Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:01:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006442.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_SRR1006442 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006442.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:01:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006442.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,260,768
Mapped reads	1,170,499 / 92.84%
Unmapped reads	90,269 / 7.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,768 / 0.3%
Read min/max/mean length	30 / 59 / 56.65
Duplicated reads (estimated)	27,231 / 2.16%
Duplication rate	1.7%
Clipped reads	180,824 / 14.34%

2.2. ACGT Content

Number/percentage of A's	17,896,441 / 27.74%
Number/percentage of C's	13,717,577 / 21.26%
Number/percentage of T's	18,546,777 / 28.75%
Number/percentage of G's	14,352,824 / 22.25%
Number/percentage of N's	1,367 / 0%
GC Percentage	43.51%

2.3. Coverage

Mean	0.0208

Standard Deviation	0.2678

2.4. Mapping Quality

Mean Mapping Quality	44.53

2.5. Mismatches and indels

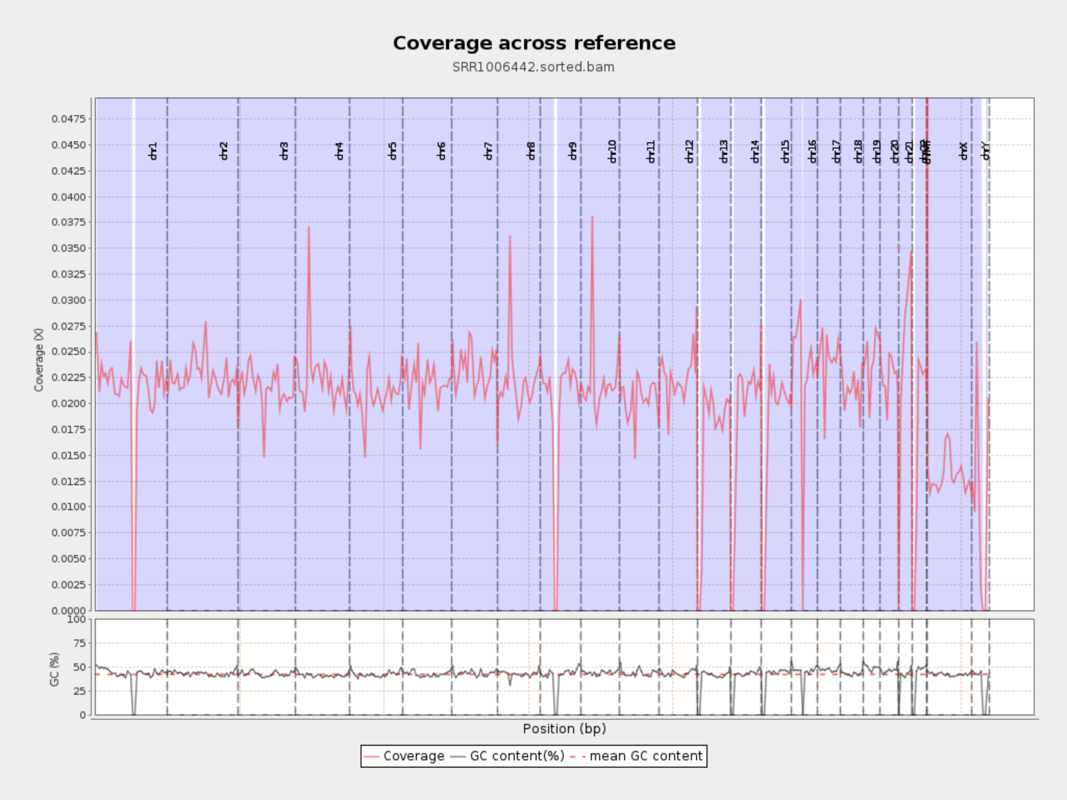
General error rate	0.44%
Mismatches	274,900
Insertions	4,305
Mapped reads with at least one insertion	0.37%
Deletions	12,777
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.03%

2.6. Chromosome stats

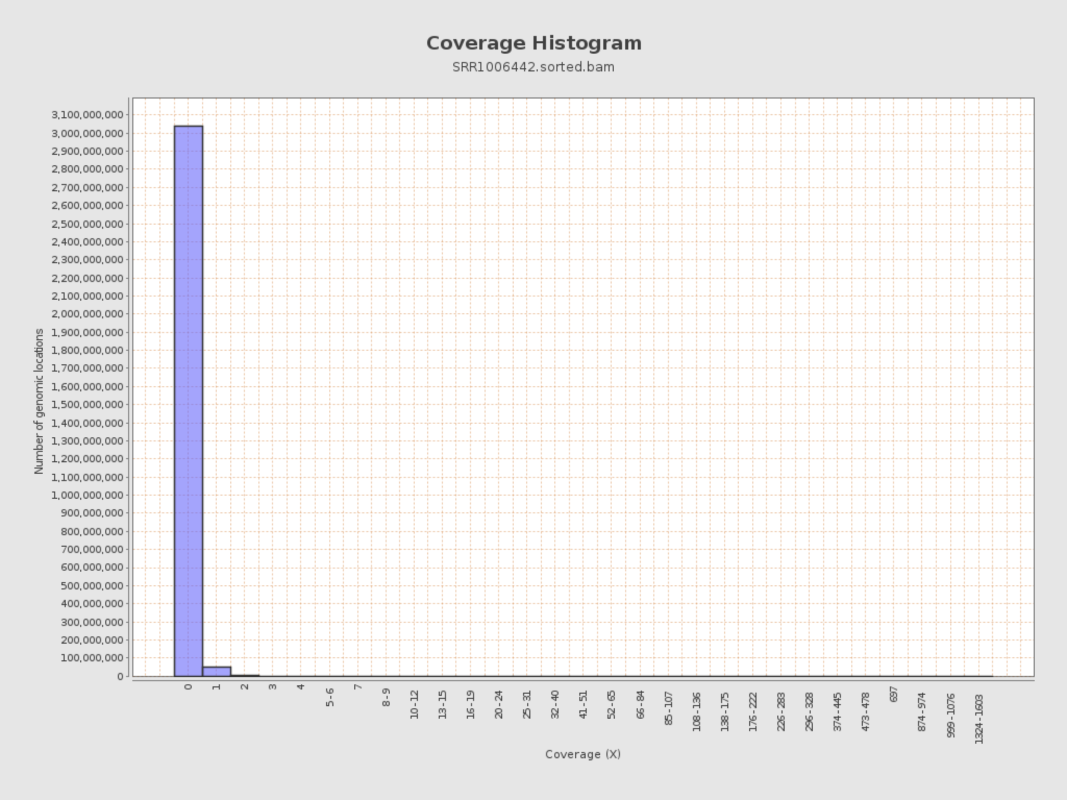
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5185203	0.0208	0.2349
chr2	243199373	5531124	0.0227	0.2022
chr3	198022430	4249904	0.0215	0.1636
chr4	191154276	4316371	0.0226	0.1829
chr5	180915260	3789644	0.0209	0.1623
chr6	171115067	3767717	0.022	0.1716
chr7	159138663	3728279	0.0234	0.2034

chr8	146364022	3260317	0.0223	0.9017
chr9	141213431	2760840	0.0196	0.1647
chr10	135534747	3027054	0.0223	0.2168
chr11	135006516	2779220	0.0206	0.1693
chr12	133851895	3017993	0.0225	0.1696
chr13	115169878	1882282	0.0163	0.143
chr14	107349540	1943545	0.0181	0.1539
chr15	102531392	1779374	0.0174	0.1478
chr16	90354753	2043931	0.0226	0.1822
chr17	81195210	1979630	0.0244	0.1842
chr18	78077248	1670616	0.0214	0.1955
chr19	59128983	1439016	0.0243	0.2113
chr20	63025520	1420971	0.0225	0.1729
chr21	48129895	1227703	0.0255	0.195
chr22	51304566	830009	0.0162	0.1573
chrMT	16571	264723	15.9751	9.0856
chrX	155270560	2037683	0.0131	0.1296
chrY	59373566	603517	0.0102	0.1671

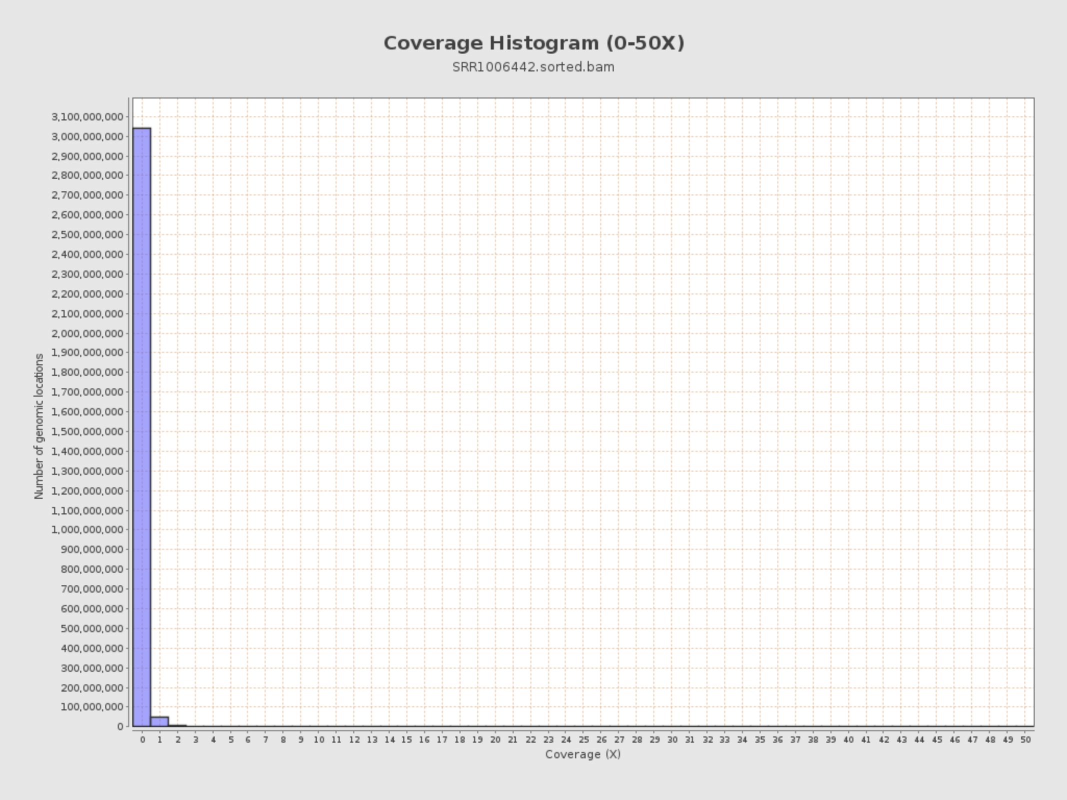
3. Results : Coverage across reference



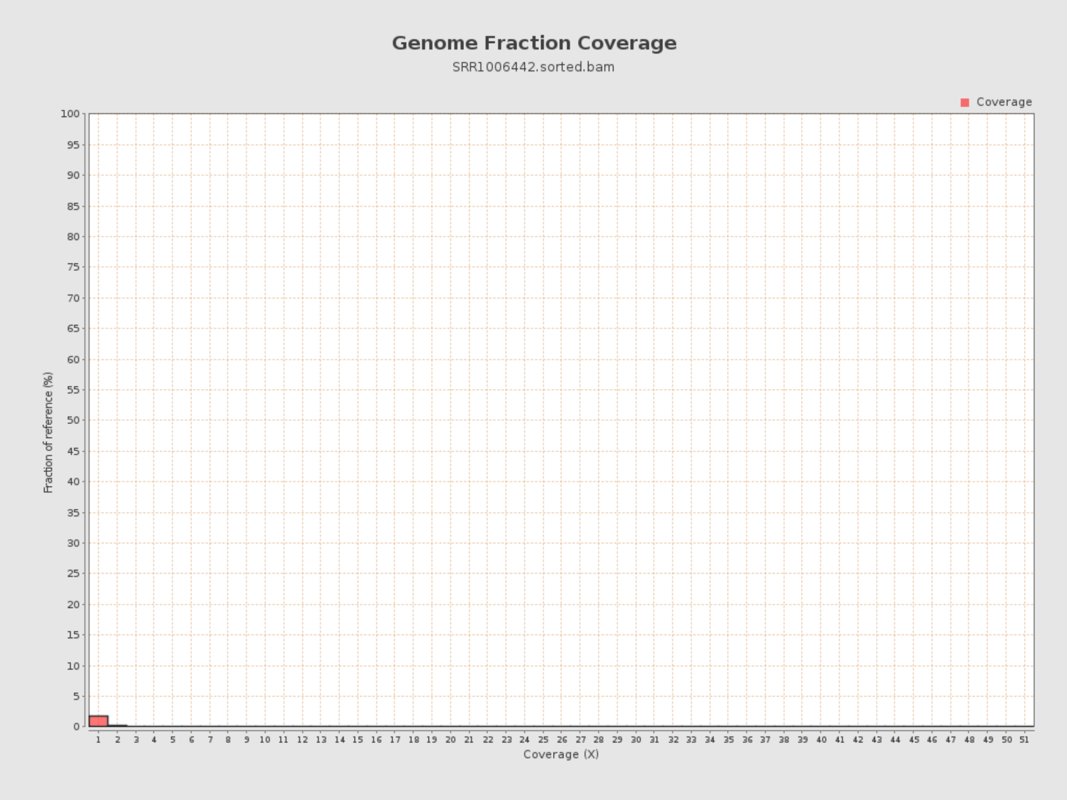
4. Results : Coverage Histogram



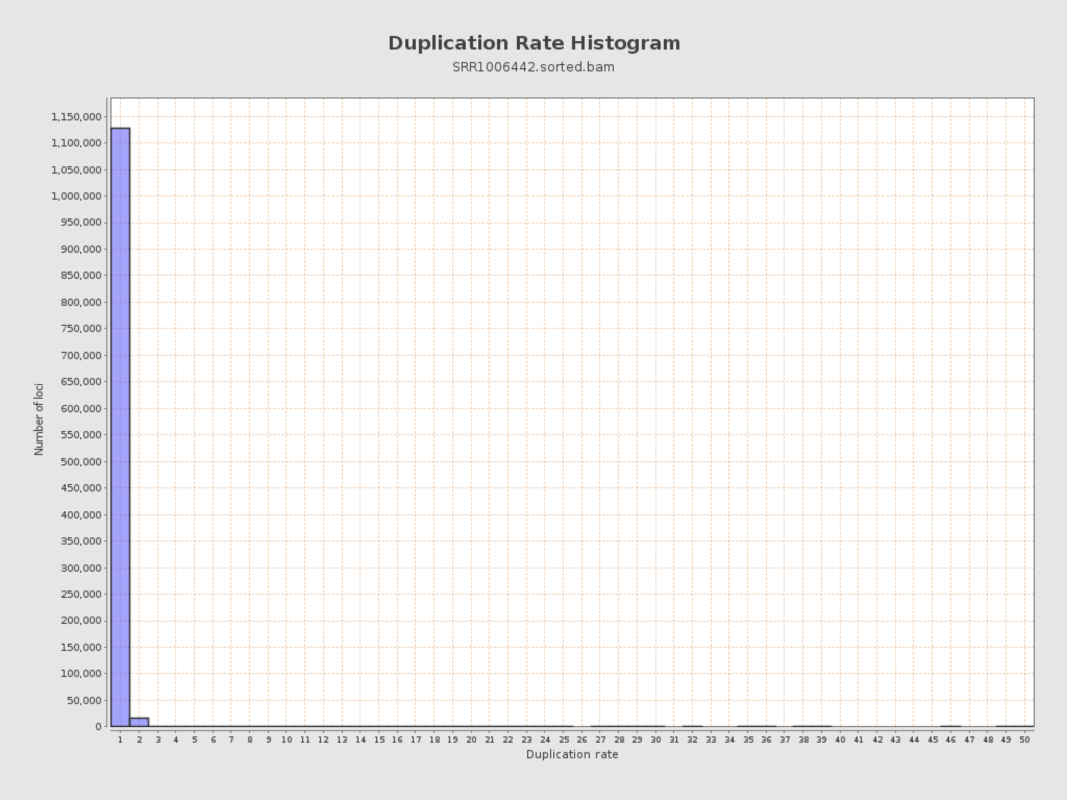
5. Results : Coverage Histogram (0-50X)



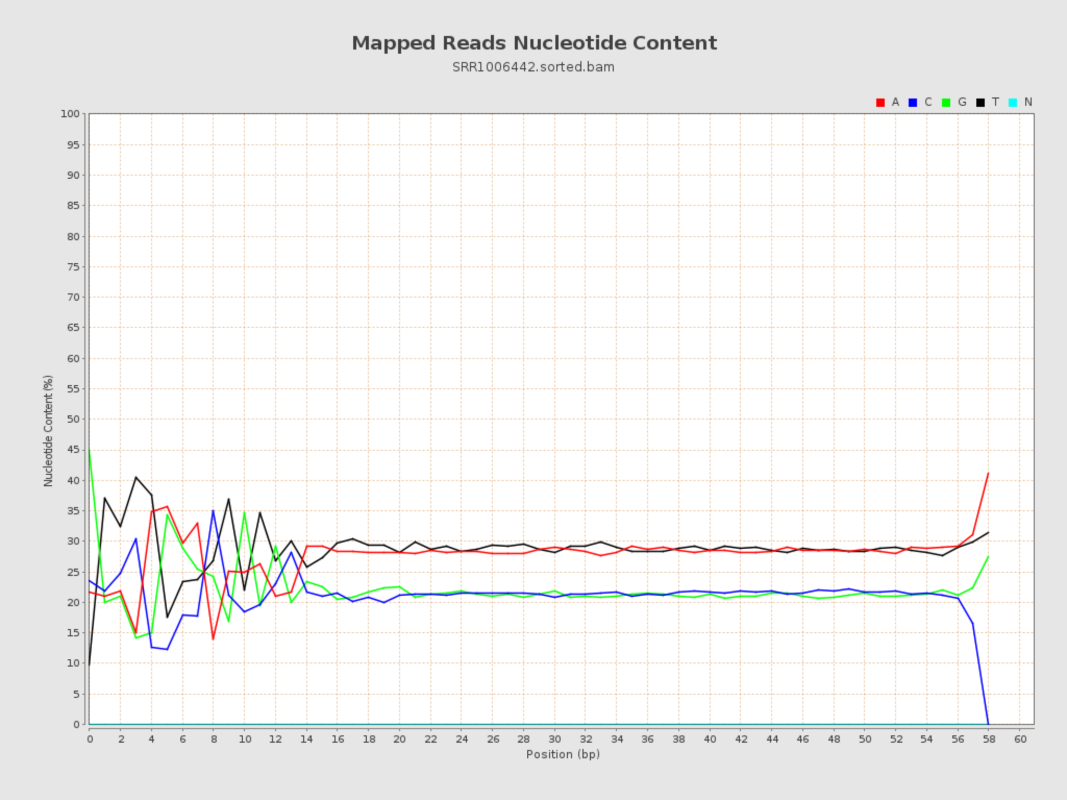
6. Results : Genome Fraction Coverage



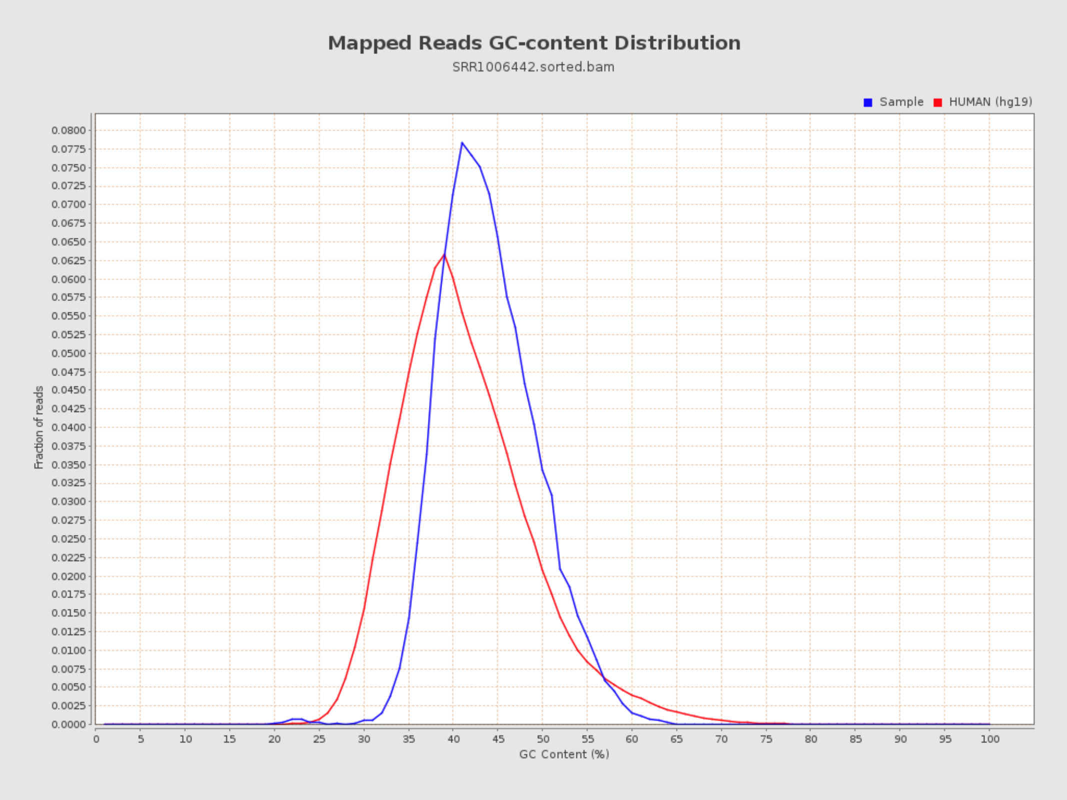
7. Results : Duplication Rate Histogram



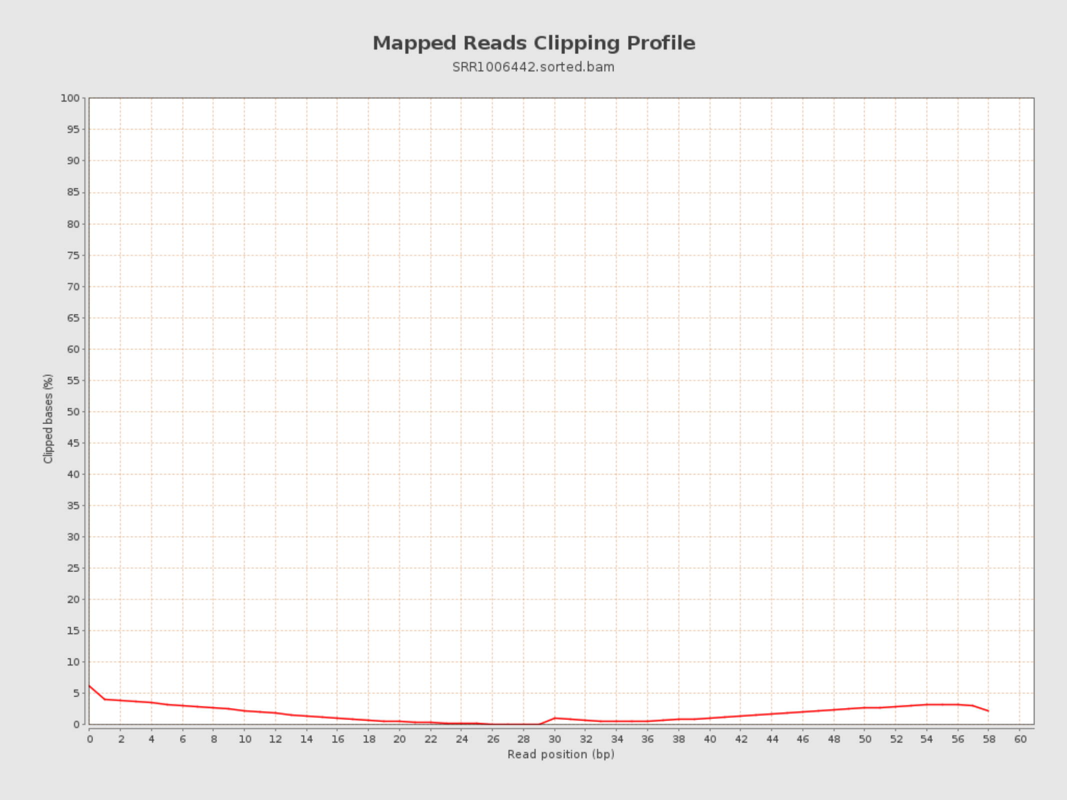
8. Results : Mapped Reads Nucleotide Content



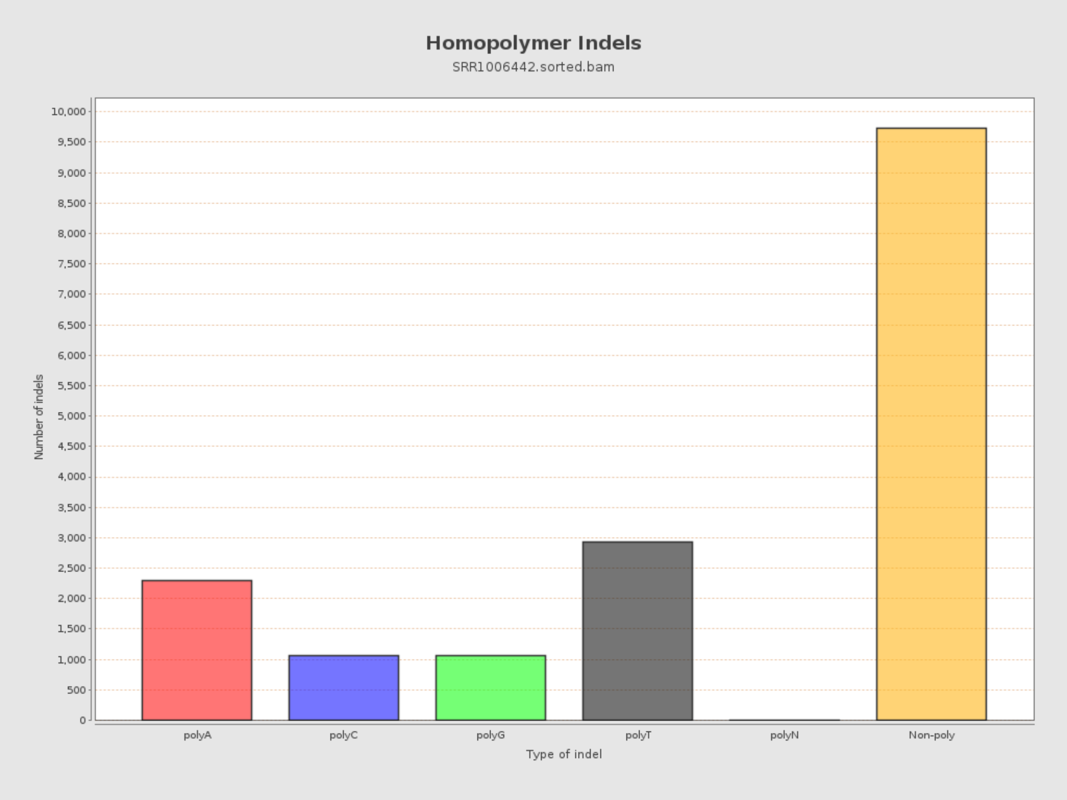
9. Results : Mapped Reads GC-content Distribution



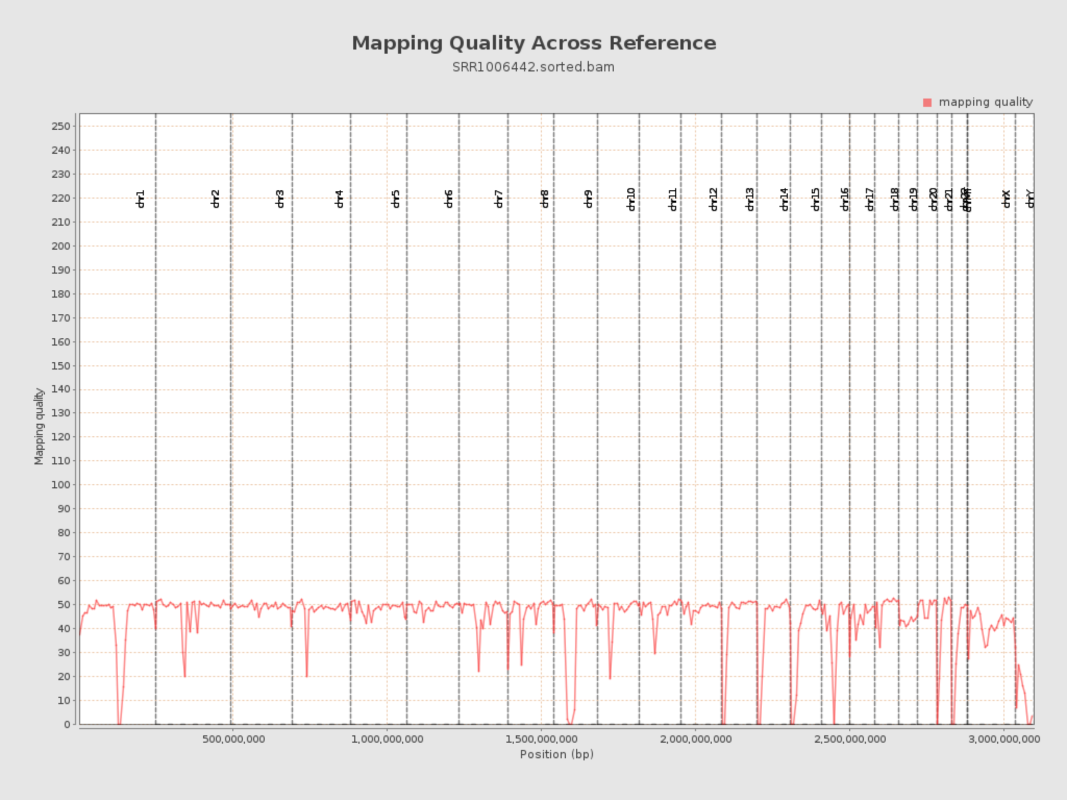
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram