

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 03:49:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089751.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_SRR089751 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089751.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 03:49:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089751.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,641,887
Mapped reads	29,250,938 / 84.44%
Unmapped reads	5,390,949 / 15.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,307 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	5,596,918 / 16.16%
Duplication rate	11.91%
Clipped reads	1,913,603 / 5.52%

2.2. ACGT Content

Number/percentage of A's	425,519,475 / 30.71%
Number/percentage of C's	272,270,815 / 19.65%
Number/percentage of T's	401,023,101 / 28.94%
Number/percentage of G's	286,577,017 / 20.68%
Number/percentage of N's	201,126 / 0.01%
GC Percentage	40.33%

2.3. Coverage

Mean	0.4477

Standard Deviation	2.6266
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2.4. Mapping Quality

Mean Mapping Quality	46
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2.5. Mismatches and indels

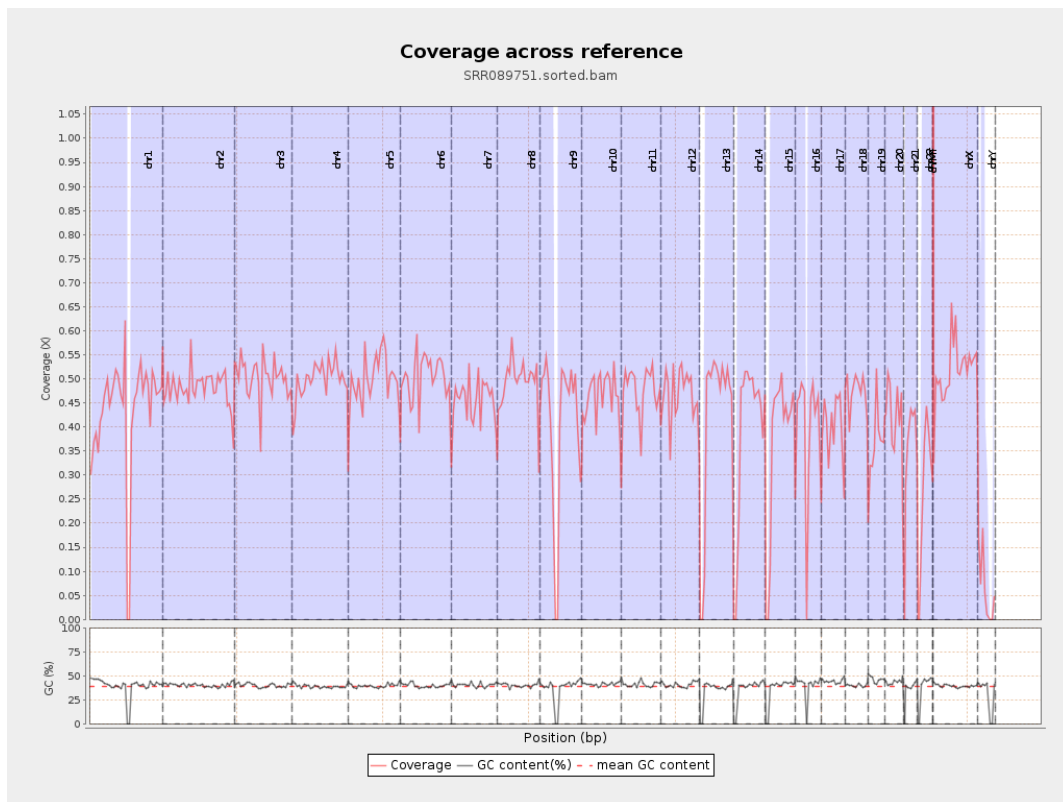
General error rate	0.43%
Mismatches	5,860,177
Insertions	50,692
Mapped reads with at least one insertion	0.17%
Deletions	166,937
Mapped reads with at least one deletion	0.57%
Homopolymer indels	47.91%

2.6. Chromosome stats

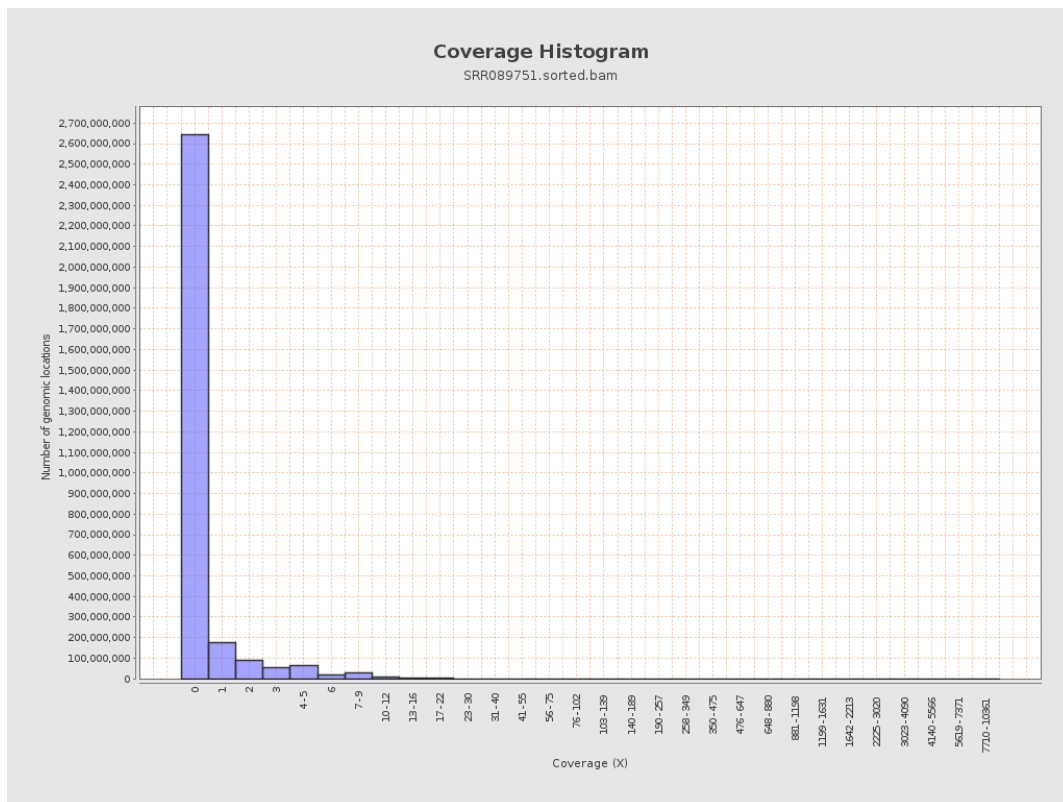
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	108225406	0.4342	4.7544
chr2	243199373	116990897	0.481	2.2167
chr3	198022430	99575721	0.5029	1.6904
chr4	191154276	95526750	0.4997	1.7575
chr5	180915260	90189462	0.4985	1.7082
chr6	171115067	86468626	0.5053	1.9075
chr7	159138663	72436609	0.4552	2.5676

chr8	146364022	72239526	0.4936	5.7039
chr9	141213431	57628388	0.4081	2.0792
chr10	135534747	63200293	0.4663	2.1713
chr11	135006516	64112916	0.4749	2.2169
chr12	133851895	62619433	0.4678	1.7338
chr13	115169878	48216066	0.4187	1.556
chr14	107349540	42567867	0.3965	1.5849
chr15	102531392	37026002	0.3611	1.4225
chr16	90354753	35077085	0.3882	1.5503
chr17	81195210	32852127	0.4046	1.7785
chr18	78077248	37024937	0.4742	3.9265
chr19	59128983	21938671	0.371	3.2259
chr20	63025520	26971262	0.4279	1.6346
chr21	48129895	16680950	0.3466	1.6341
chr22	51304566	13750069	0.268	1.2077
chrMT	16571	178268	10.7578	9.5659
chrX	155270560	80557929	0.5188	1.9298
chrY	59373566	3786997	0.0638	1.1232

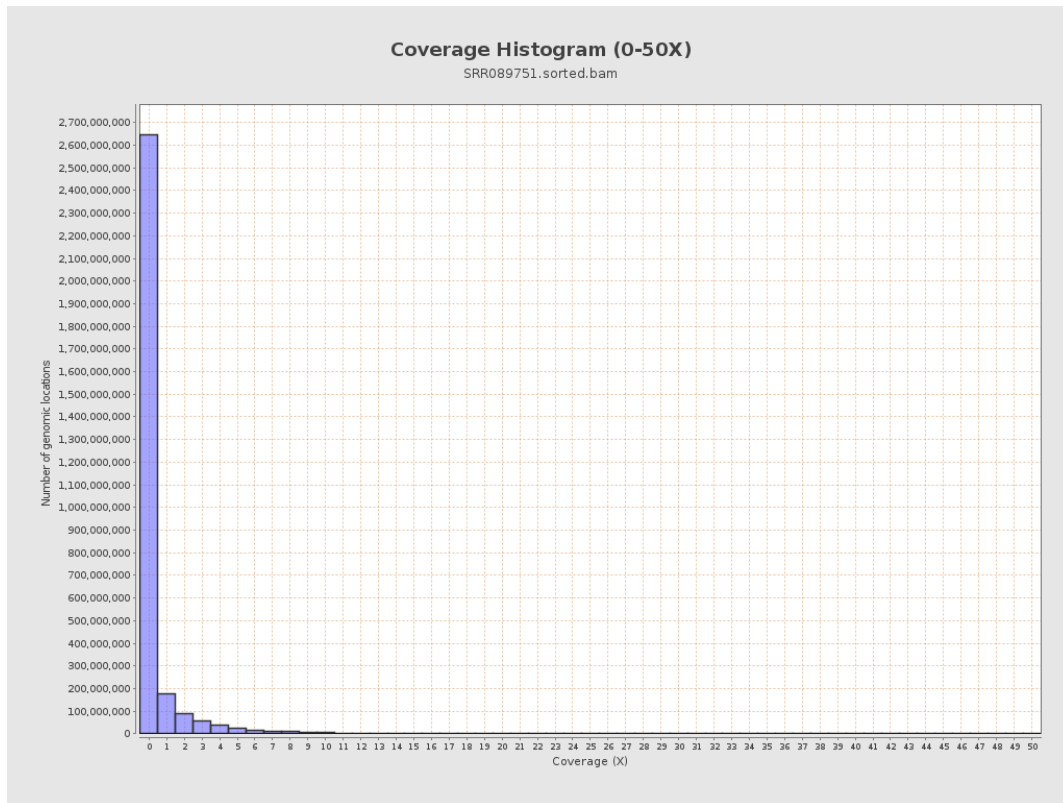
3. Results : Coverage across reference



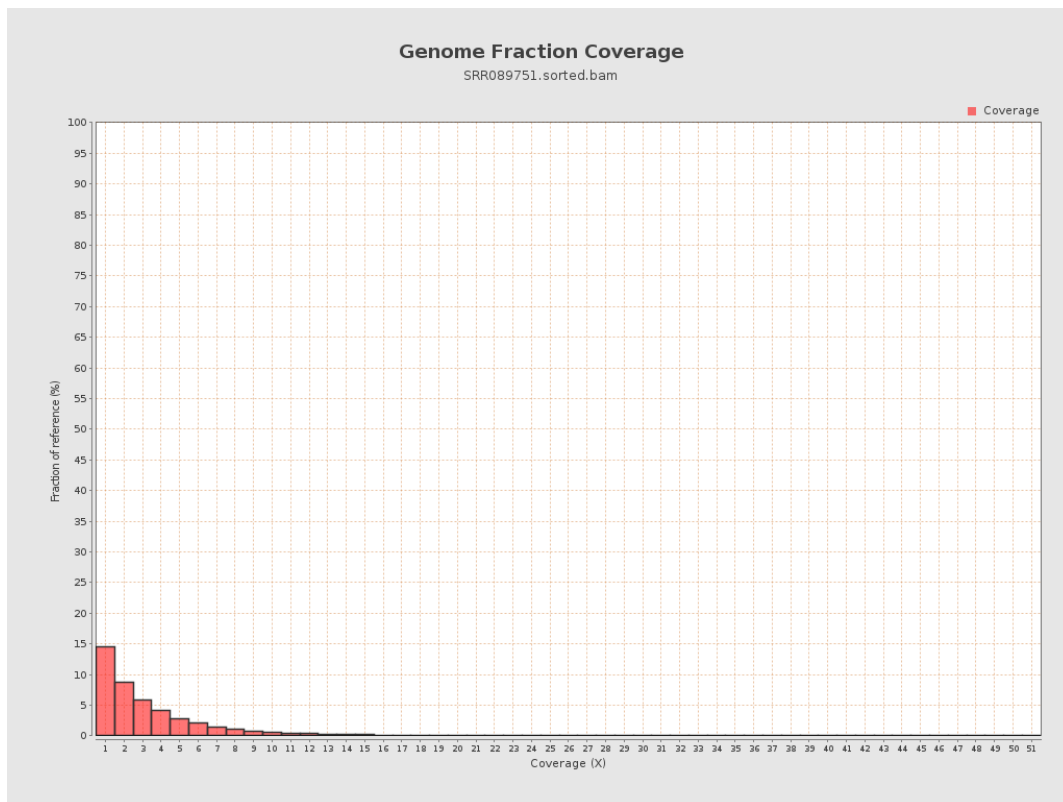
4. Results : Coverage Histogram



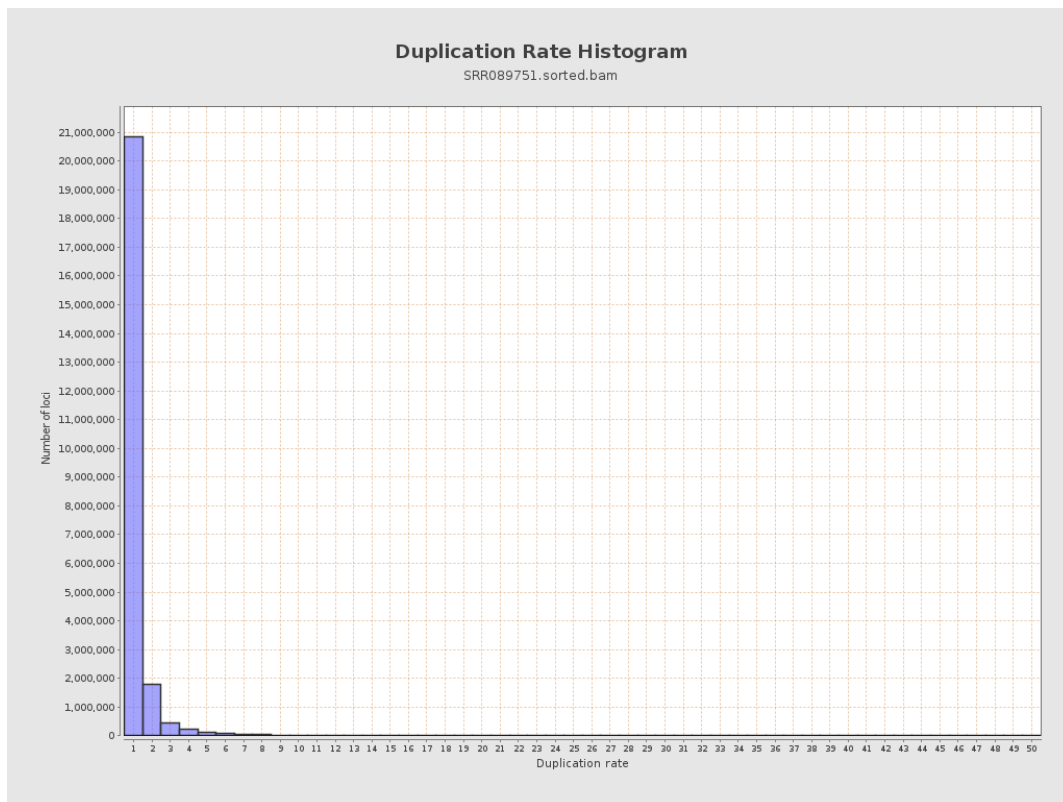
5. Results : Coverage Histogram (0-50X)



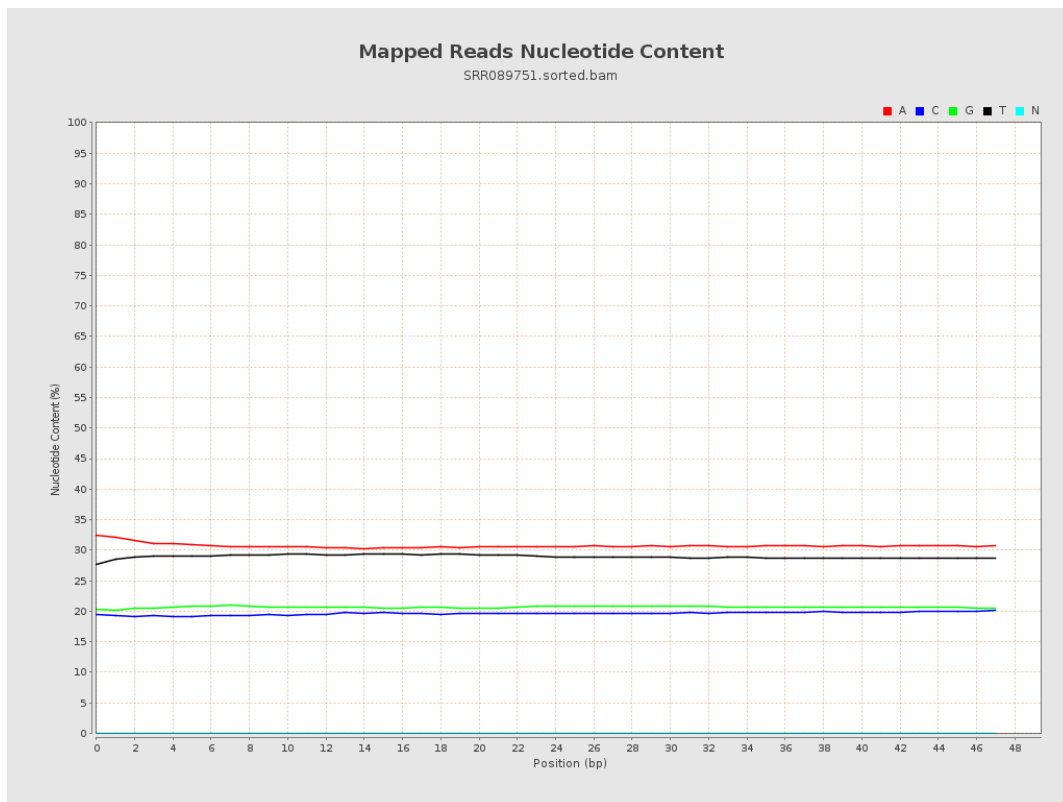
6. Results : Genome Fraction Coverage



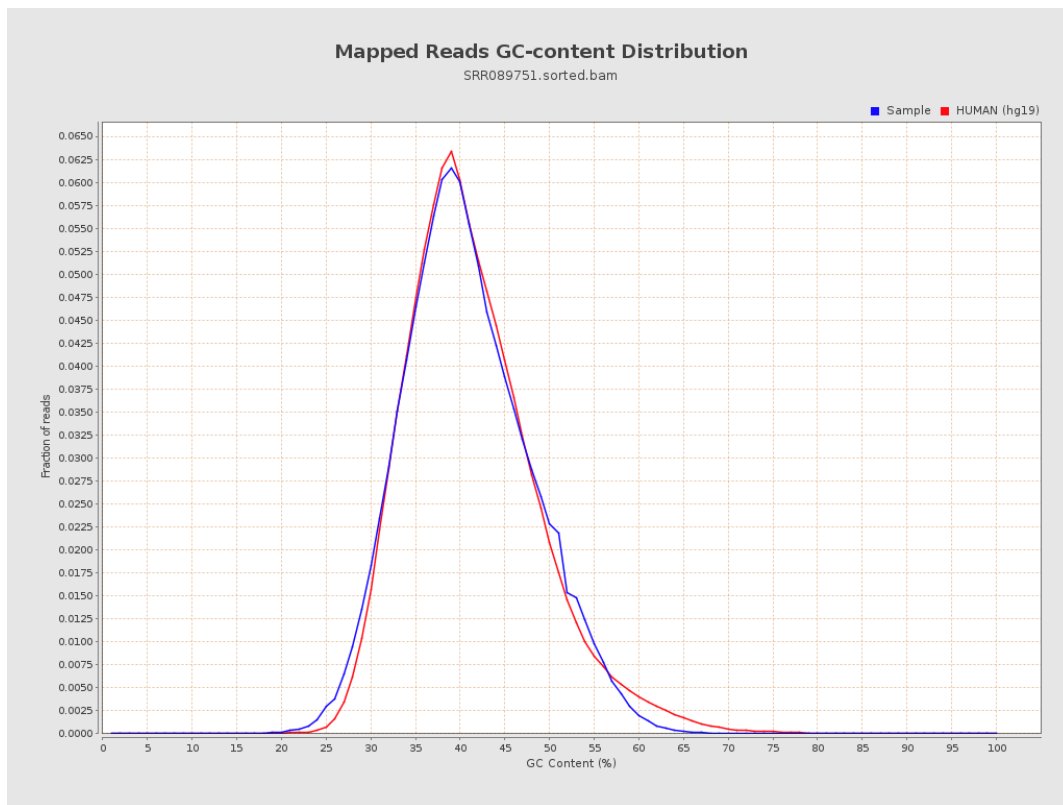
7. Results : Duplication Rate Histogram



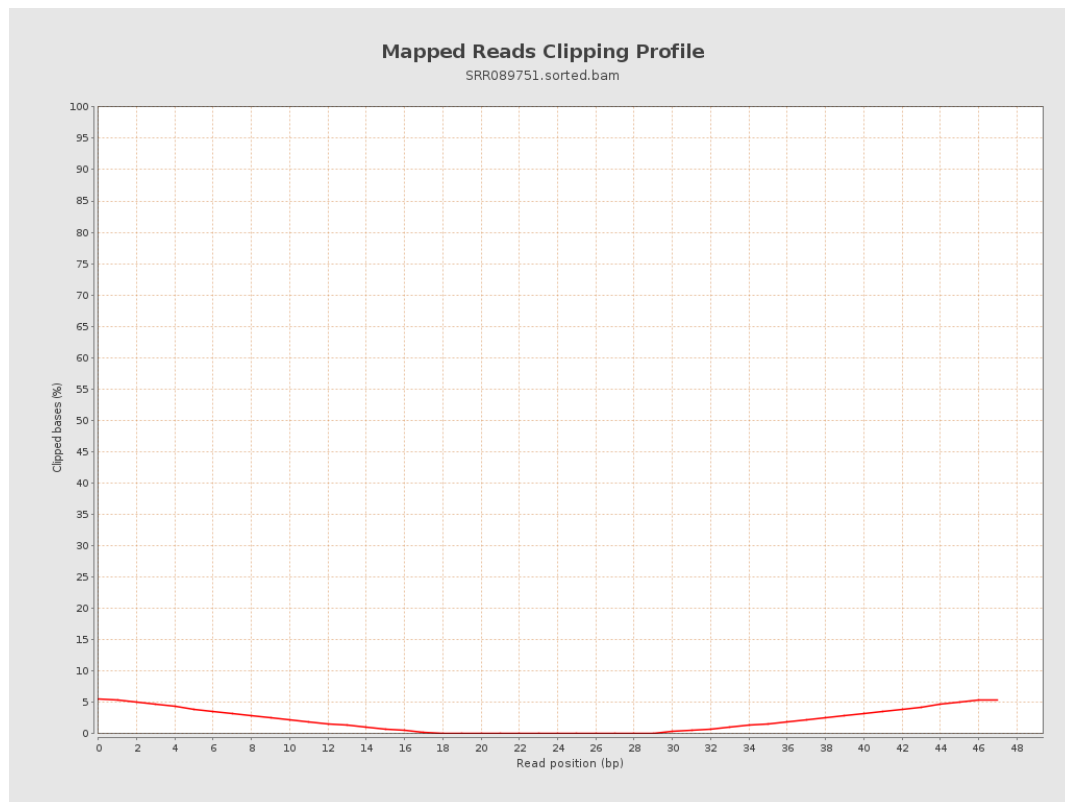
8. Results : Mapped Reads Nucleotide Content



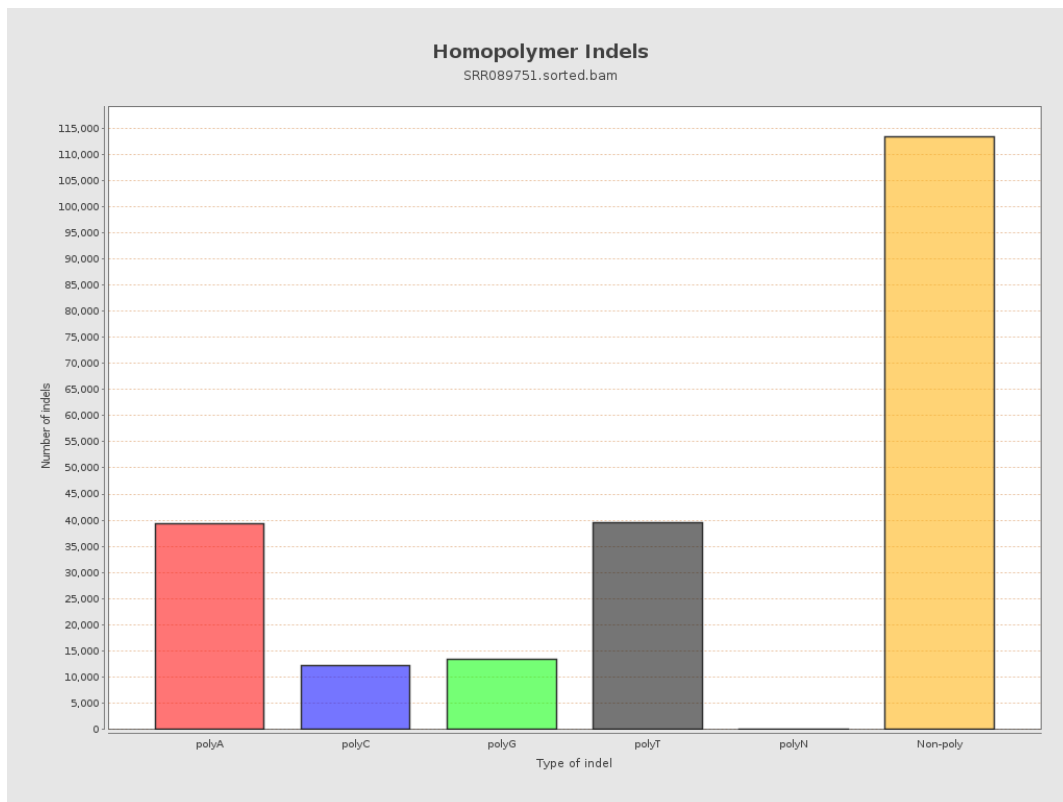
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

