Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:03:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080656.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_SRR3080656 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080656.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:03:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080656.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,460,392
Mapped reads	1,311,114 / 89.78%
Unmapped reads	149,278 / 10.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,570 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	46,475 / 3.18%
Duplication rate	2.78%
Clipped reads	714,867 / 48.95%

2.2. ACGT Content

Number/percentage of A's	22,287,334 / 26.33%
Number/percentage of C's	15,500,419 / 18.31%
Number/percentage of T's	26,718,119 / 31.56%
Number/percentage of G's	20,137,569 / 23.79%
Number/percentage of N's	3,417 / 0%
GC Percentage	42.1%

2.3. Coverage

Mean	0.0274

Standard Deviation	0.2667

2.4. Mapping Quality

Mean Mapping Quality	43.58

2.5. Mismatches and indels

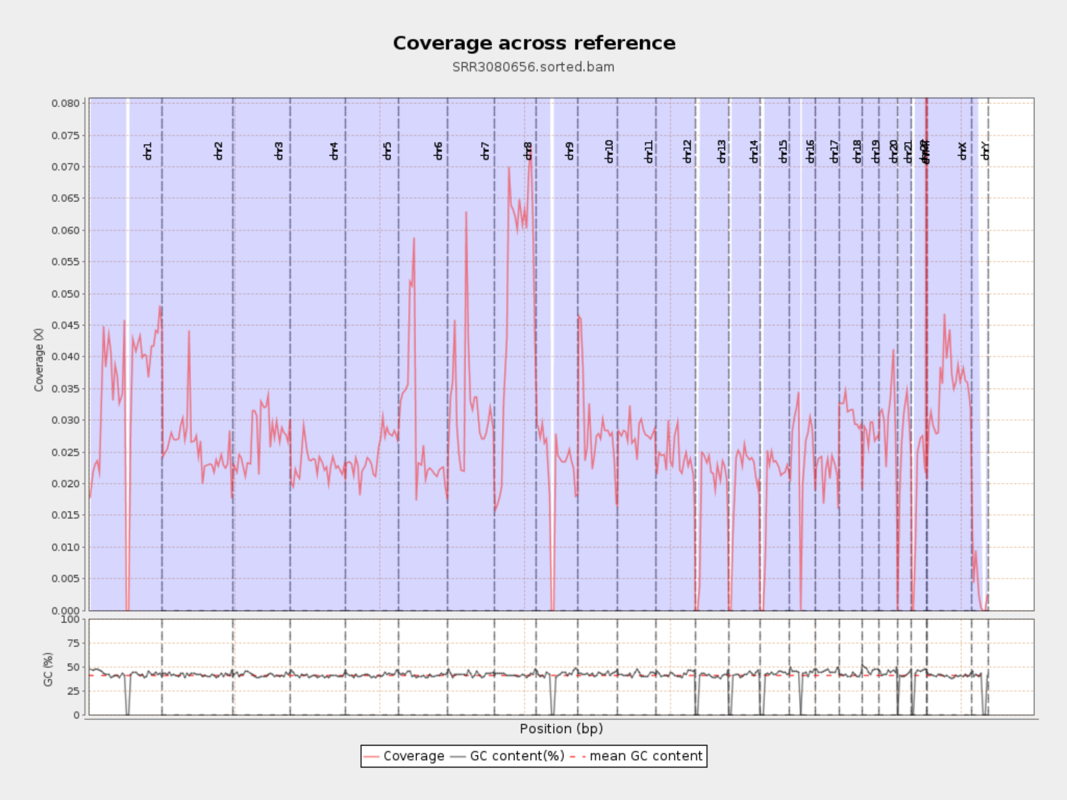
General error rate	0.76%
Mismatches	633,174
Insertions	6,894
Mapped reads with at least one insertion	0.52%
Deletions	23,231
Mapped reads with at least one deletion	1.75%
Homopolymer indels	45.04%

2.6. Chromosome stats

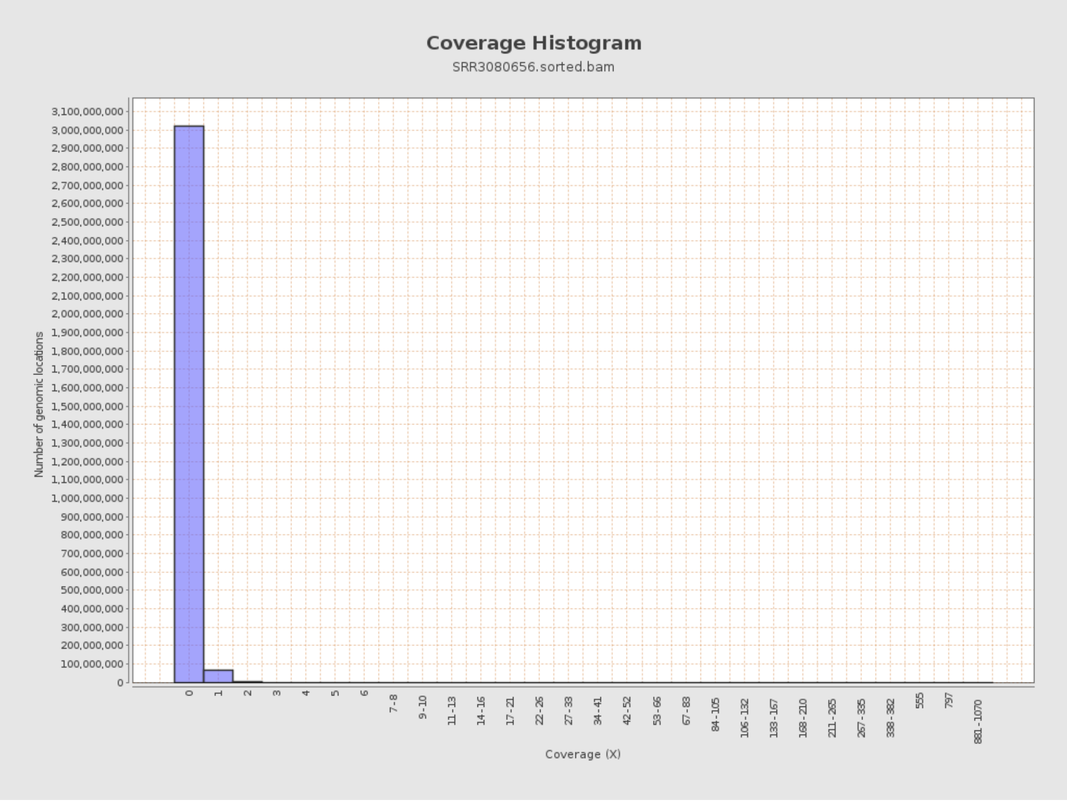
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8640256	0.0347	0.3352
chr2	243199373	6268612	0.0258	0.4861
chr3	198022430	5376616	0.0272	0.1804
chr4	191154276	4378367	0.0229	0.175
chr5	180915260	4458180	0.0246	0.172
chr6	171115067	4902003	0.0286	0.2326
chr7	159138663	5158214	0.0324	0.4521

chr8	146364022	7405675	0.0506	0.2945
chr9	141213431	3103692	0.022	0.2142
chr10	135534747	3976551	0.0293	0.2159
chr11	135006516	3748056	0.0278	0.2379
chr12	133851895	3220614	0.0241	0.172
chr13	115169878	2153709	0.0187	0.1499
chr14	107349540	2124773	0.0198	0.1723
chr15	102531392	1910271	0.0186	0.1575
chr16	90354753	2286574	0.0253	0.1839
chr17	81195210	1788863	0.022	0.1774
chr18	78077248	2445149	0.0313	0.3155
chr19	59128983	1636882	0.0277	0.244
chr20	63025520	1918851	0.0304	0.1961
chr21	48129895	1207744	0.0251	0.1791
chr22	51304566	910571	0.0177	0.1457
chrMT	16571	9843	0.594	0.8564
chrX	155270560	5444880	0.0351	0.2186
chrY	59373566	209483	0.0035	0.0798

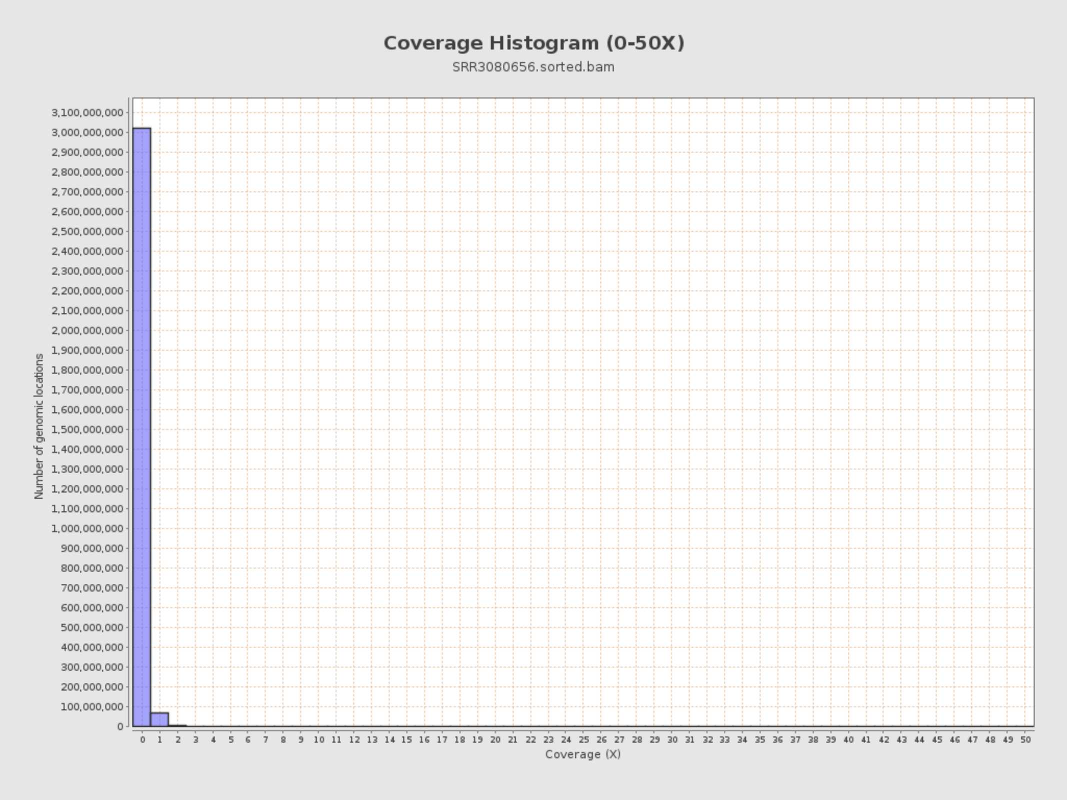
3. Results : Coverage across reference



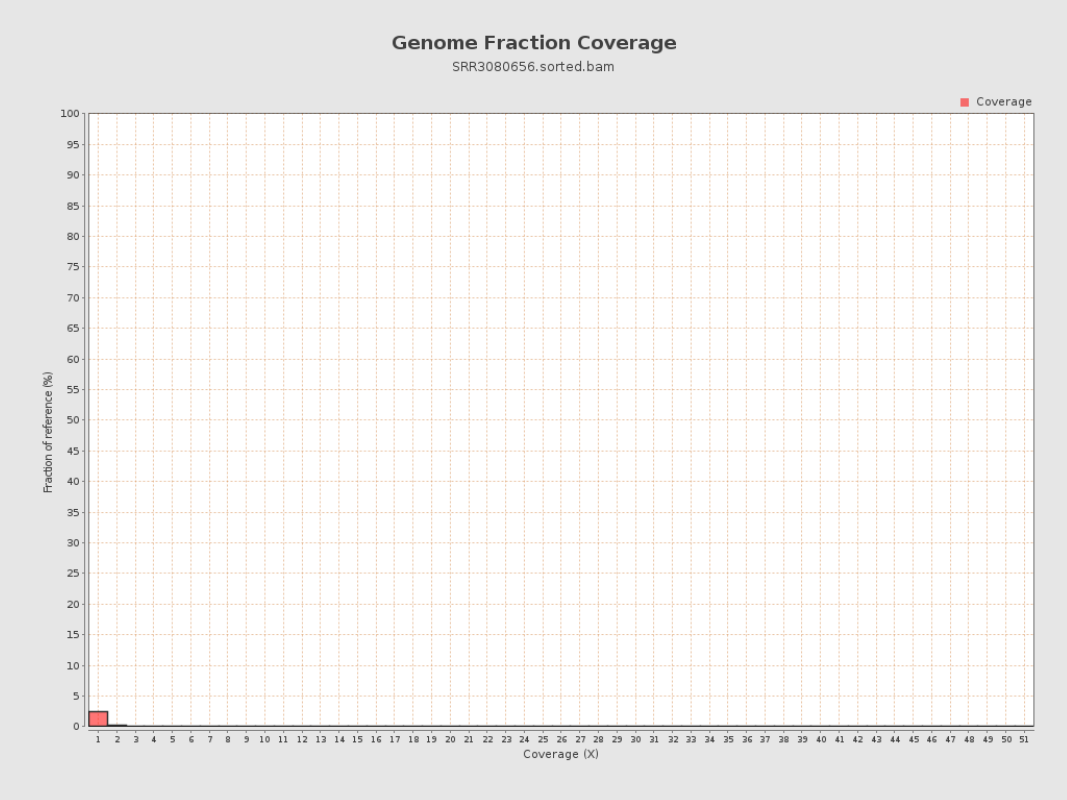
4. Results : Coverage Histogram



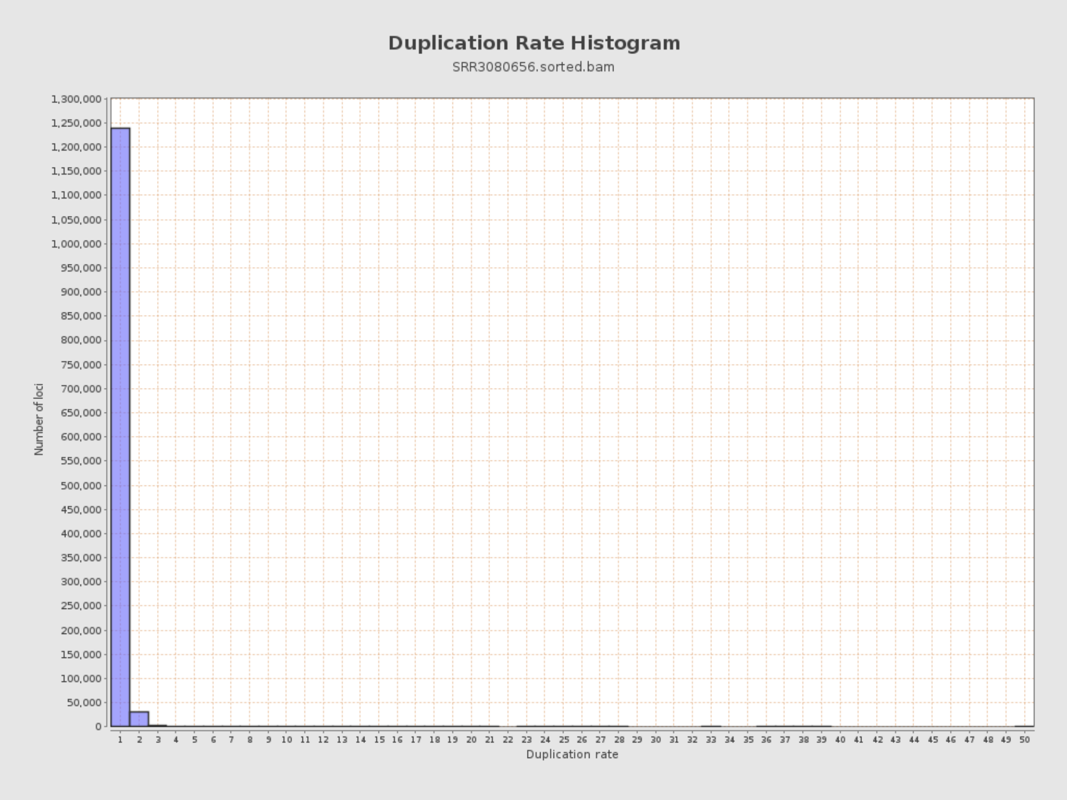
5. Results : Coverage Histogram (0-50X)



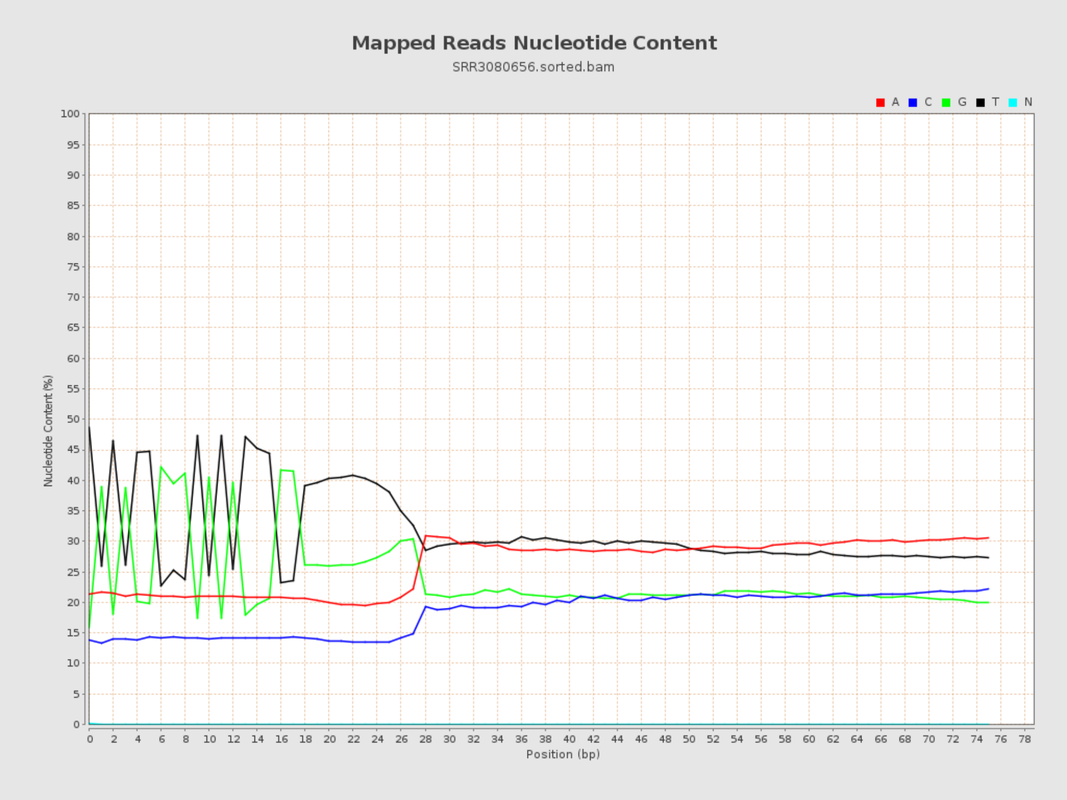
6. Results : Genome Fraction Coverage



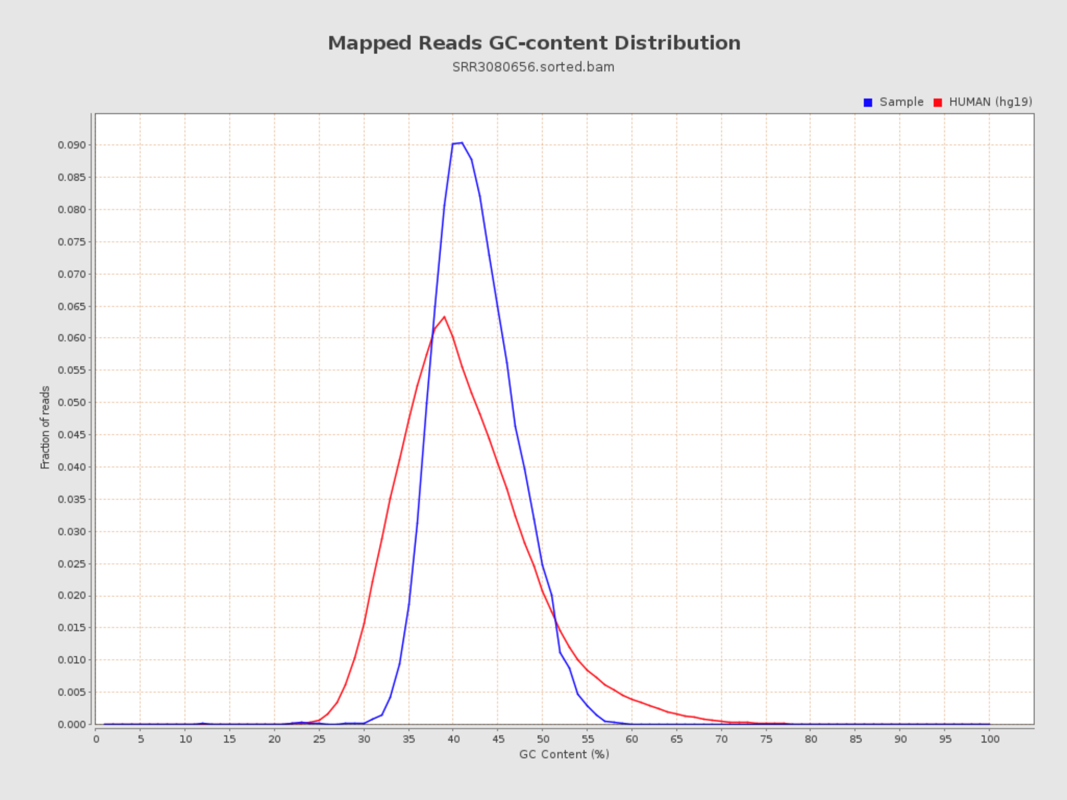
7. Results : Duplication Rate Histogram



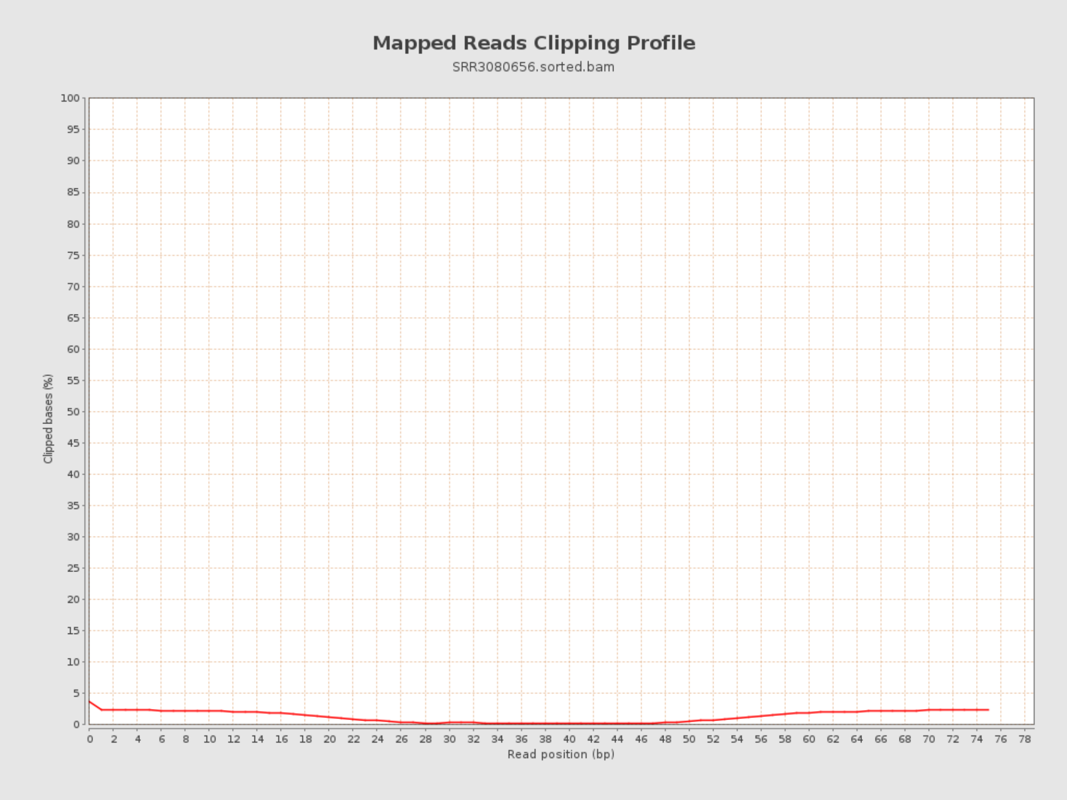
8. Results : Mapped Reads Nucleotide Content



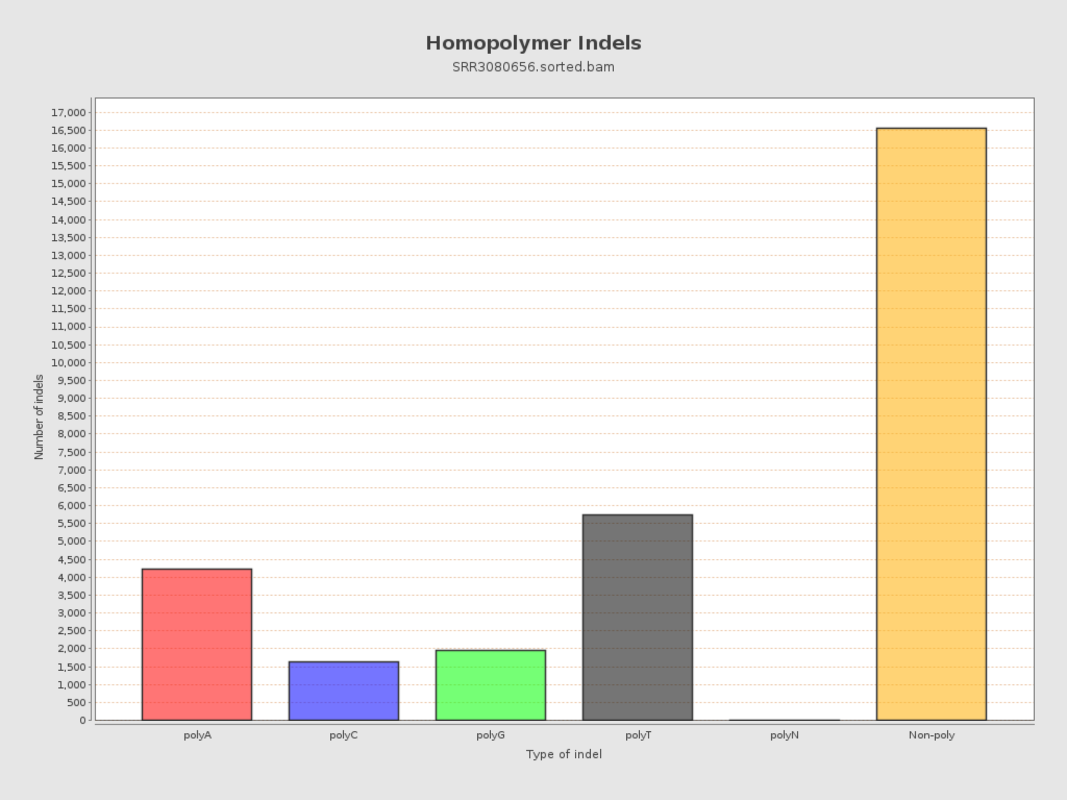
9. Results : Mapped Reads GC-content Distribution



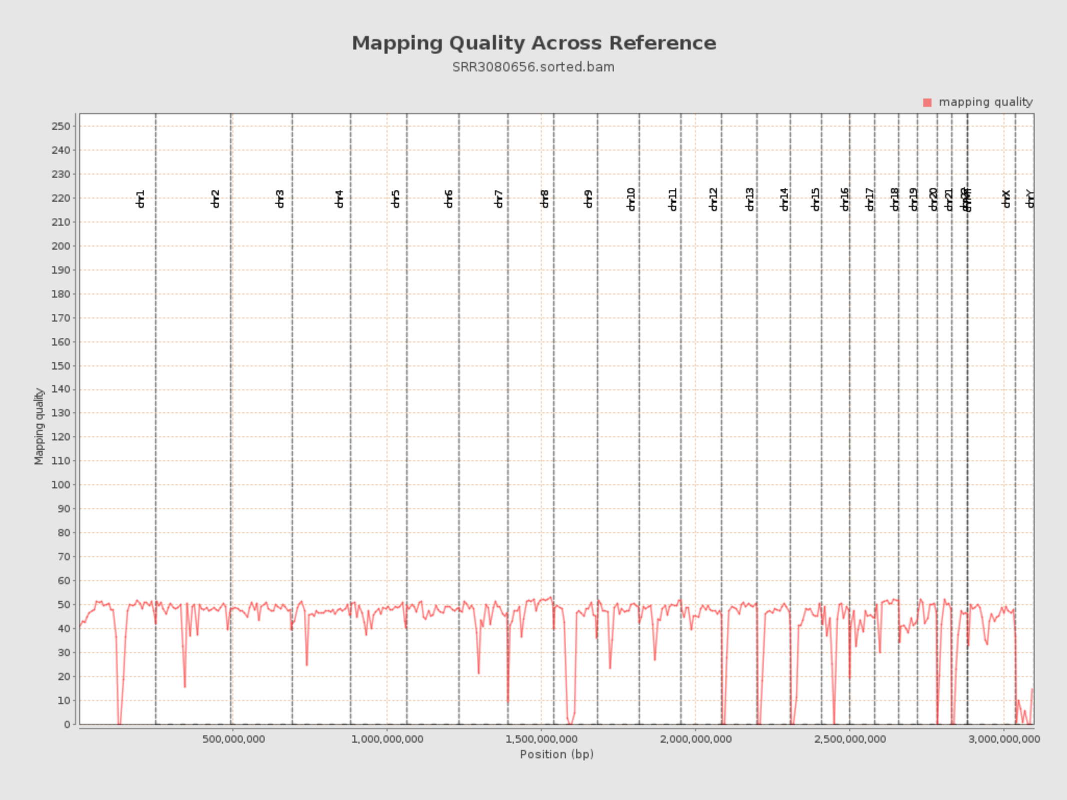
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram