

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 10:37:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089397.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_SRR089397 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089397.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 10:37:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089397.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,259,582
Mapped reads	21,668,252 / 93.16%
Unmapped reads	1,591,330 / 6.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	147,303 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	4,331,391 / 18.62%
Duplication rate	13.1%
Clipped reads	10,904,125 / 46.88%

2.2. ACGT Content

Number/percentage of A's	378,775,624 / 26.69%
Number/percentage of C's	275,483,041 / 19.41%
Number/percentage of T's	431,752,866 / 30.43%
Number/percentage of G's	332,854,697 / 23.46%
Number/percentage of N's	89,499 / 0.01%
GC Percentage	42.87%

2.3. Coverage

Mean	0.4585

Standard Deviation	2.8197
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2.4. Mapping Quality

Mean Mapping Quality	46.48
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2.5. Mismatches and indels

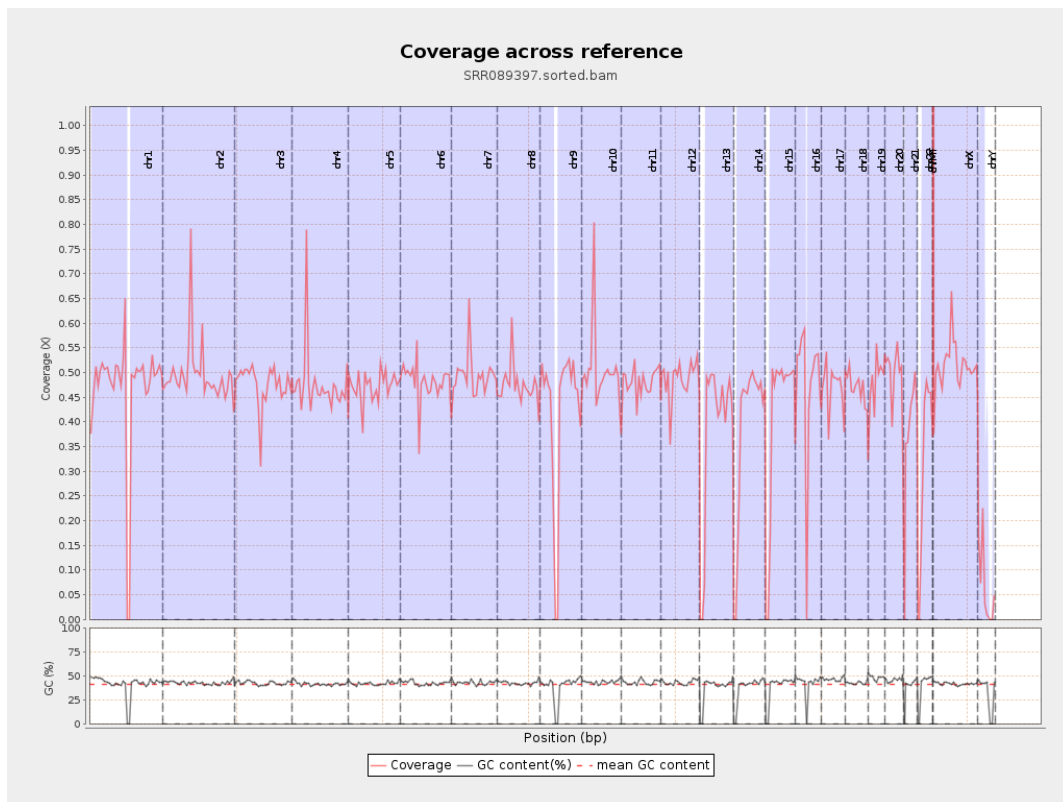
General error rate	0.63%
Mismatches	8,735,148
Insertions	91,277
Mapped reads with at least one insertion	0.42%
Deletions	263,618
Mapped reads with at least one deletion	1.2%
Homopolymer indels	44.51%

2.6. Chromosome stats

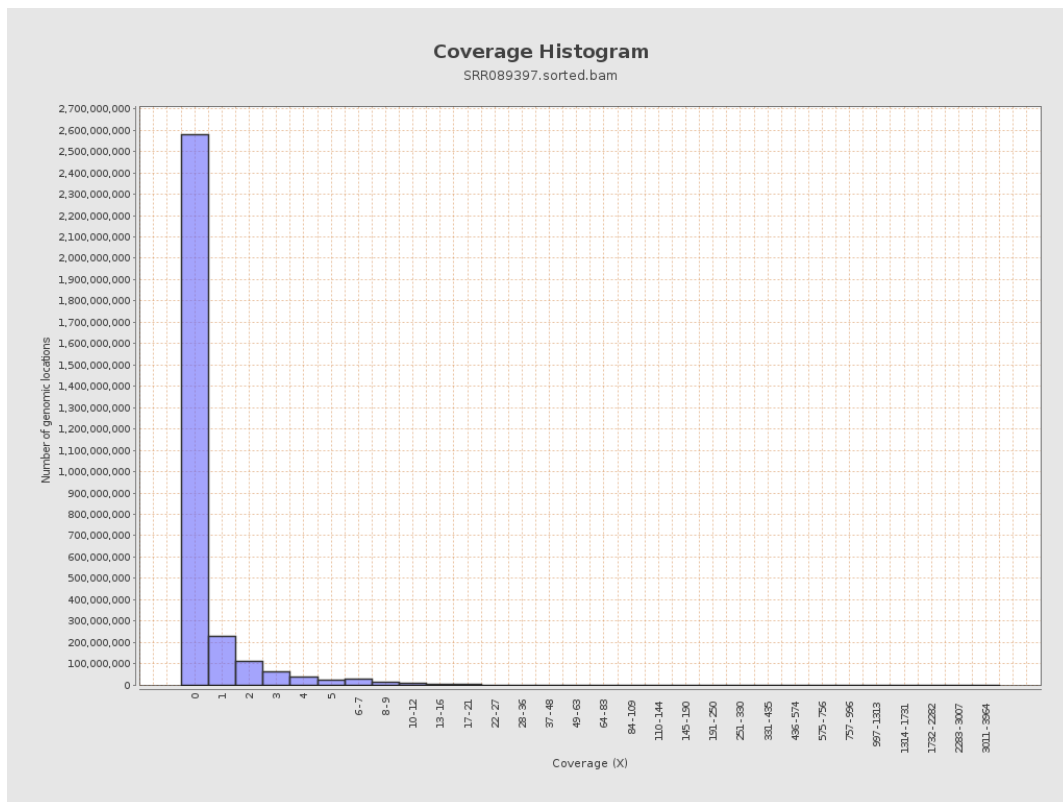
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	116341974	0.4668	4.1672
chr2	243199373	120755461	0.4965	3.8624
chr3	198022430	94214659	0.4758	1.6096
chr4	191154276	91009760	0.4761	2.2047
chr5	180915260	85414241	0.4721	1.6374
chr6	171115067	82403428	0.4816	2.0818
chr7	159138663	78704584	0.4946	3.8013

chr8	146364022	69359136	0.4739	3.1104
chr9	141213431	59628346	0.4223	2.7352
chr10	135534747	68213864	0.5033	3.5797
chr11	135006516	64834605	0.4802	3.0803
chr12	133851895	65493317	0.4893	1.7387
chr13	115169878	43975183	0.3818	1.4415
chr14	107349540	42262782	0.3937	2.0948
chr15	102531392	41182256	0.4017	1.4899
chr16	90354753	41870016	0.4634	2.0551
chr17	81195210	38433106	0.4733	2.1742
chr18	78077248	36767057	0.4709	4.717
chr19	59128983	28584142	0.4834	3.8595
chr20	63025520	31303405	0.4967	1.8188
chr21	48129895	18387306	0.382	2.1078
chr22	51304566	16211695	0.316	1.3136
chrMT	16571	362409	21.8701	16.9914
chrX	155270560	79843253	0.5142	2.186
chrY	59373566	3860679	0.065	1.7977

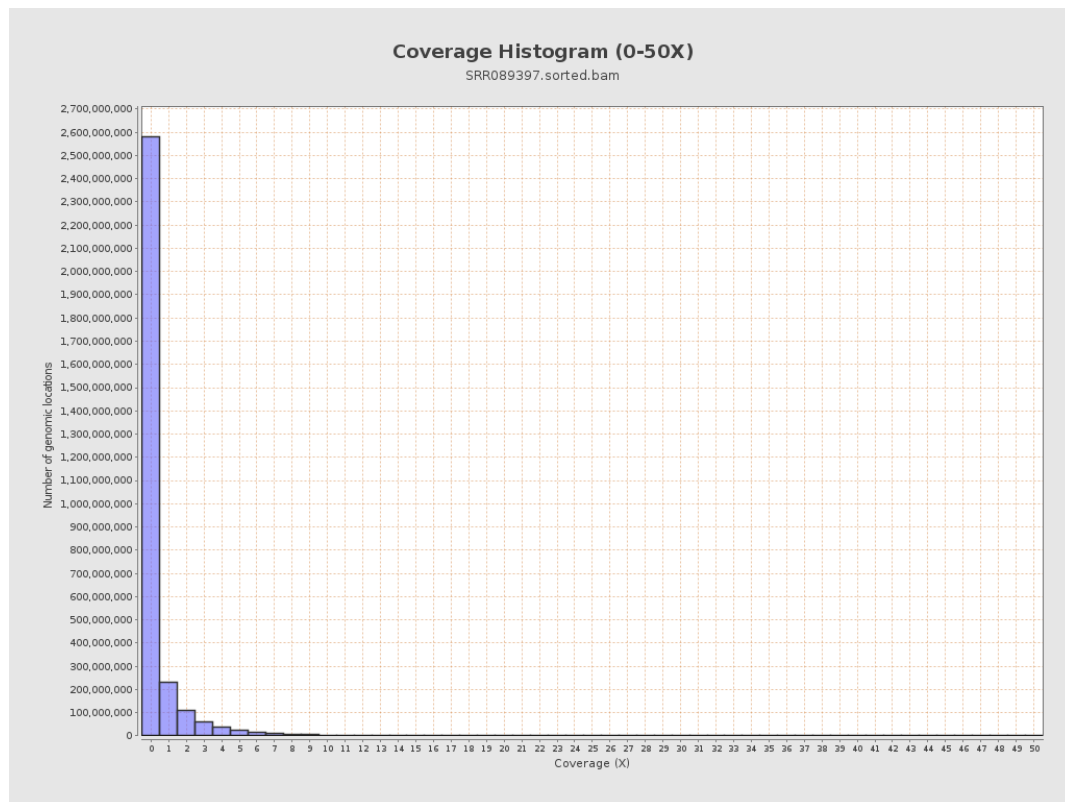
3. Results : Coverage across reference



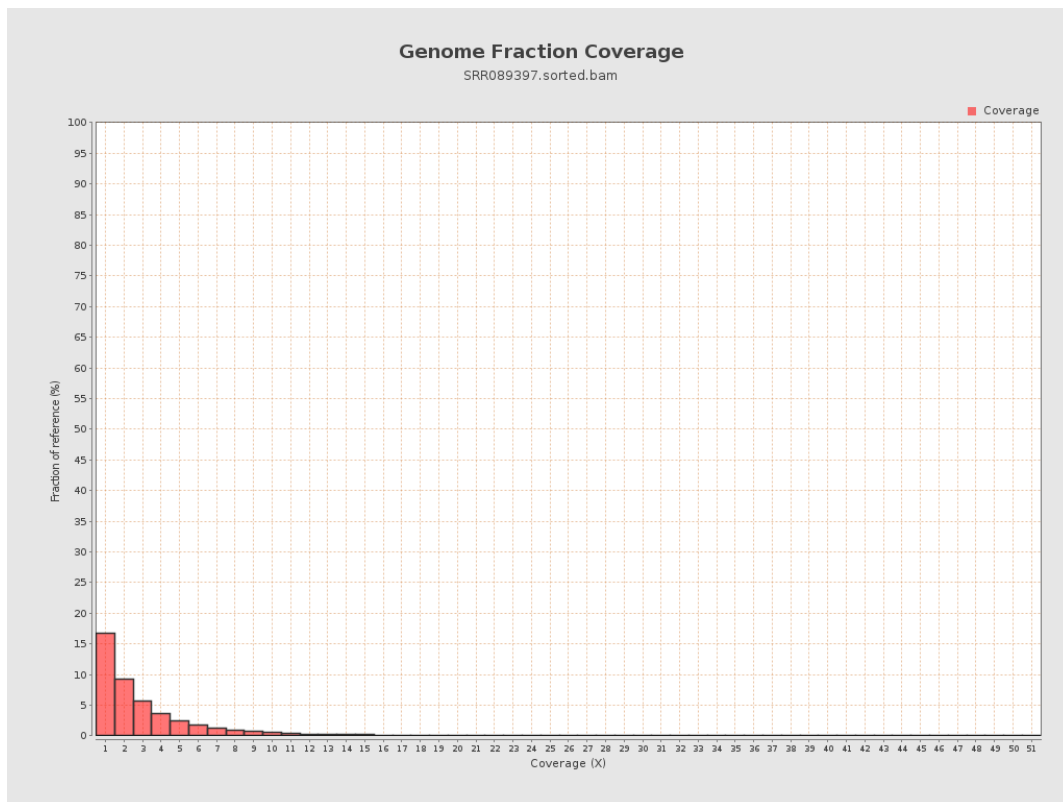
4. Results : Coverage Histogram



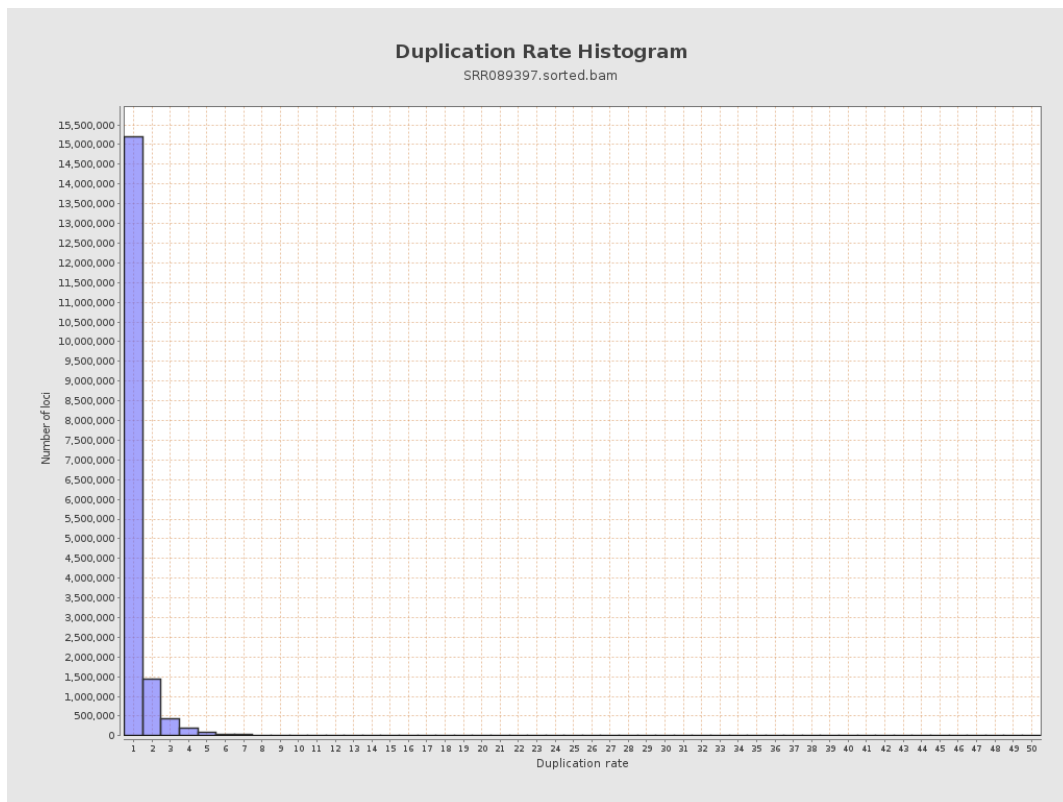
5. Results : Coverage Histogram (0-50X)



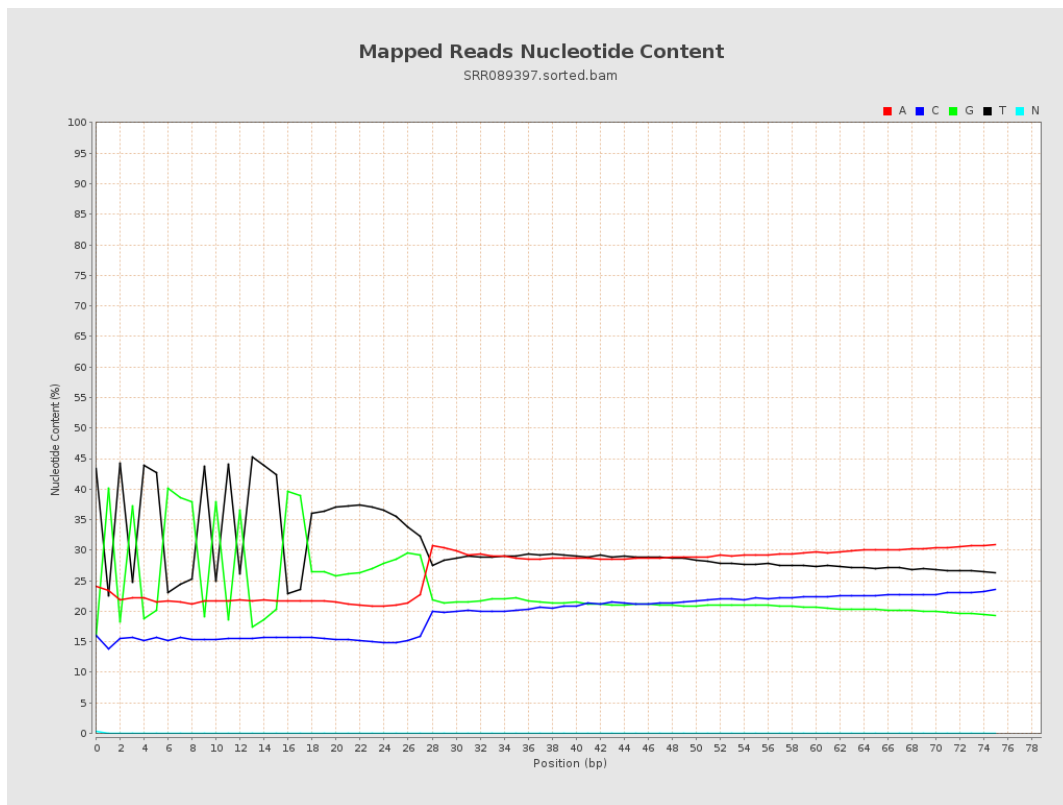
6. Results : Genome Fraction Coverage



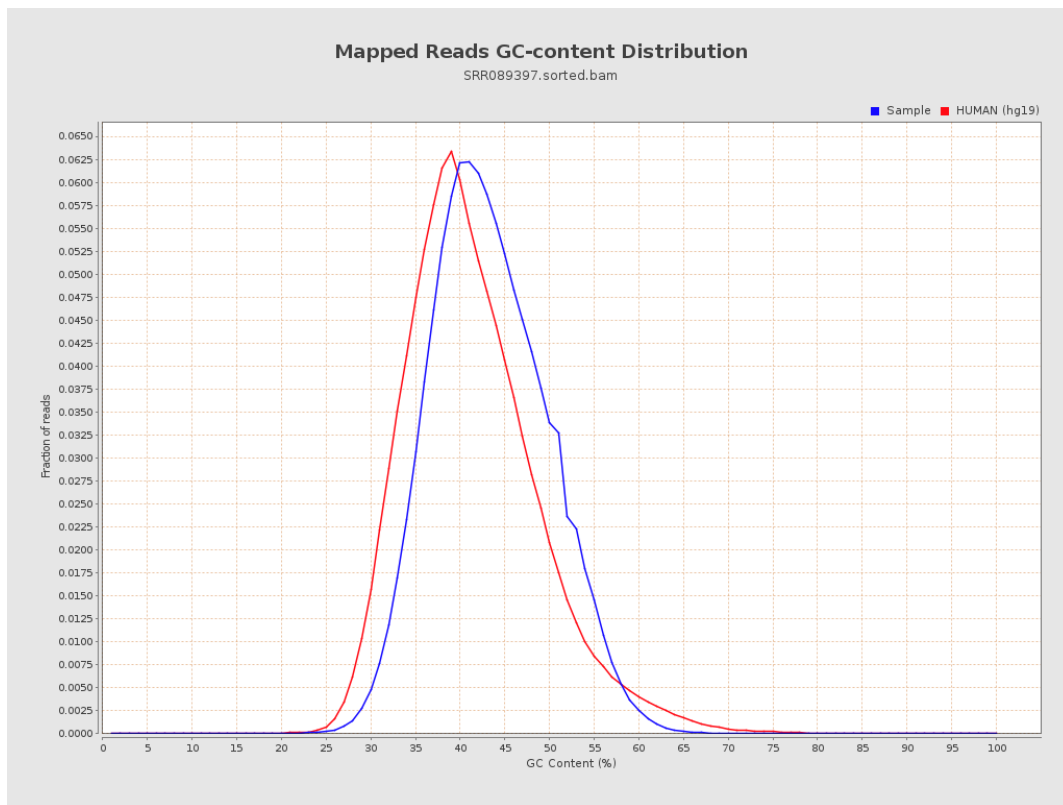
7. Results : Duplication Rate Histogram



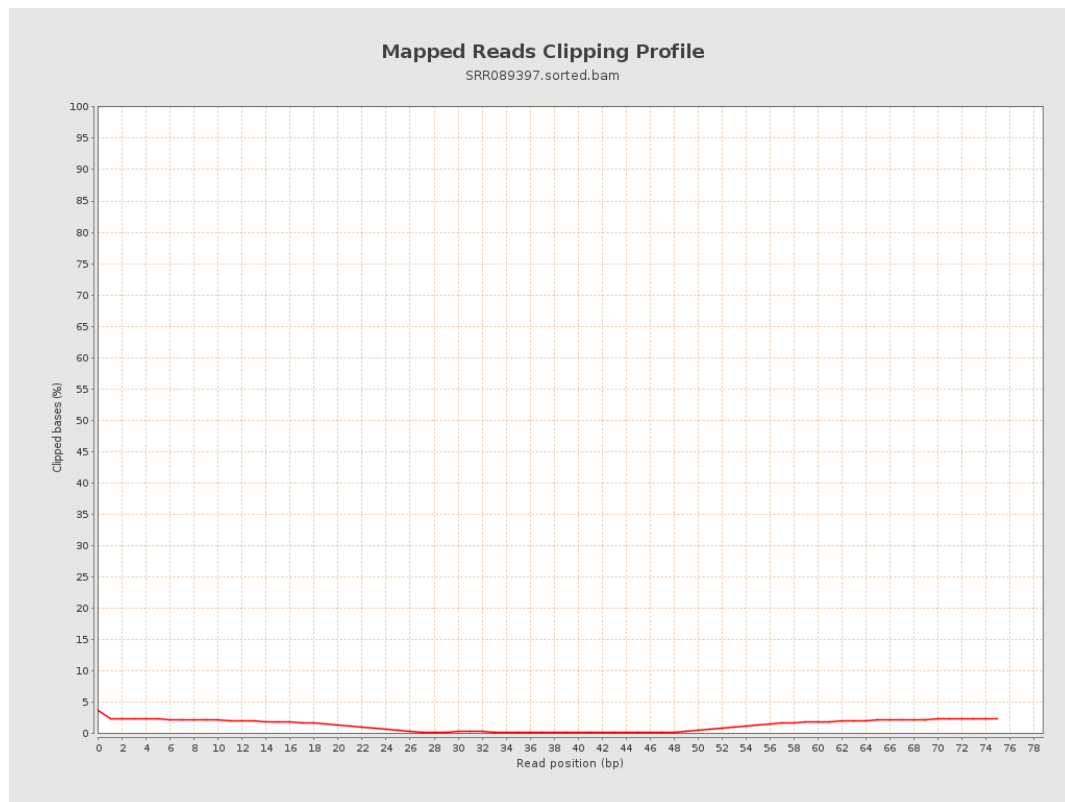
8. Results : Mapped Reads Nucleotide Content



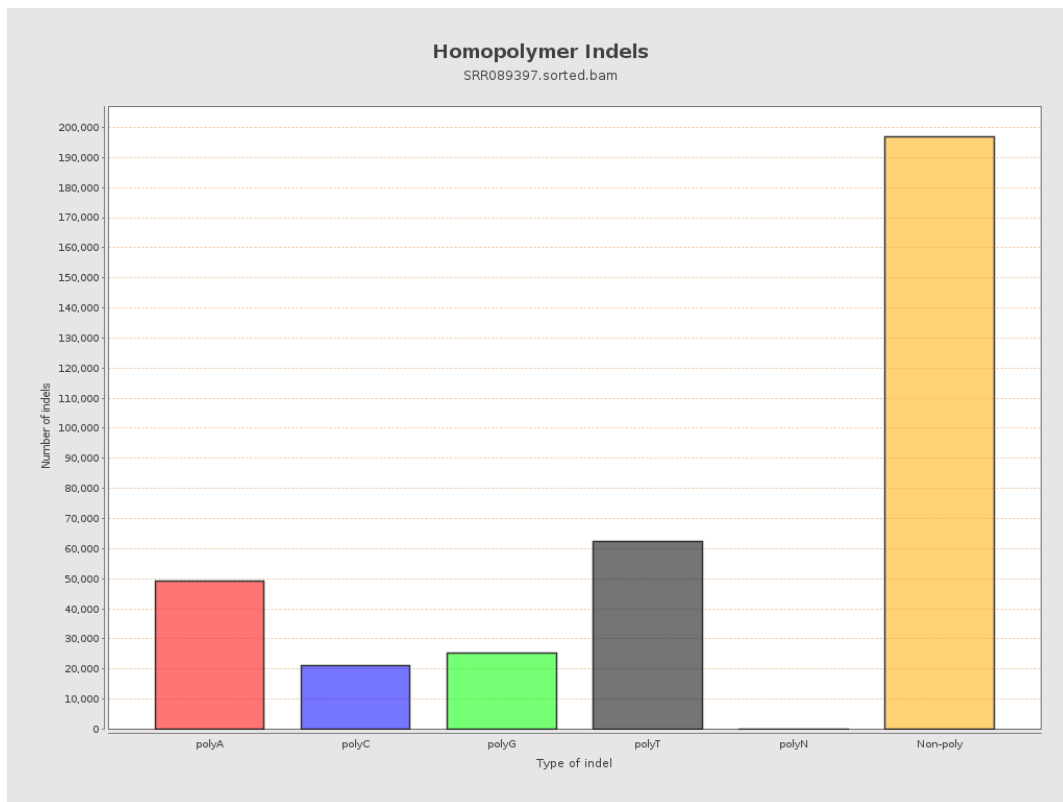
9. Results : Mapped Reads GC-content Distribution



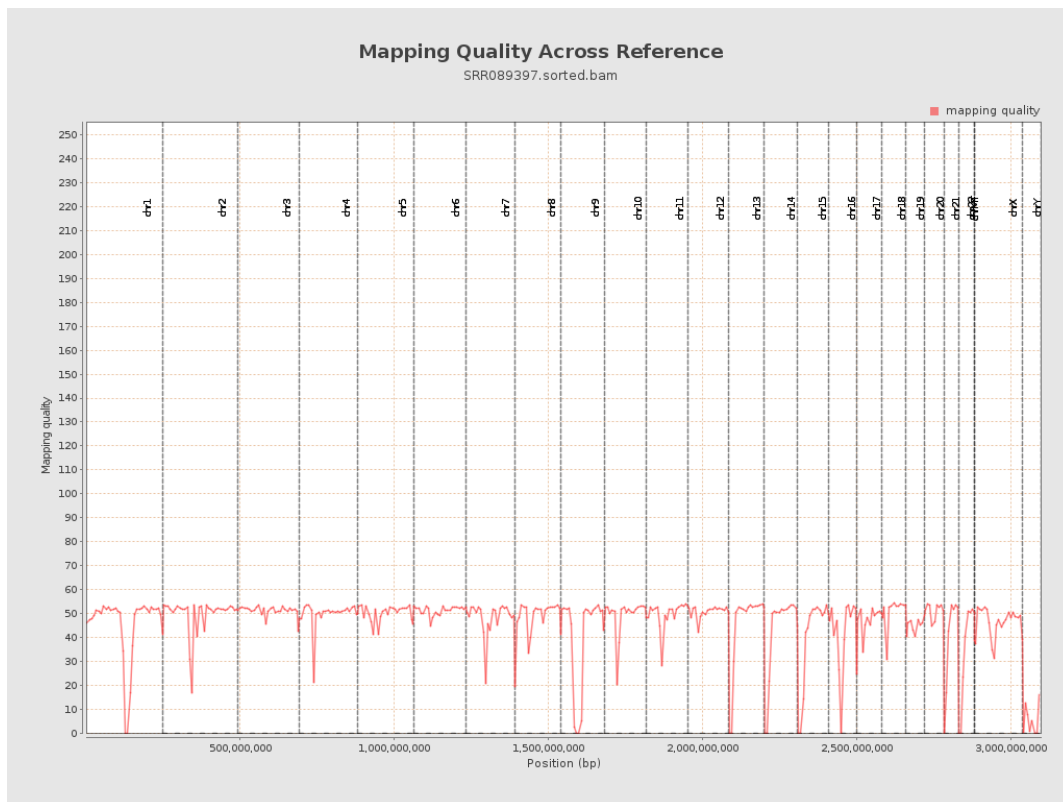
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

