

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:29:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080754.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_SRR3080754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080754.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:29:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080754.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,047,515
Mapped reads	6,563,175 / 81.56%
Unmapped reads	1,484,340 / 18.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,503 / 0.35%
Read min/max/mean length	30 / 66 / 66.12
Duplicated reads (estimated)	798,146 / 9.92%
Duplication rate	9.23%
Clipped reads	835,278 / 10.38%

2.2. ACGT Content

Number/percentage of A's	129,139,975 / 30.68%
Number/percentage of C's	84,557,688 / 20.09%
Number/percentage of T's	112,398,223 / 26.71%
Number/percentage of G's	93,797,203 / 22.29%
Number/percentage of N's	971,757 / 0.23%
GC Percentage	42.38%

2.3. Coverage

Mean	0.136

Standard Deviation	0.8452
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2.4. Mapping Quality

Mean Mapping Quality	45.49
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2.5. Mismatches and indels

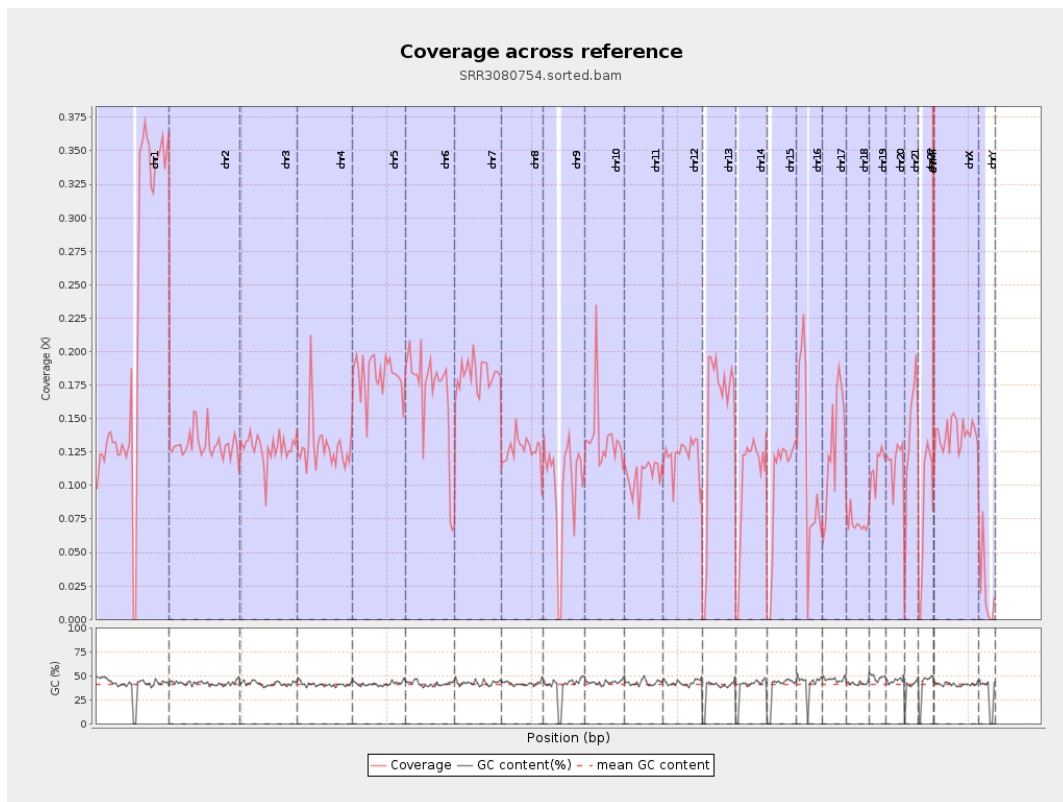
General error rate	0.97%
Mismatches	4,040,648
Insertions	29,089
Mapped reads with at least one insertion	0.44%
Deletions	71,487
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.63%

2.6. Chromosome stats

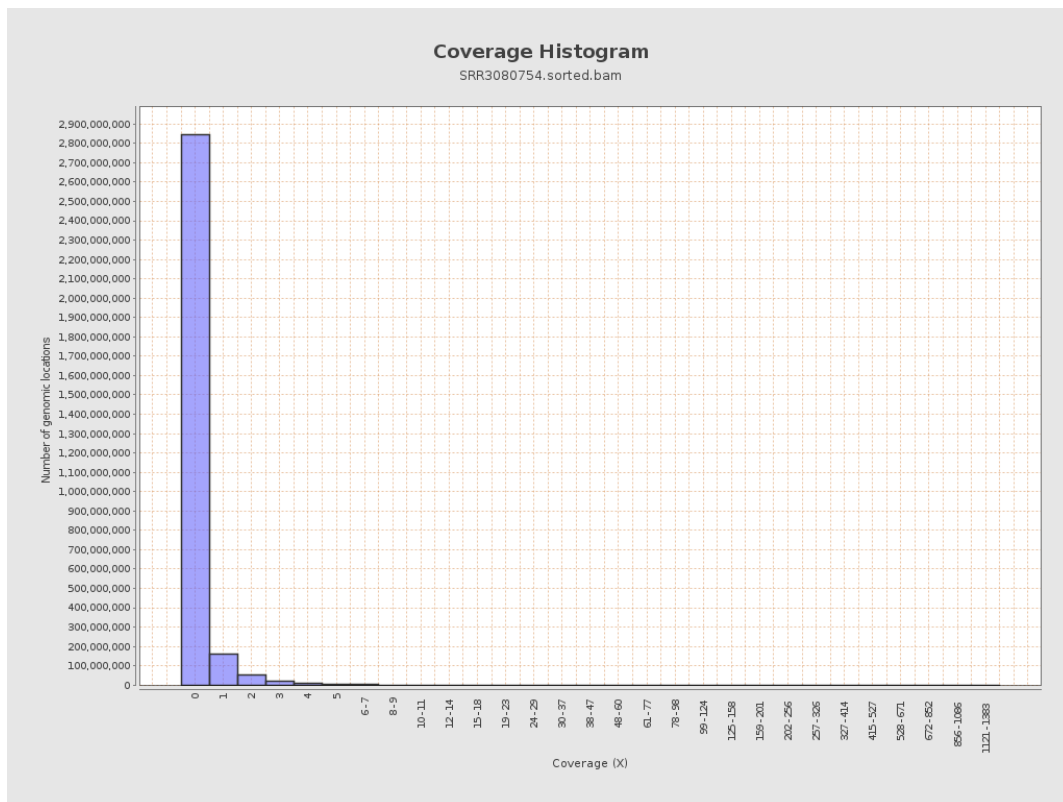
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	53329837	0.214	1.3329
chr2	243199373	31818306	0.1308	0.7804
chr3	198022430	25306953	0.1278	0.5632
chr4	191154276	24570614	0.1285	0.7044
chr5	180915260	32859230	0.1816	0.6761
chr6	171115067	28906034	0.1689	0.8941
chr7	159138663	29131376	0.1831	1.2935

chr8	146364022	18518311	0.1265	1.0783
chr9	141213431	14011383	0.0992	0.6207
chr10	135534747	18326358	0.1352	1.0704
chr11	135006516	14545706	0.1077	0.6966
chr12	133851895	16304179	0.1218	0.5574
chr13	115169878	17391836	0.151	0.6159
chr14	107349540	10982573	0.1023	0.6274
chr15	102531392	10261391	0.1001	0.4873
chr16	90354753	10420696	0.1153	0.6143
chr17	81195210	10657799	0.1313	0.6012
chr18	78077248	5610067	0.0719	1.0525
chr19	59128983	6725031	0.1137	1.0941
chr20	63025520	7425508	0.1178	0.589
chr21	48129895	6621012	0.1376	0.7144
chr22	51304566	4285773	0.0835	0.4565
chrMT	16571	297718	17.9662	13.1939
chrX	155270560	21434003	0.138	0.6232
chrY	59373566	1258094	0.0212	0.7008

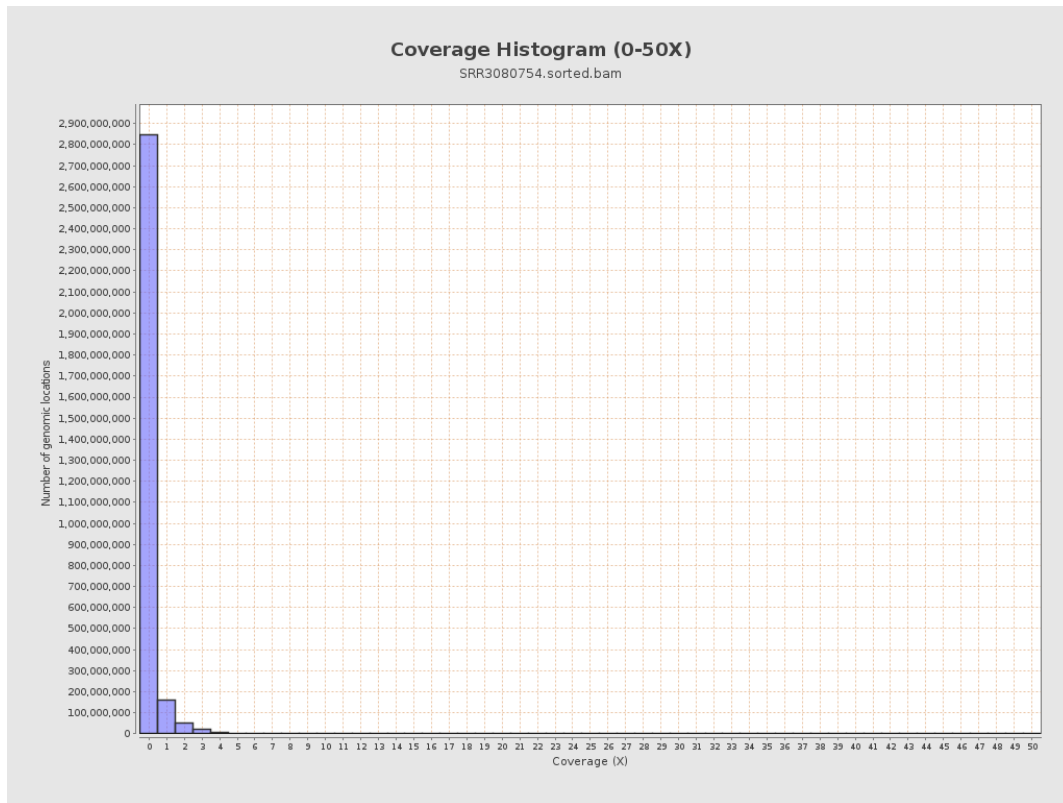
3. Results : Coverage across reference



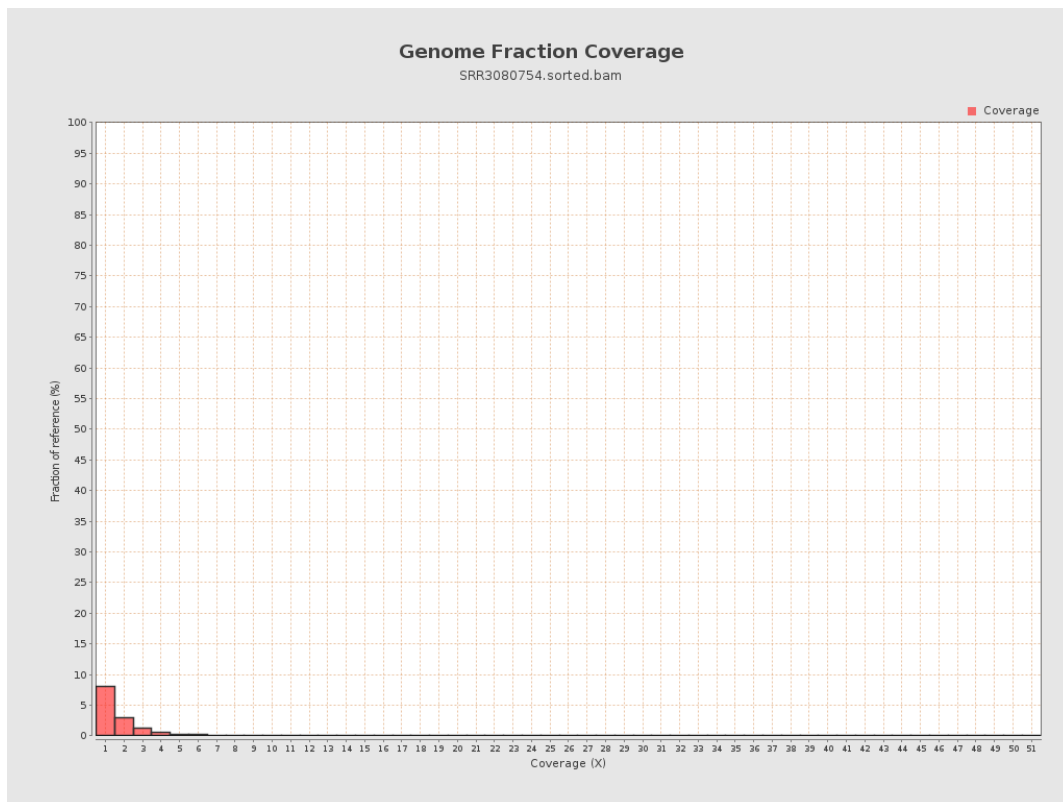
4. Results : Coverage Histogram



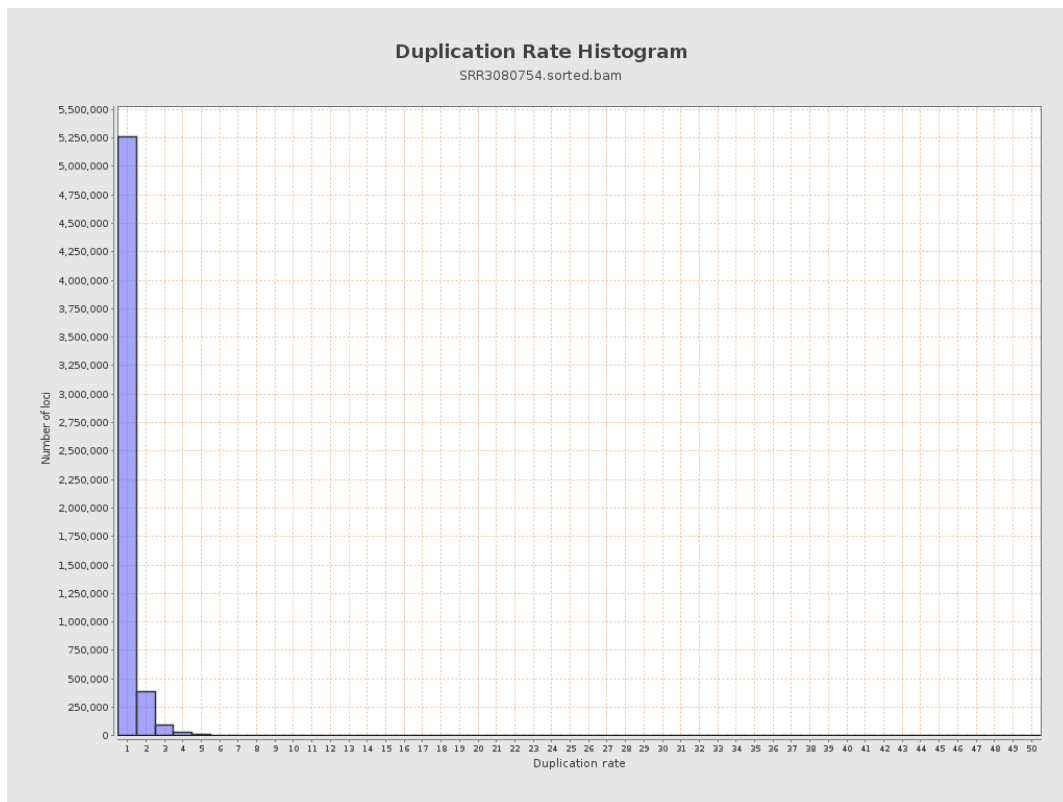
5. Results : Coverage Histogram (0-50X)



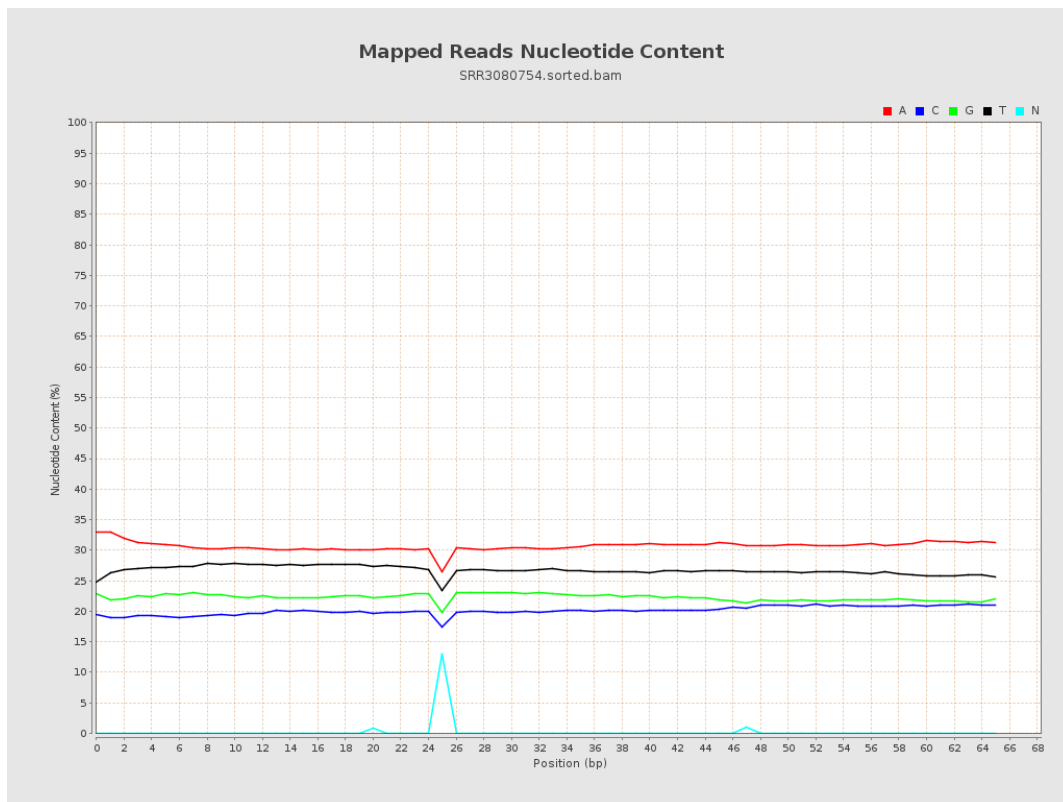
6. Results : Genome Fraction Coverage



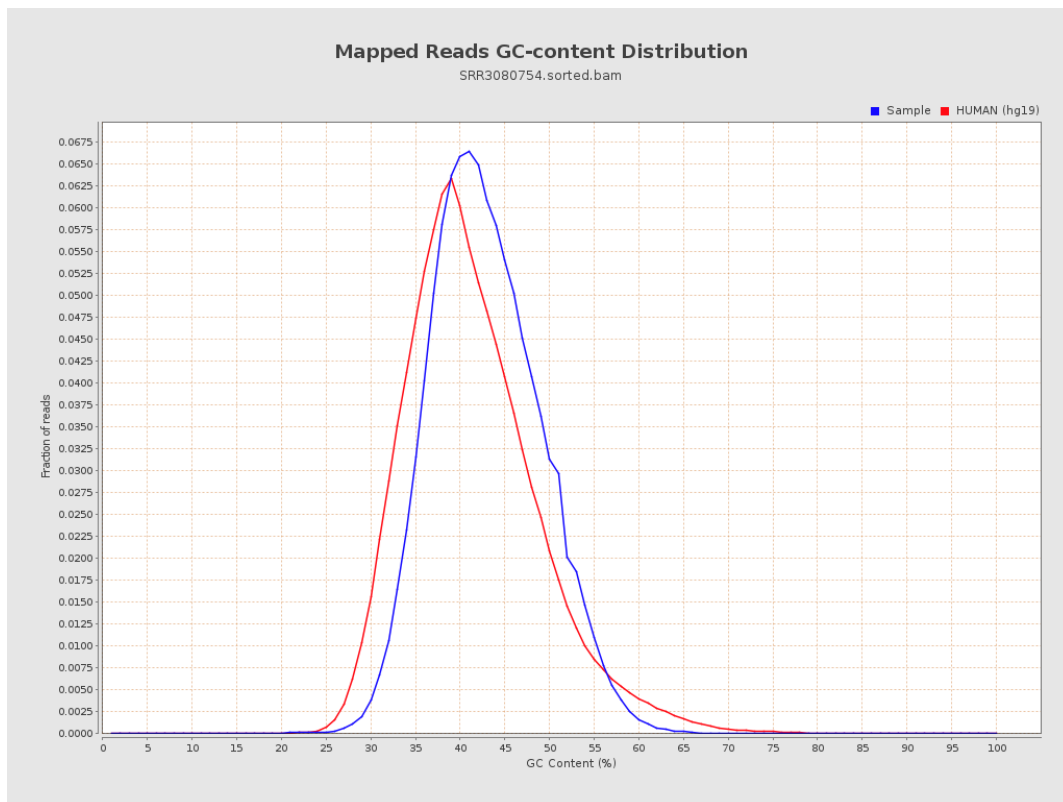
7. Results : Duplication Rate Histogram



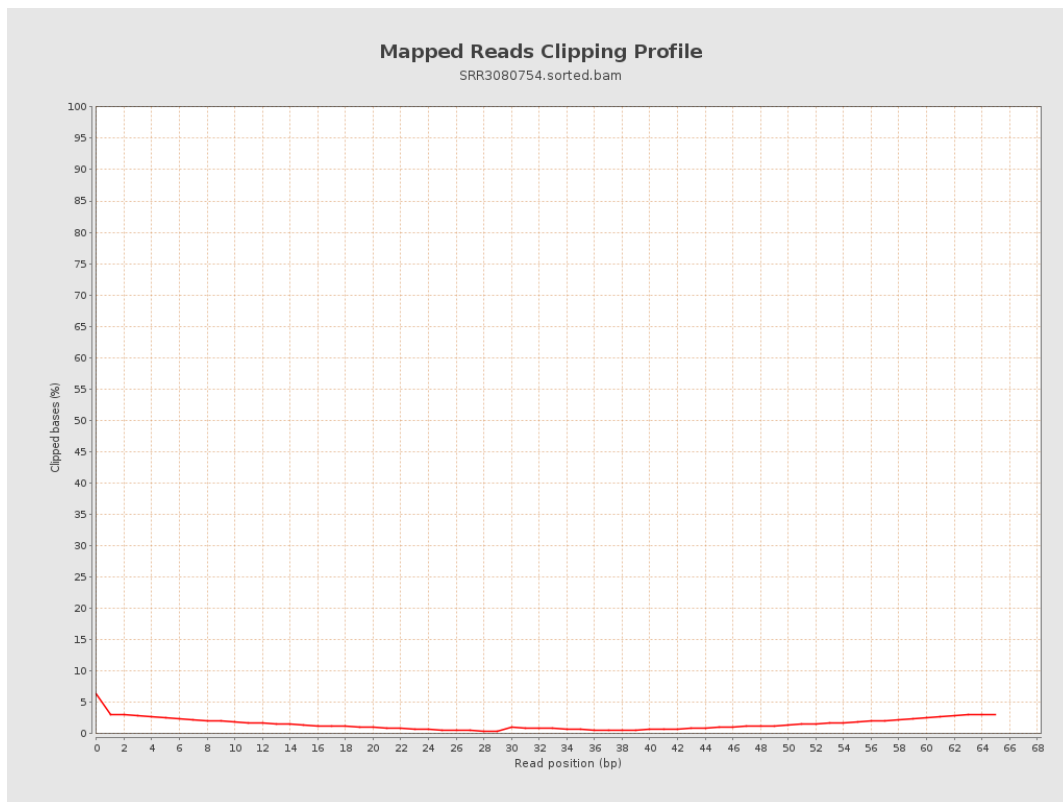
8. Results : Mapped Reads Nucleotide Content



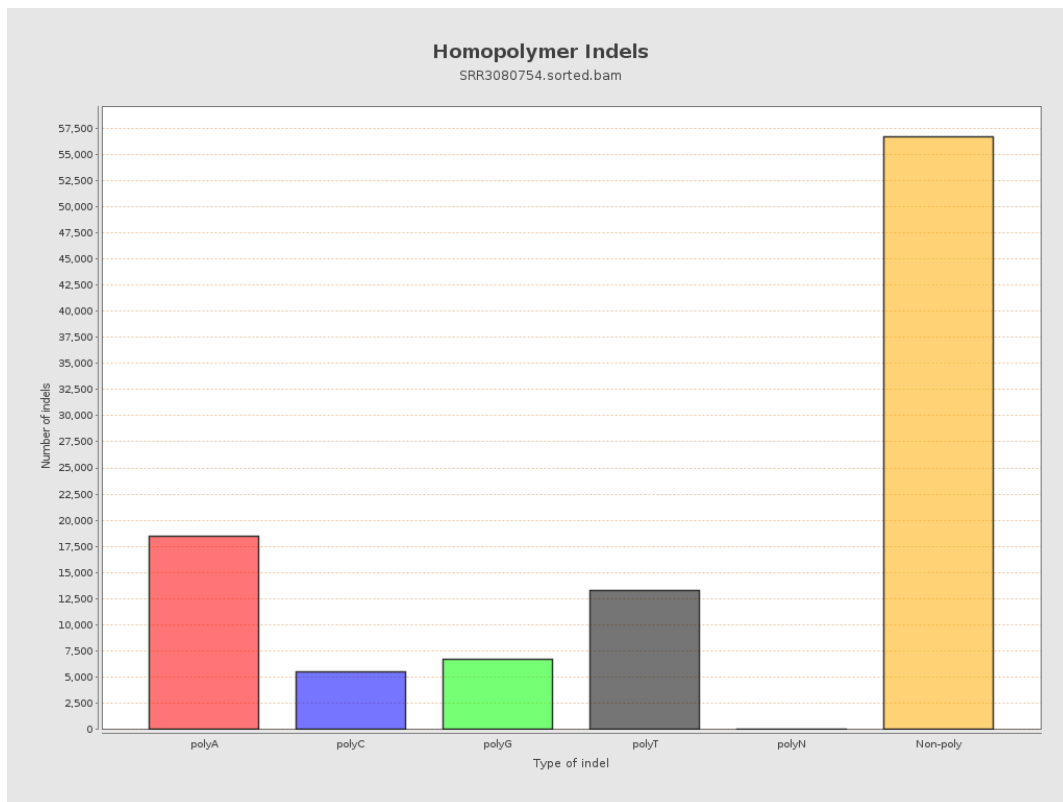
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

