Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 17:17:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089604.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_SRR089604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089604.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 17:17:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,050,157
Mapped reads	7,388,733 / 81.64%
Unmapped reads	1,661,424 / 18.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	296 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,538,193 / 28.05%
Duplication rate	25.93%
Clipped reads	818,661 / 9.05%

2.2. ACGT Content

Number/percentage of A's	110,975,830 / 31.96%
Number/percentage of C's	67,246,273 / 19.36%
Number/percentage of T's	91,989,221 / 26.49%
Number/percentage of G's	76,983,558 / 22.17%
Number/percentage of N's	64,246 / 0.02%
GC Percentage	41.53%

2.3. Coverage

Mean	0.1122

Standard Deviation	1.0001

2.4. Mapping Quality

Mean Mapping Quality	43.25

2.5. Mismatches and indels

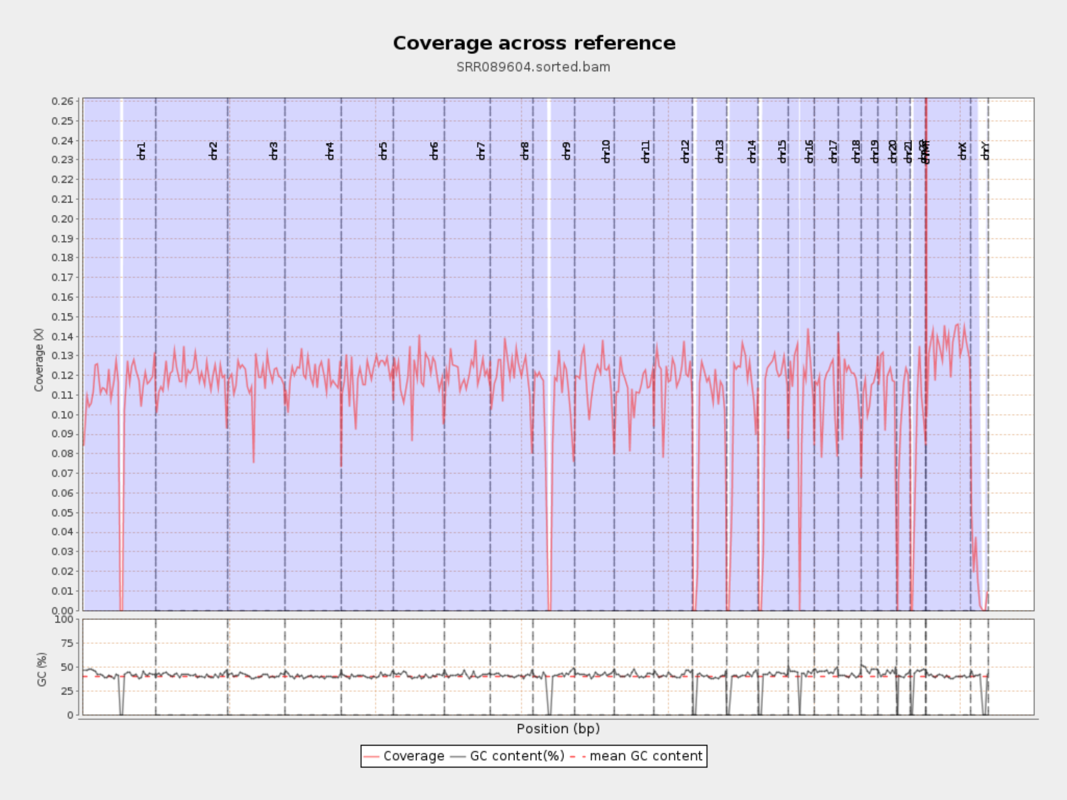
General error rate	0.54%
Mismatches	1,846,052
Insertions	15,218
Mapped reads with at least one insertion	0.21%
Deletions	46,648
Mapped reads with at least one deletion	0.63%
Homopolymer indels	45.4%

2.6. Chromosome stats

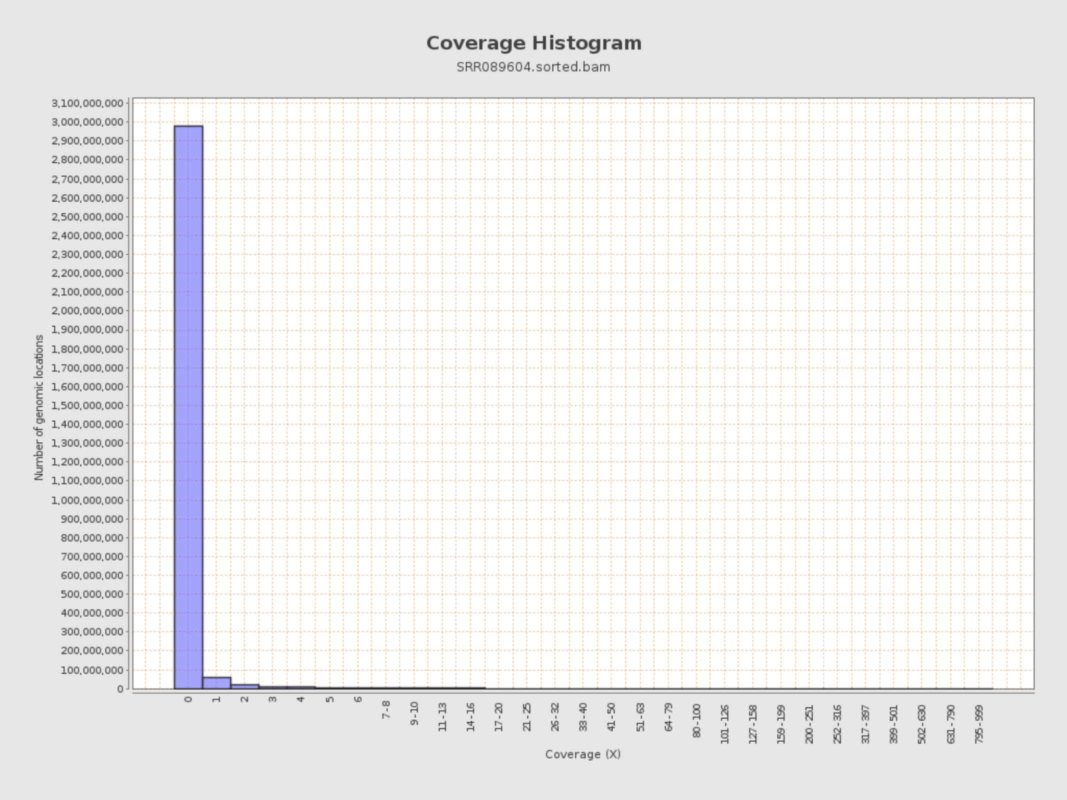
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27041550	0.1085	1.0738
chr2	243199373	29120406	0.1197	1.1075
chr3	198022430	23380160	0.1181	0.9653
chr4	191154276	22934724	0.12	1.0133
chr5	180915260	21694536	0.1199	0.976
chr6	171115067	20558102	0.1201	1.0587
chr7	159138663	19313785	0.1214	1.0578

chr8	146364022	17576342	0.1201	1.1569
chr9	141213431	13982347	0.099	0.8929
chr10	135534747	16160632	0.1192	1.0142
chr11	135006516	15237260	0.1129	1.0465
chr12	133851895	16156007	0.1207	0.9736
chr13	115169878	11006900	0.0956	0.8606
chr14	107349540	10761920	0.1003	0.9303
chr15	102531392	10140928	0.0989	0.8832
chr16	90354753	9804818	0.1085	0.9312
chr17	81195210	9129943	0.1124	0.9196
chr18	78077248	9108253	0.1167	1.0182
chr19	59128983	6565985	0.111	1.0008
chr20	63025520	7297373	0.1158	0.9571
chr21	48129895	4523573	0.094	0.8942
chr22	51304566	3998082	0.0779	0.8268
chrMT	16571	152240	9.1871	17.0068
chrX	155270560	20774910	0.1338	1.0652
chrY	59373566	908431	0.0153	0.304

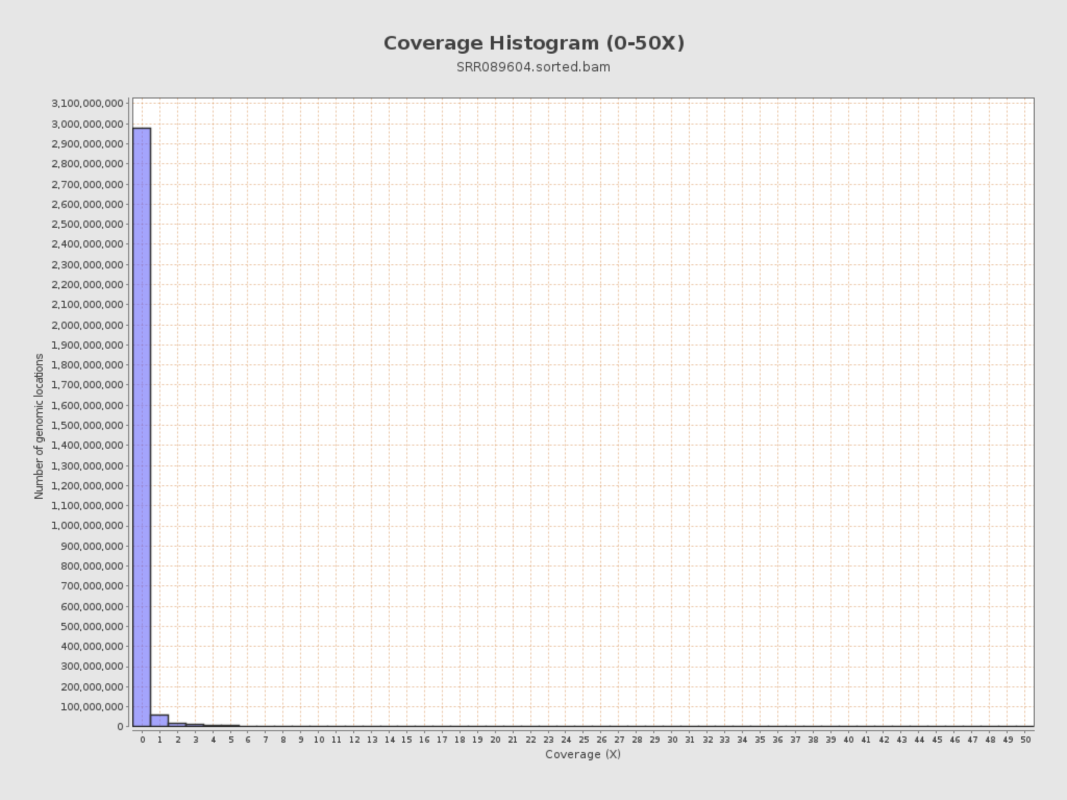
3. Results : Coverage across reference



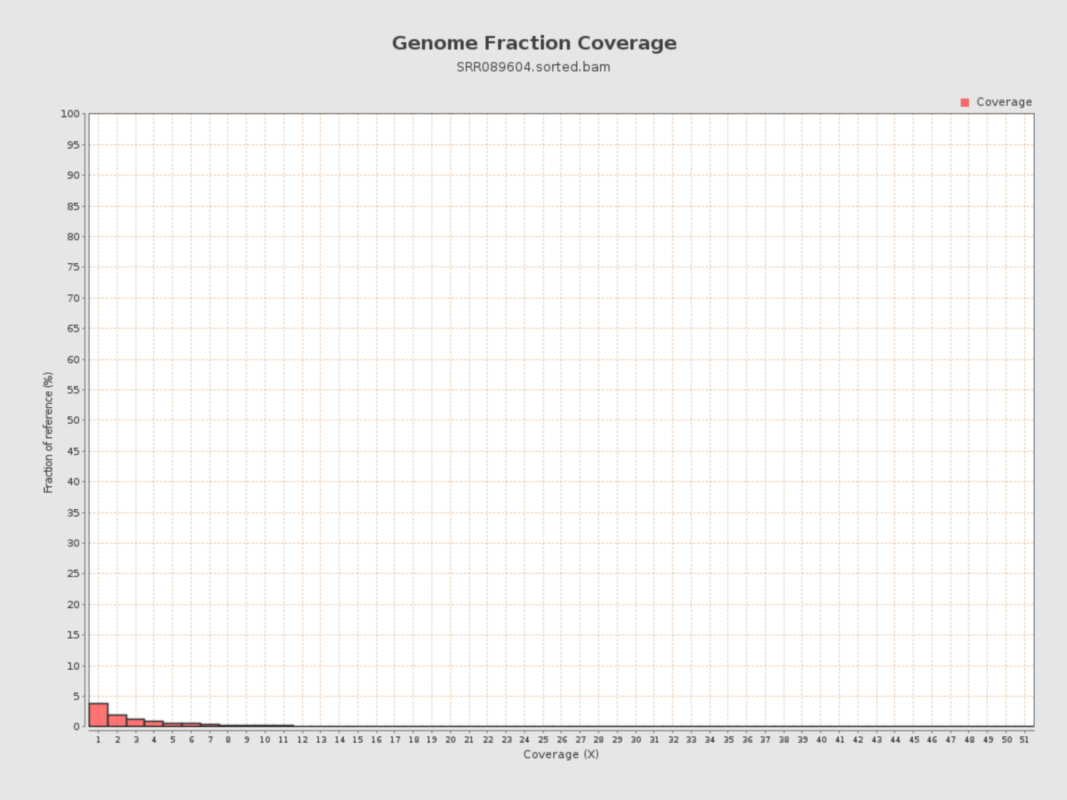
4. Results : Coverage Histogram



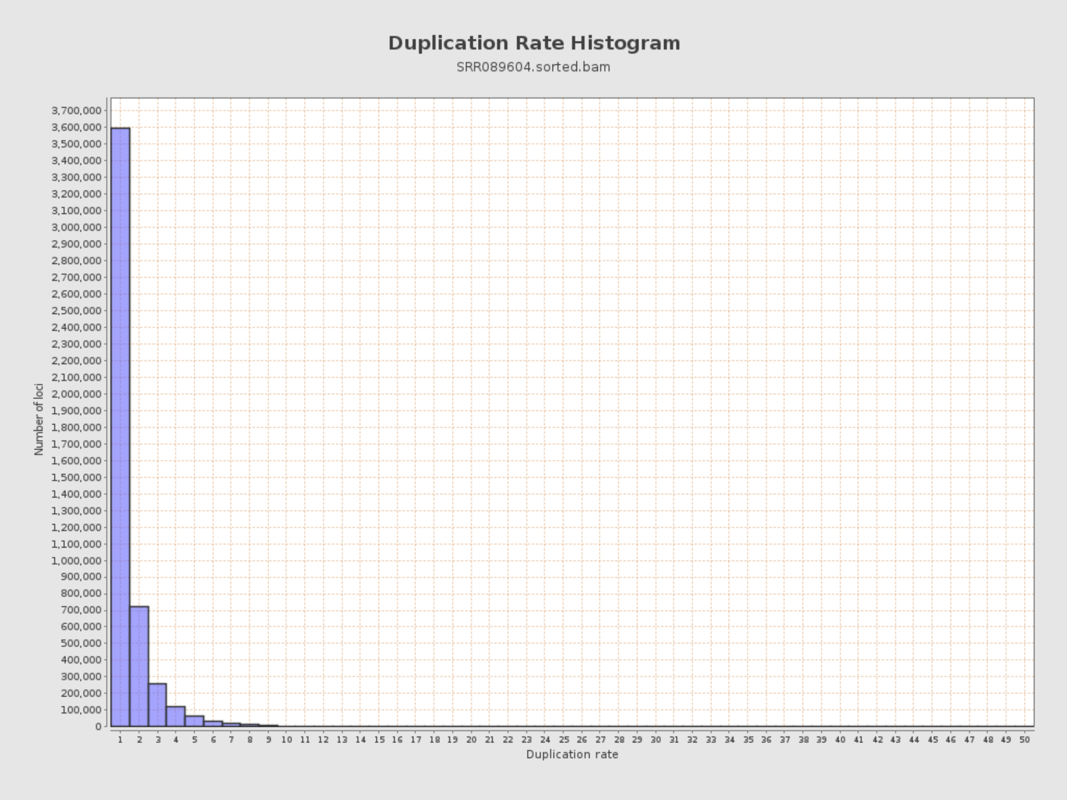
5. Results : Coverage Histogram (0-50X)



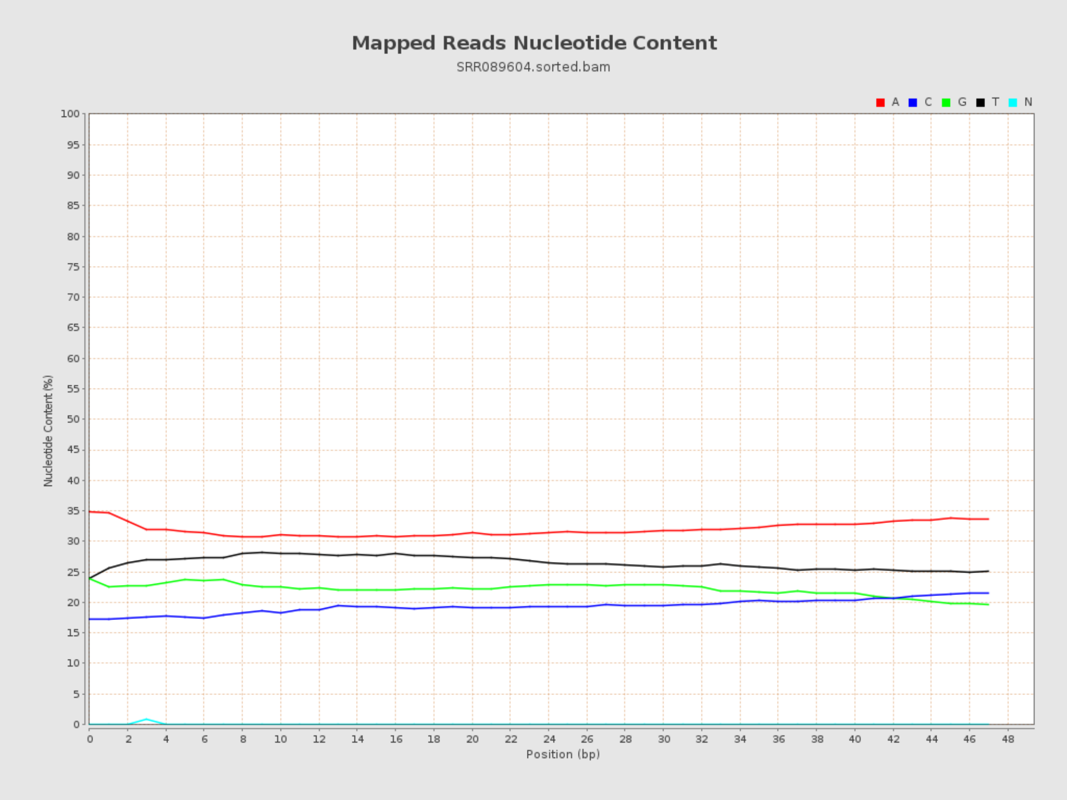
6. Results : Genome Fraction Coverage



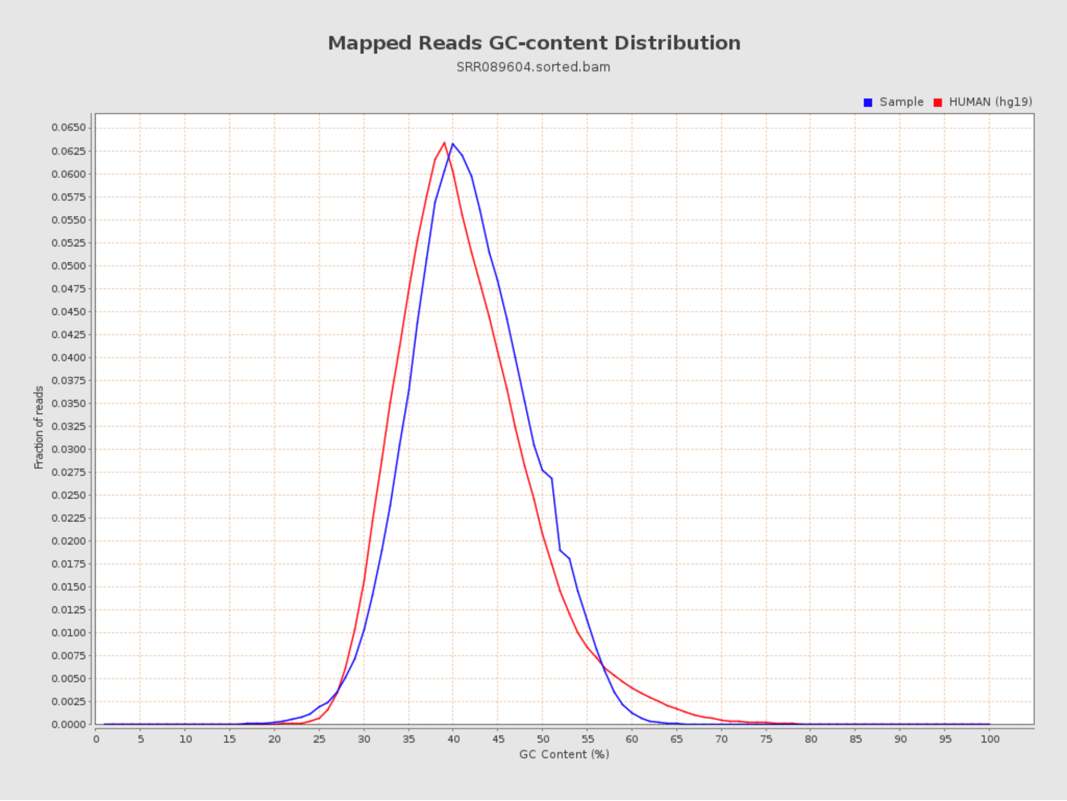
7. Results : Duplication Rate Histogram



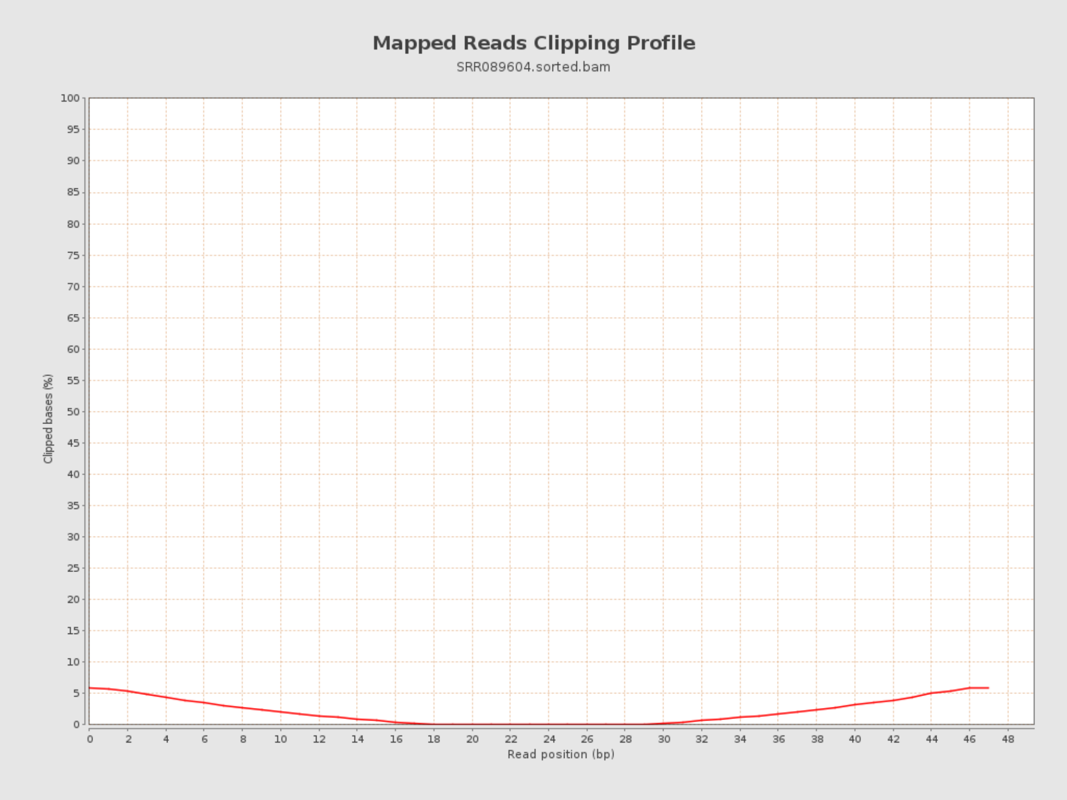
8. Results : Mapped Reads Nucleotide Content



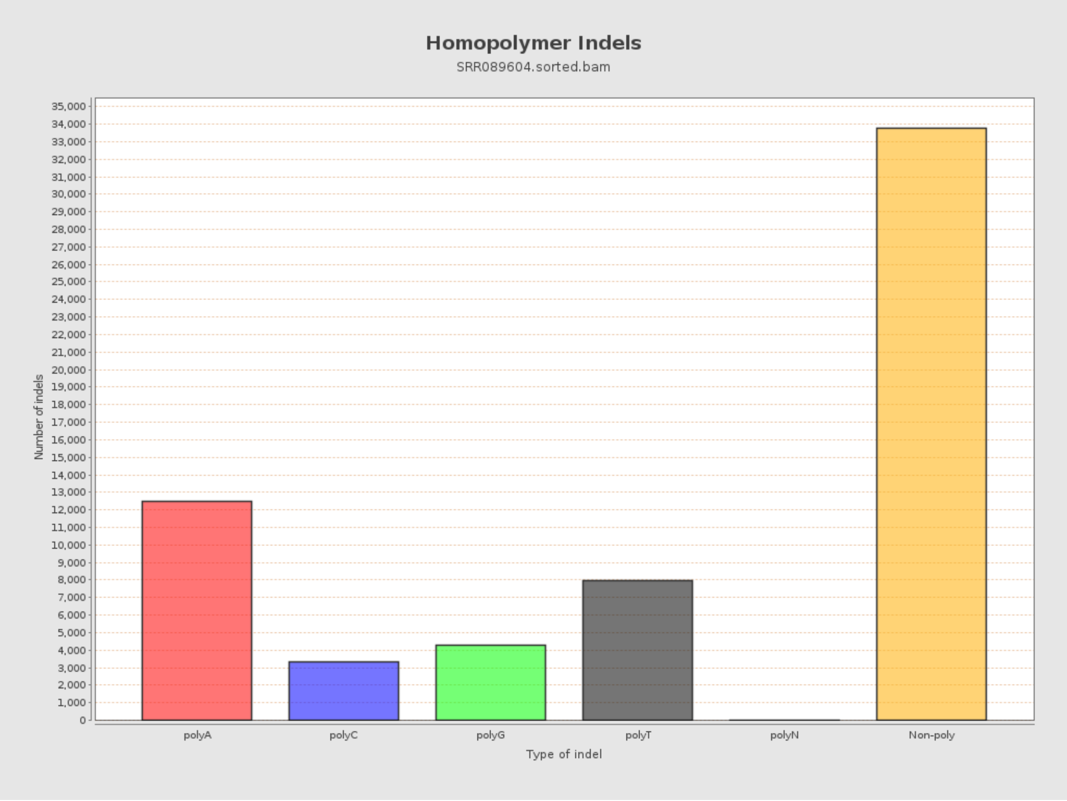
9. Results : Mapped Reads GC-content Distribution



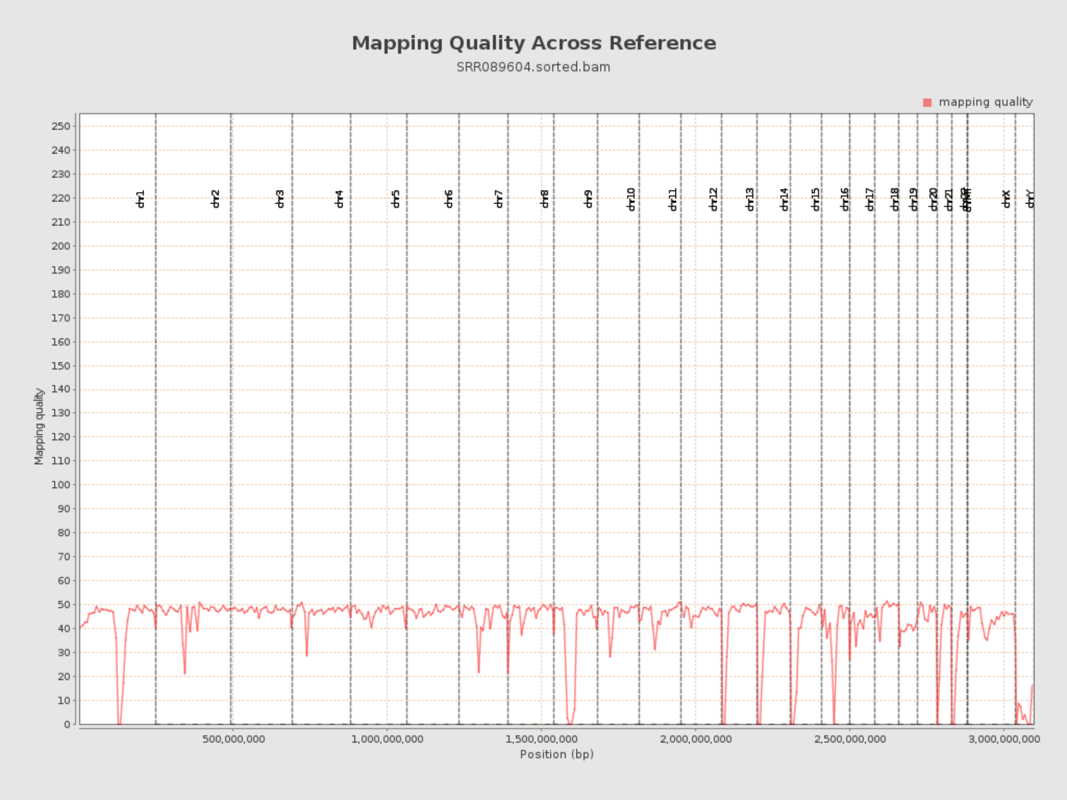
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram