

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:36:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004115.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_SRR6004115 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004115.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:36:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,484,939
Mapped reads	3,973,710 / 88.6%
Unmapped reads	511,229 / 11.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,008 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	230,763 / 5.15%
Duplication rate	4.5%
Clipped reads	1,479,730 / 32.99%

2.2. ACGT Content

Number/percentage of A's	76,893,562 / 28.16%
Number/percentage of C's	51,620,921 / 18.9%
Number/percentage of T's	86,546,426 / 31.69%
Number/percentage of G's	57,998,095 / 21.24%
Number/percentage of N's	37,926 / 0.01%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0883

Standard Deviation	0.7467
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2.4. Mapping Quality

Mean Mapping Quality	46.38
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2.5. Mismatches and indels

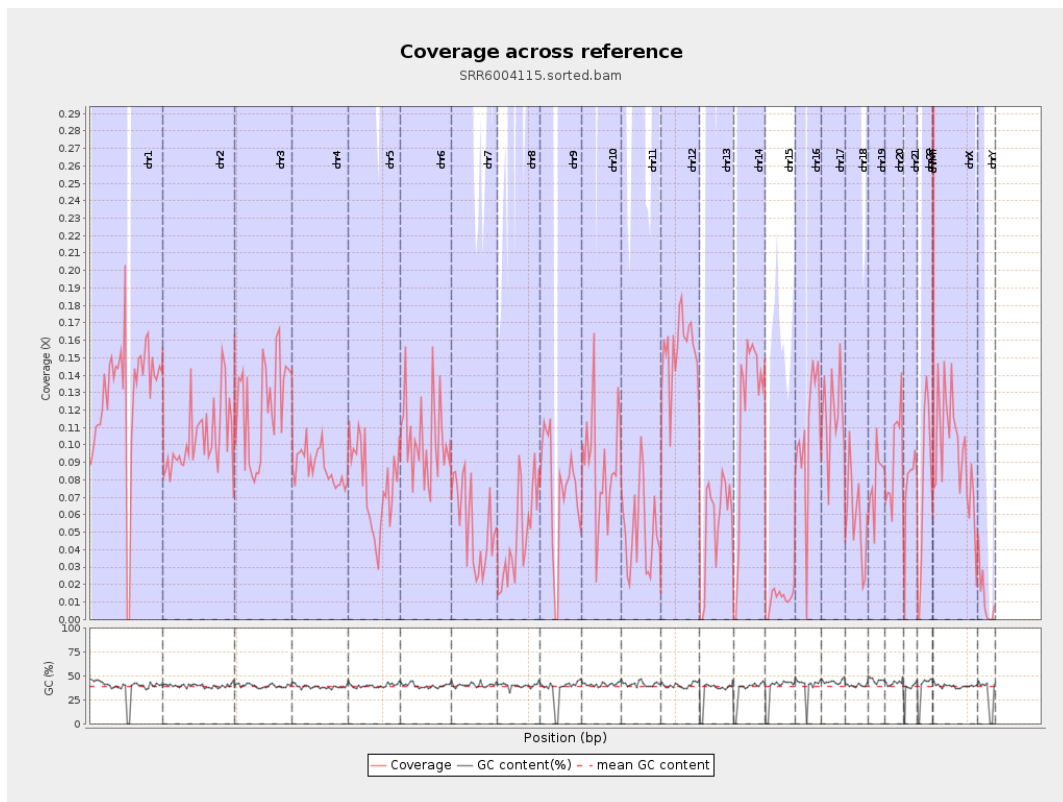
General error rate	0.95%
Mismatches	2,540,338
Insertions	22,893
Mapped reads with at least one insertion	0.57%
Deletions	68,359
Mapped reads with at least one deletion	1.7%
Homopolymer indels	47.68%

2.6. Chromosome stats

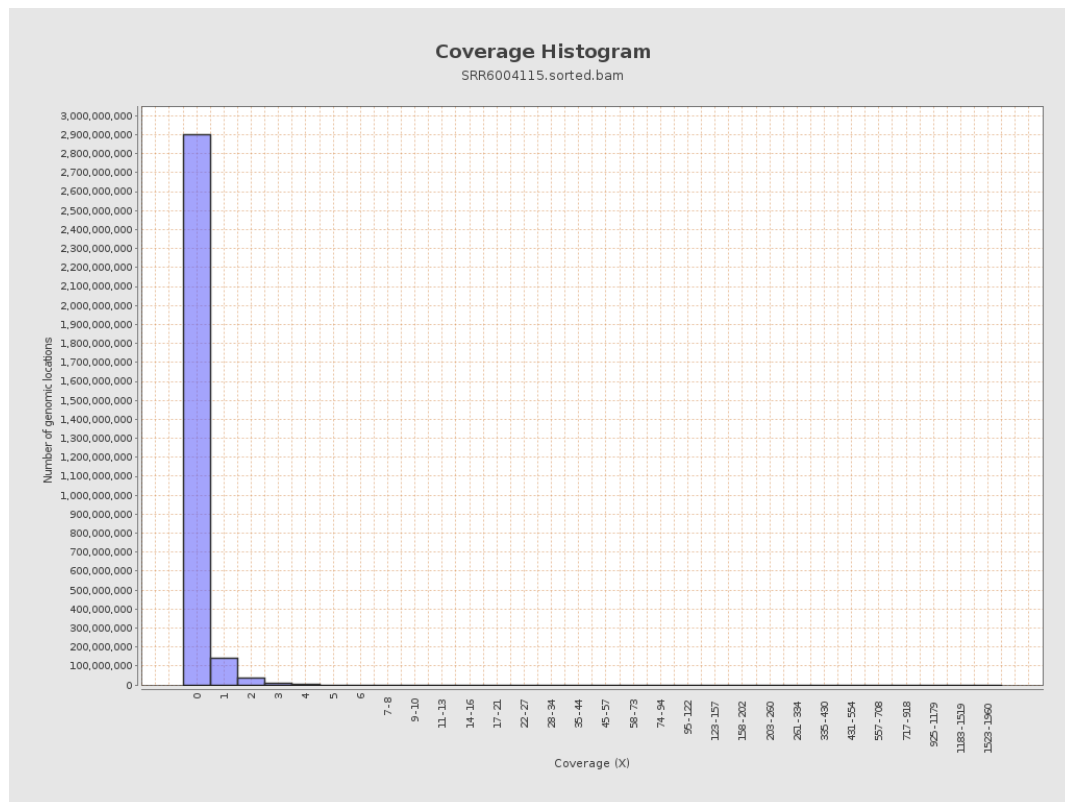
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	32032648	0.1285	1.7205
chr2	243199373	25118834	0.1033	0.7767
chr3	198022430	24141602	0.1219	0.4739
chr4	191154276	16685537	0.0873	0.4132
chr5	180915260	13954532	0.0771	0.3664
chr6	171115067	17536897	0.1025	0.4449
chr7	159138663	8607342	0.0541	0.4425

chr8	146364022	7176955	0.049	0.7986
chr9	141213431	10539728	0.0746	0.6128
chr10	135534747	11851856	0.0874	0.8964
chr11	135006516	6787088	0.0503	0.4255
chr12	133851895	20763088	0.1551	0.5287
chr13	115169878	6346014	0.0551	0.3038
chr14	107349540	12742619	0.1187	0.4953
chr15	102531392	1197150	0.0117	0.1416
chr16	90354753	9590134	0.1061	0.552
chr17	81195210	9670524	0.1191	0.4802
chr18	78077248	4494898	0.0576	1.3528
chr19	59128983	4723730	0.0799	1.0379
chr20	63025520	5893050	0.0935	0.4166
chr21	48129895	3661199	0.0761	0.4052
chr22	51304566	4046976	0.0789	0.3614
chrMT	16571	31402	1.895	1.9171
chrX	155270560	14912982	0.096	0.4643
chrY	59373566	704379	0.0119	0.2445

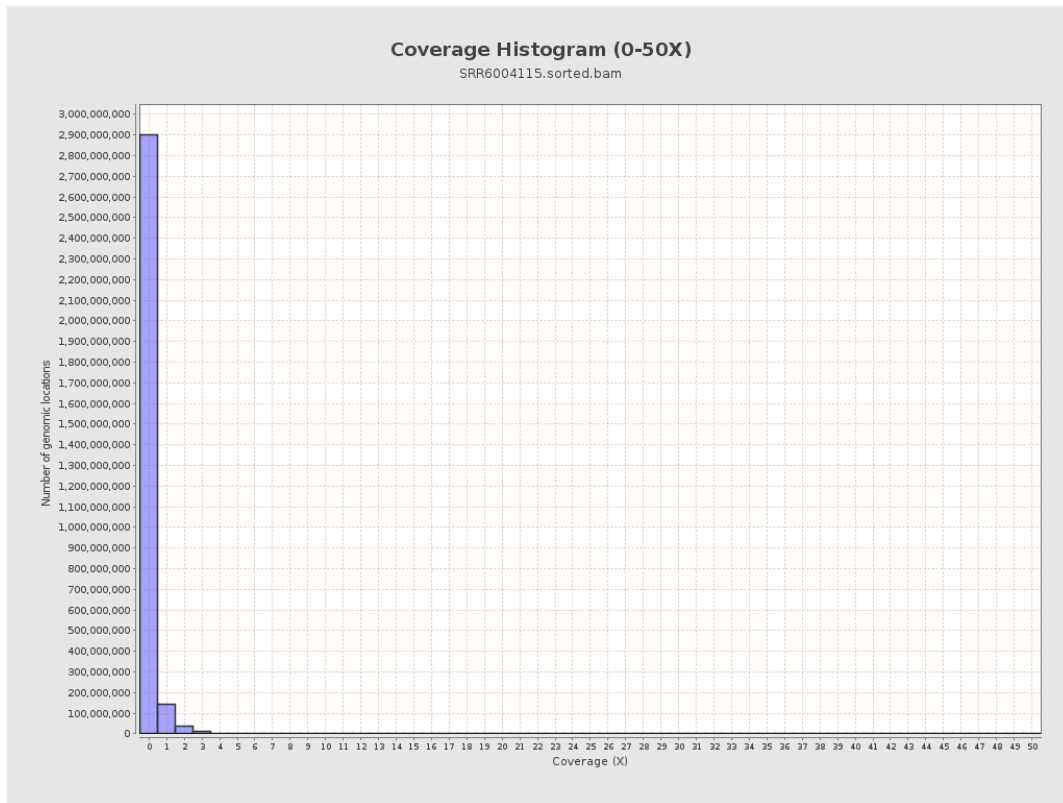
3. Results : Coverage across reference



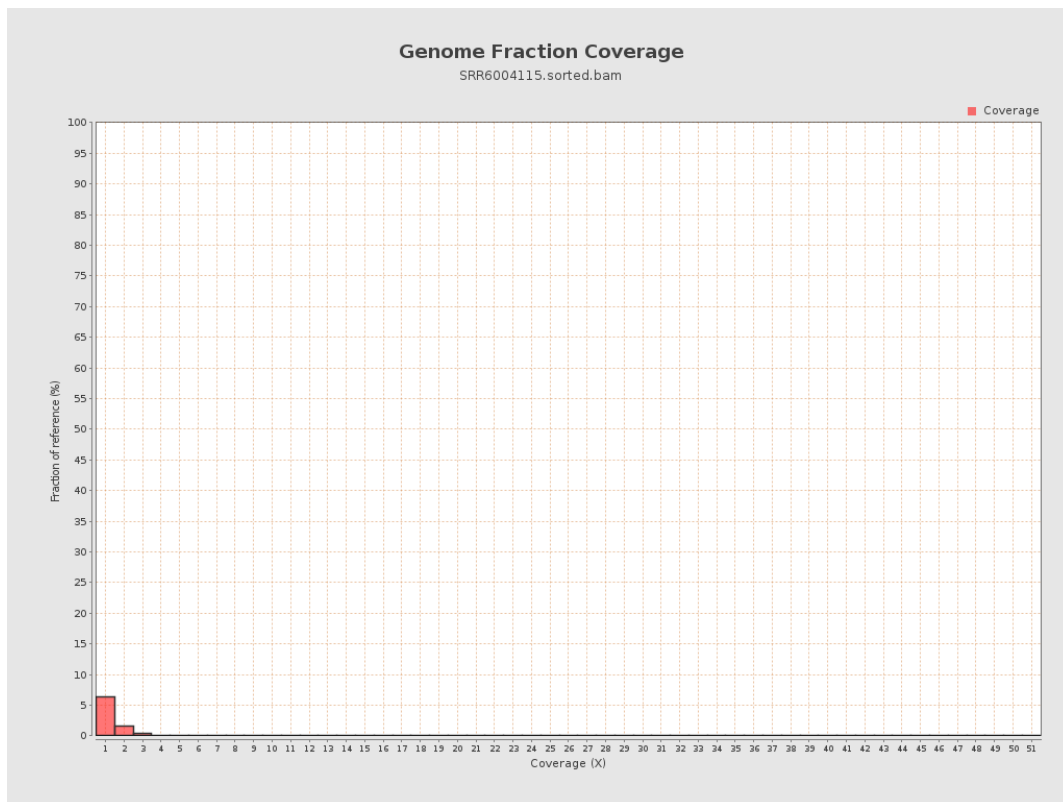
4. Results : Coverage Histogram



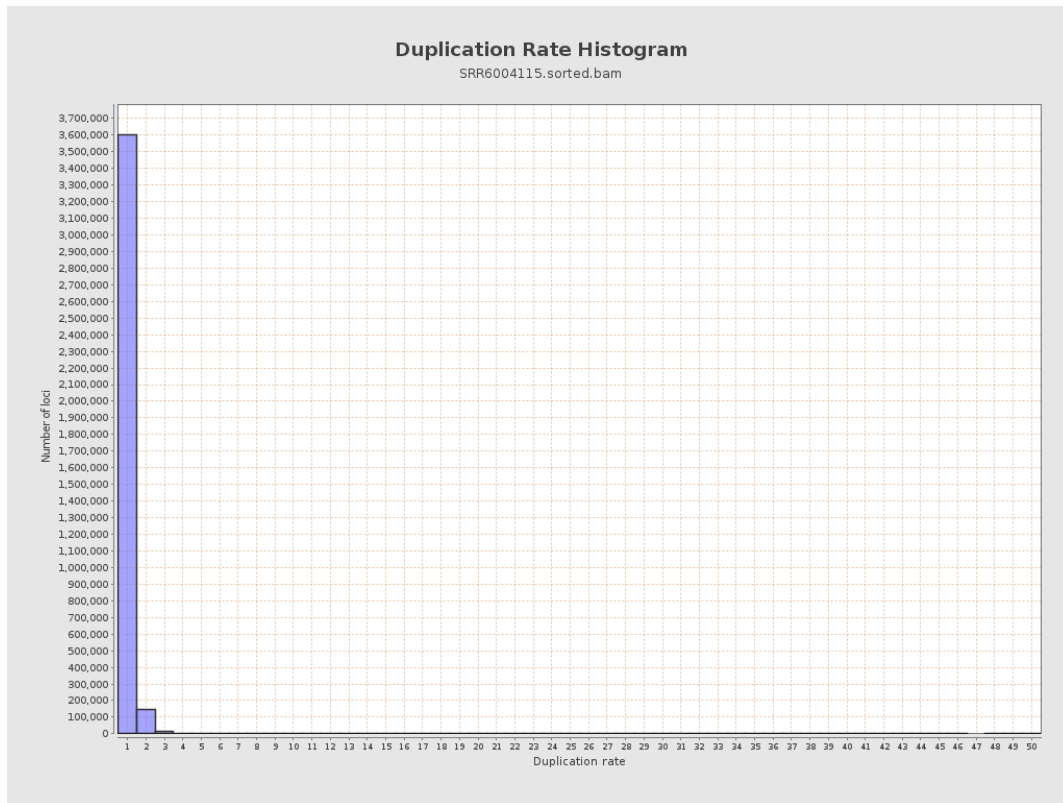
5. Results : Coverage Histogram (0-50X)



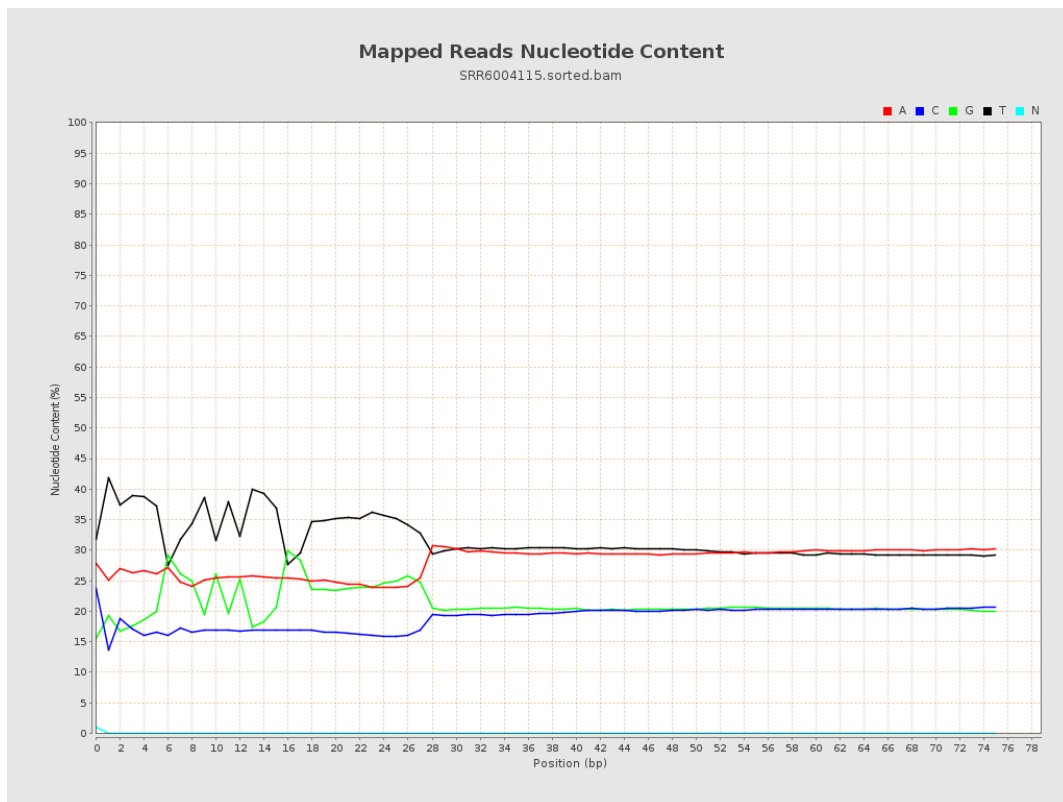
6. Results : Genome Fraction Coverage



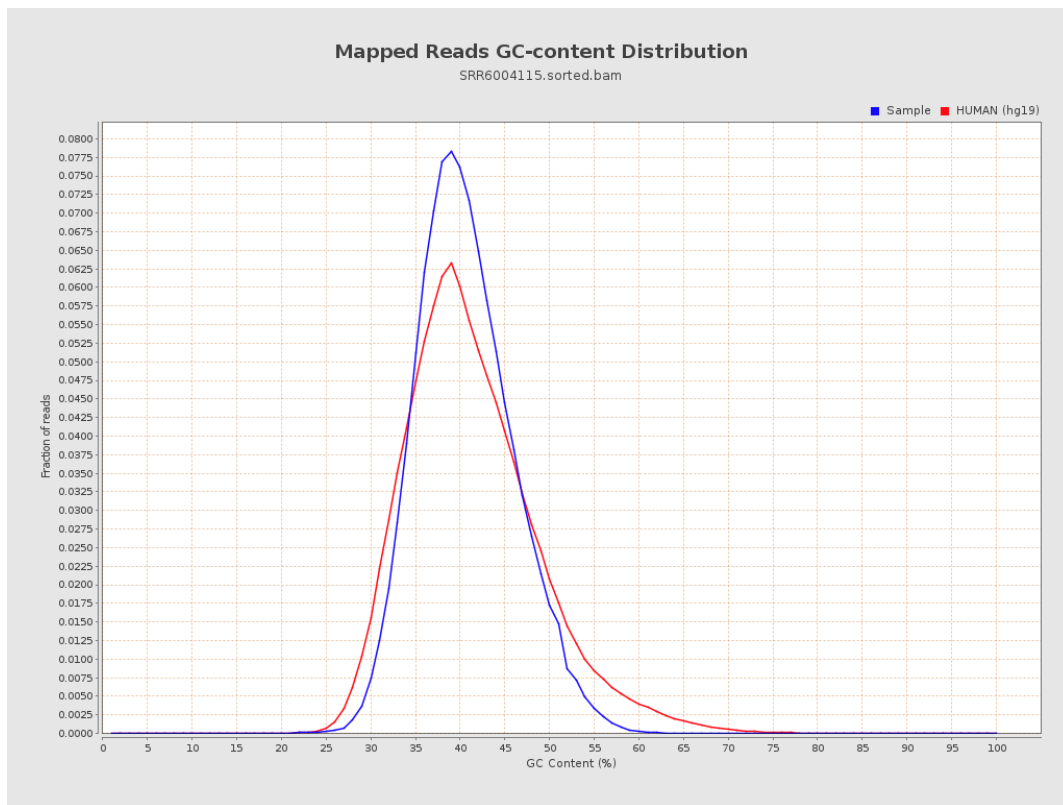
7. Results : Duplication Rate Histogram



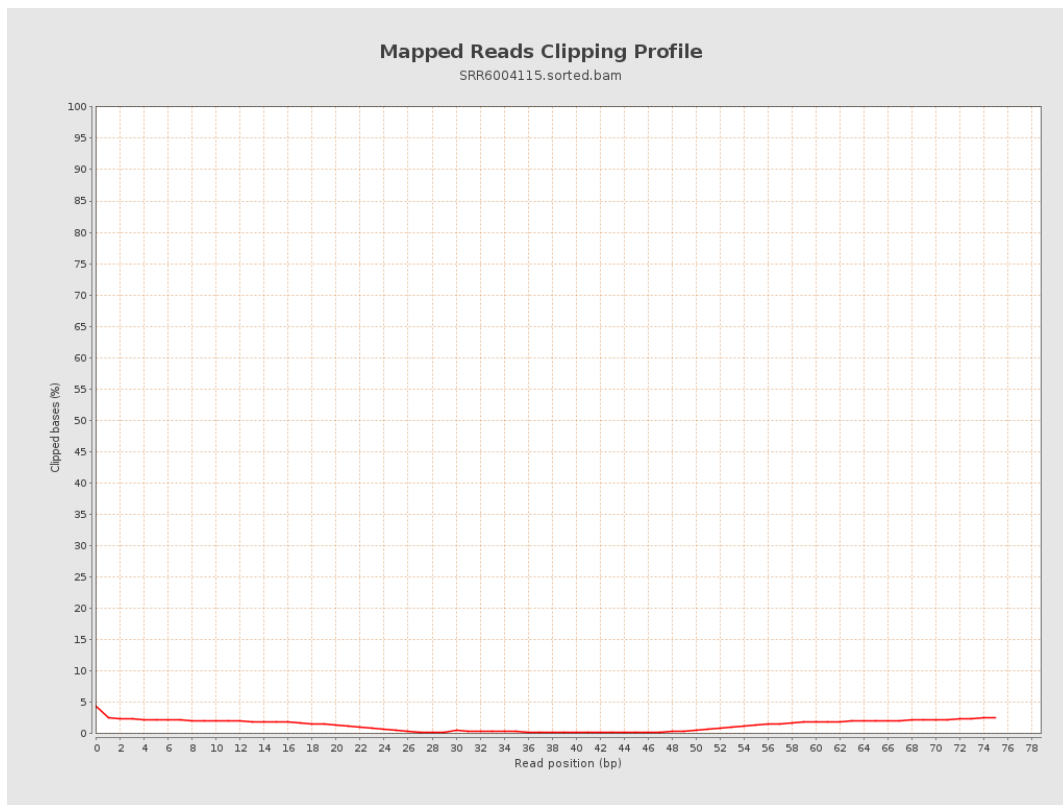
8. Results : Mapped Reads Nucleotide Content



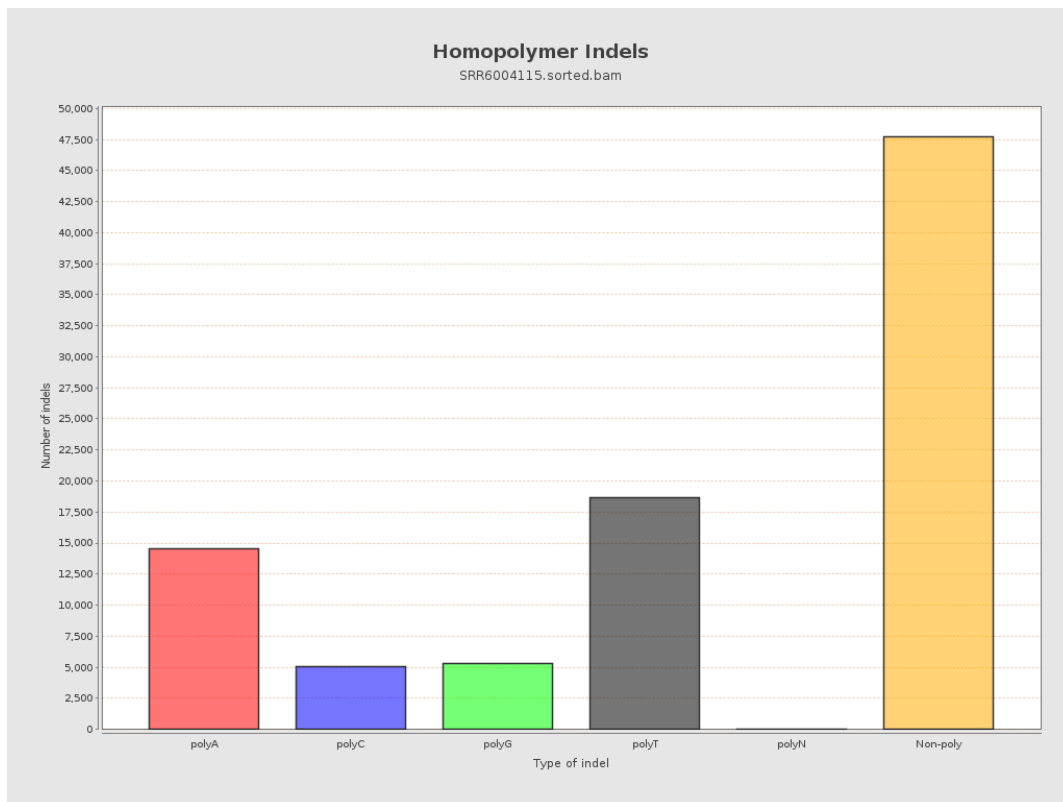
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

