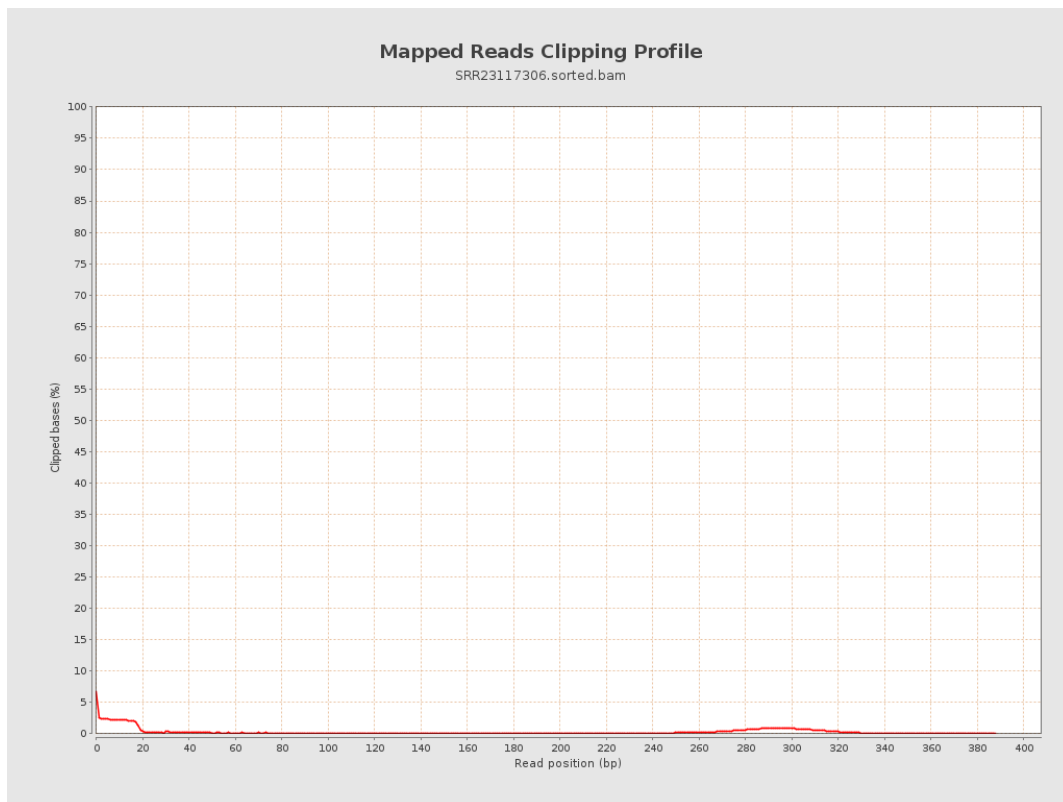
8. Results : Mapped Reads Nucleotide Content



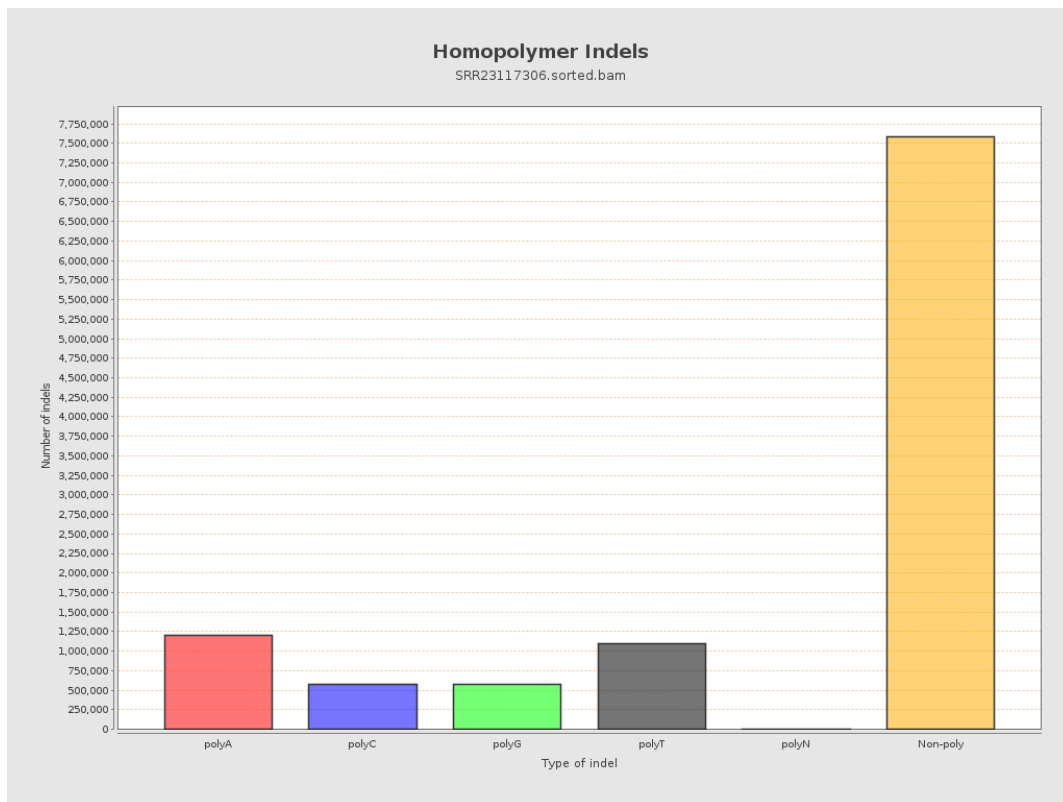
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

