Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:33:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080682.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_SRR3080682 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080682.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:33:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080682.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,334,949
Mapped reads	1,234,625 / 92.48%
Unmapped reads	100,324 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,295 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	40,158 / 3.01%
Duplication rate	2.86%
Clipped reads	522,335 / 39.13%

2.2. ACGT Content

Number/percentage of A's	22,995,004 / 27.78%
Number/percentage of C's	15,034,626 / 18.16%
Number/percentage of T's	26,519,405 / 32.03%
Number/percentage of G's	18,233,391 / 22.02%
Number/percentage of N's	3,487 / 0%
GC Percentage	40.19%

2.3. Coverage

Mean	0.0268

Standard Deviation	0.2114

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

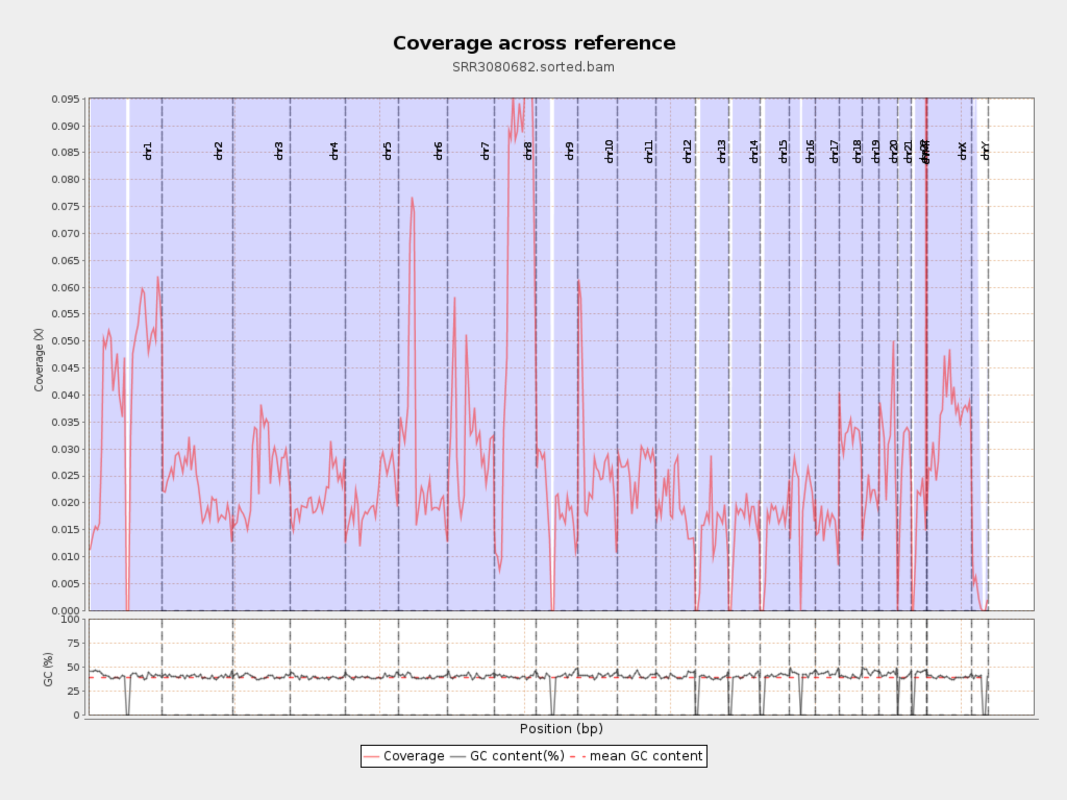
General error rate	0.69%
Mismatches	561,289
Insertions	6,145
Mapped reads with at least one insertion	0.49%
Deletions	19,190
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.9%

2.6. Chromosome stats

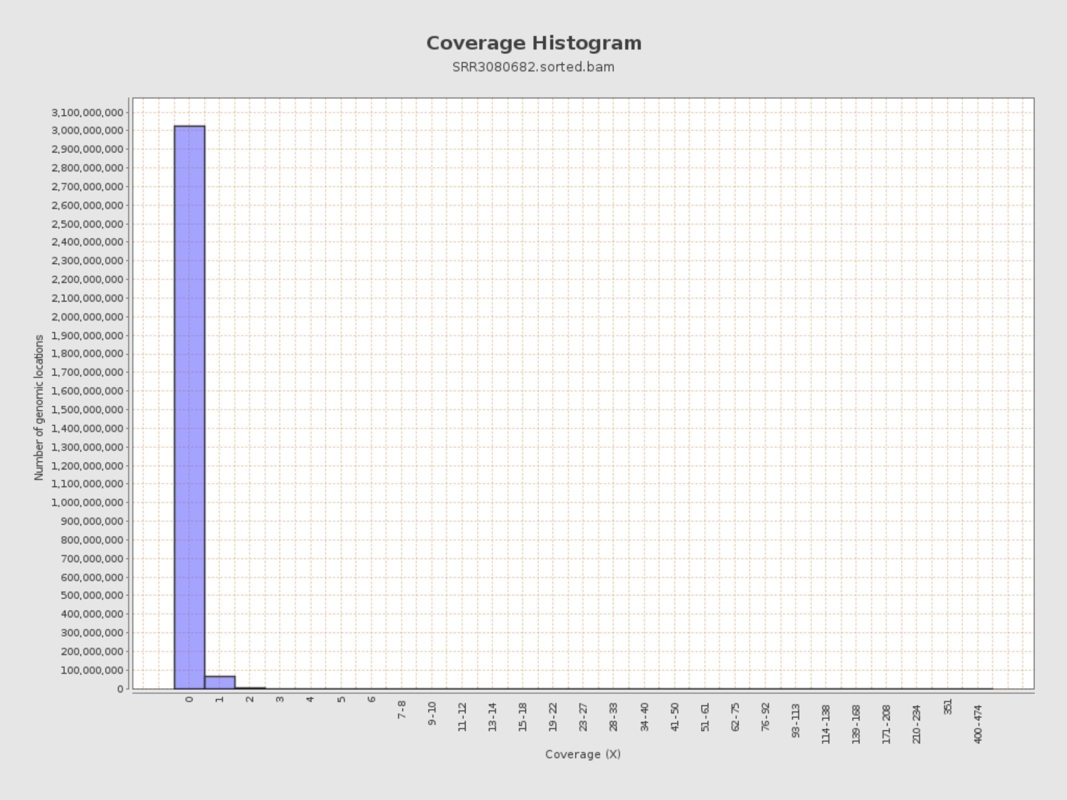
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10103001	0.0405	0.2762
chr2	243199373	5491404	0.0226	0.2694
chr3	198022430	5113081	0.0258	0.176
chr4	191154276	4083862	0.0214	0.1631
chr5	180915260	3799798	0.021	0.159
chr6	171115067	5090200	0.0297	0.2122
chr7	159138663	5173679	0.0325	0.3281

chr8	146364022	10006730	0.0684	0.3185
chr9	141213431	2618139	0.0185	0.1713
chr10	135534747	3836442	0.0283	0.1934
chr11	135006516	3547133	0.0263	0.1876
chr12	133851895	2576148	0.0192	0.1535
chr13	115169878	1613636	0.014	0.1307
chr14	107349540	1628408	0.0152	0.1372
chr15	102531392	1508943	0.0147	0.141
chr16	90354753	1889580	0.0209	0.1602
chr17	81195210	1257021	0.0155	0.1378
chr18	78077248	2570430	0.0329	0.2423
chr19	59128983	1222177	0.0207	0.1813
chr20	63025520	2021170	0.0321	0.1987
chr21	48129895	1204491	0.025	0.1753
chr22	51304566	774798	0.0151	0.1343
chrMT	16571	12658	0.7639	1.0357
chrX	155270560	5503770	0.0354	0.213
chrY	59373566	170270	0.0029	0.0618

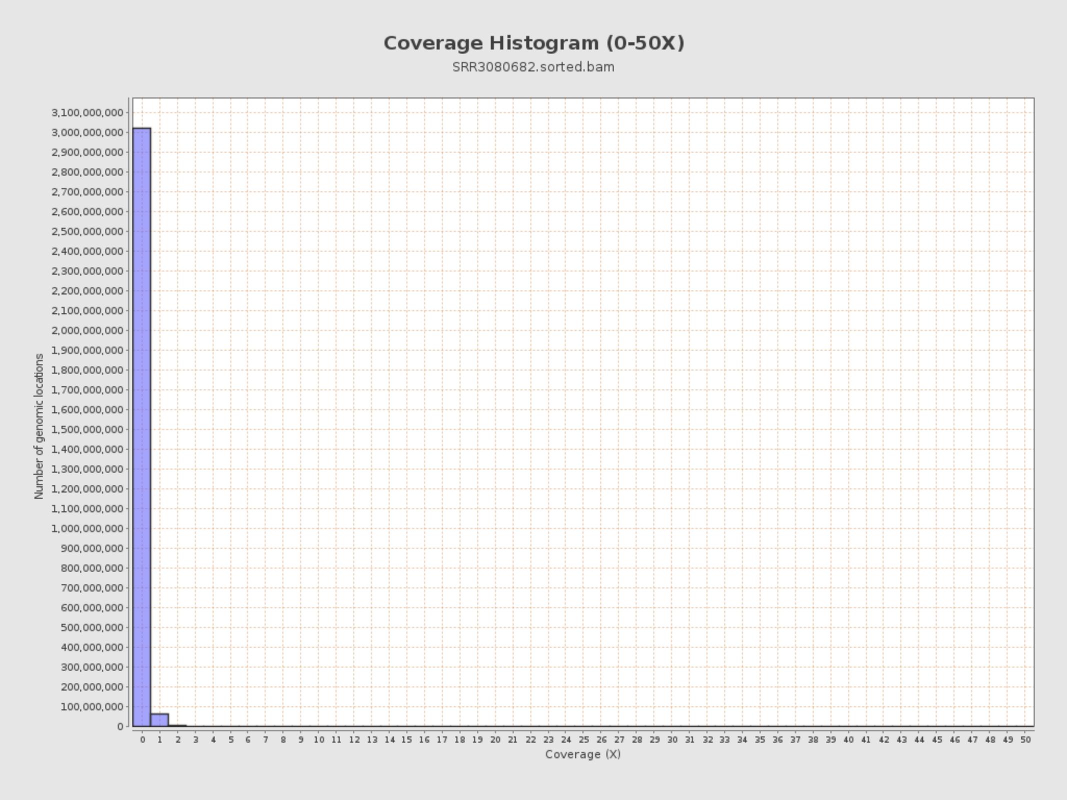
3. Results : Coverage across reference



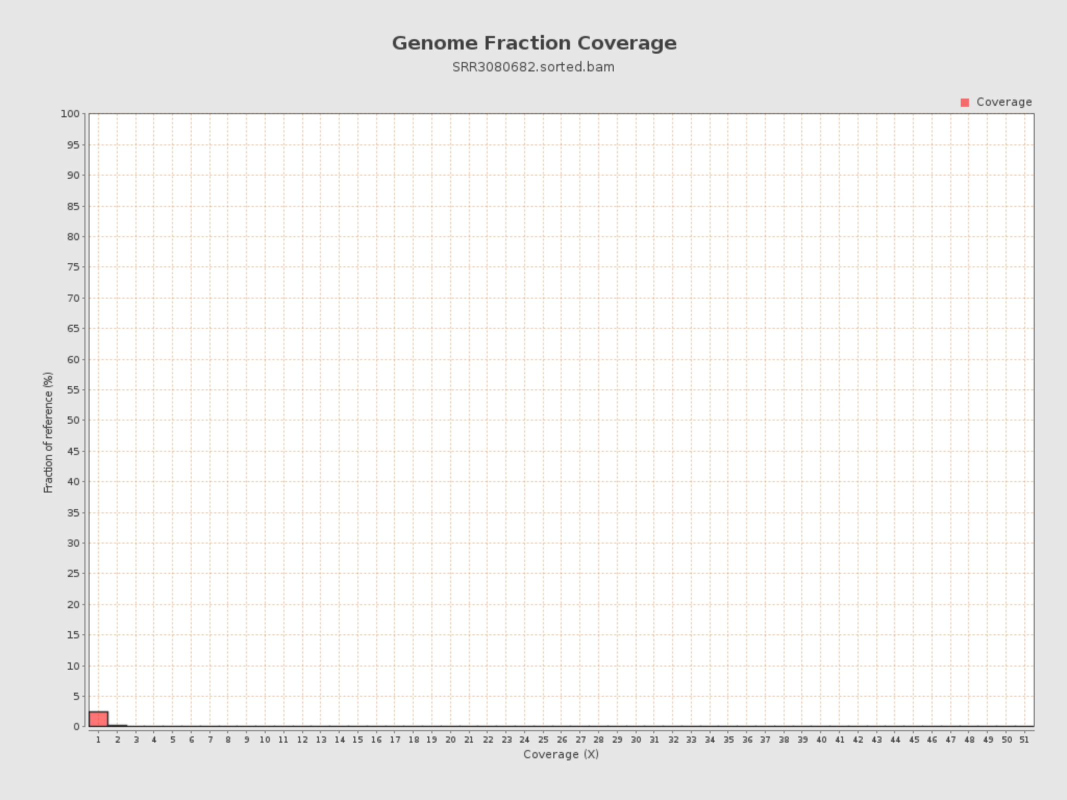
4. Results : Coverage Histogram



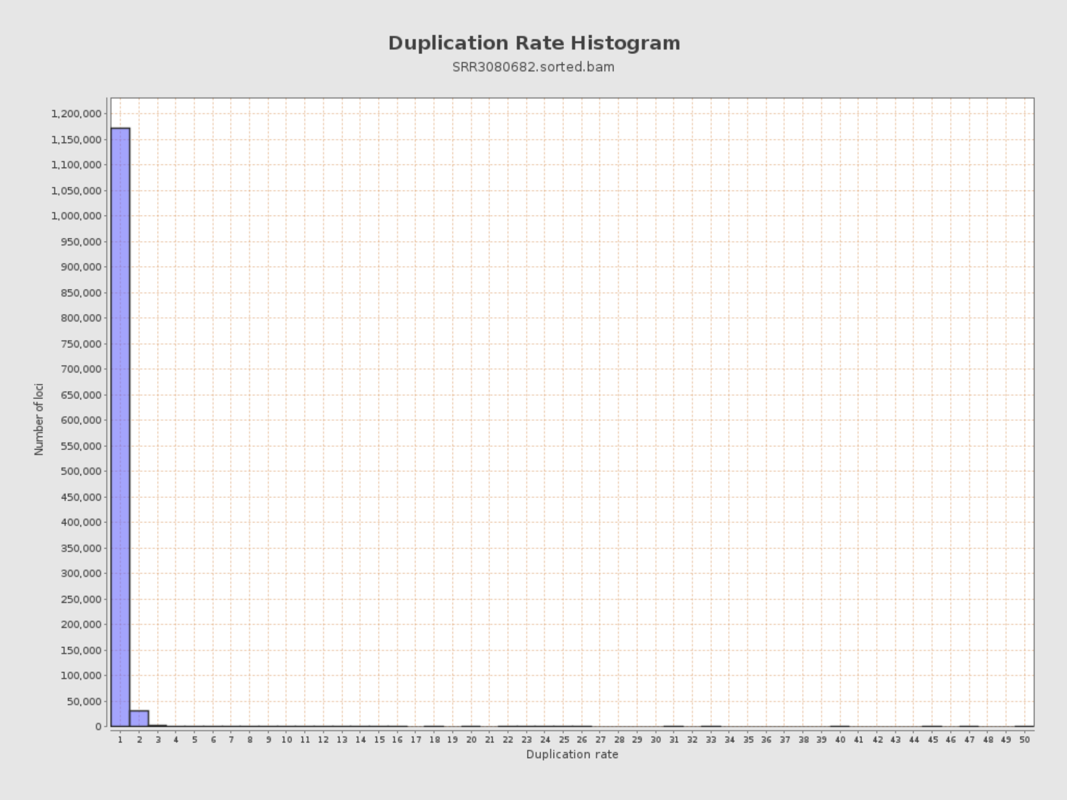
5. Results : Coverage Histogram (0-50X)



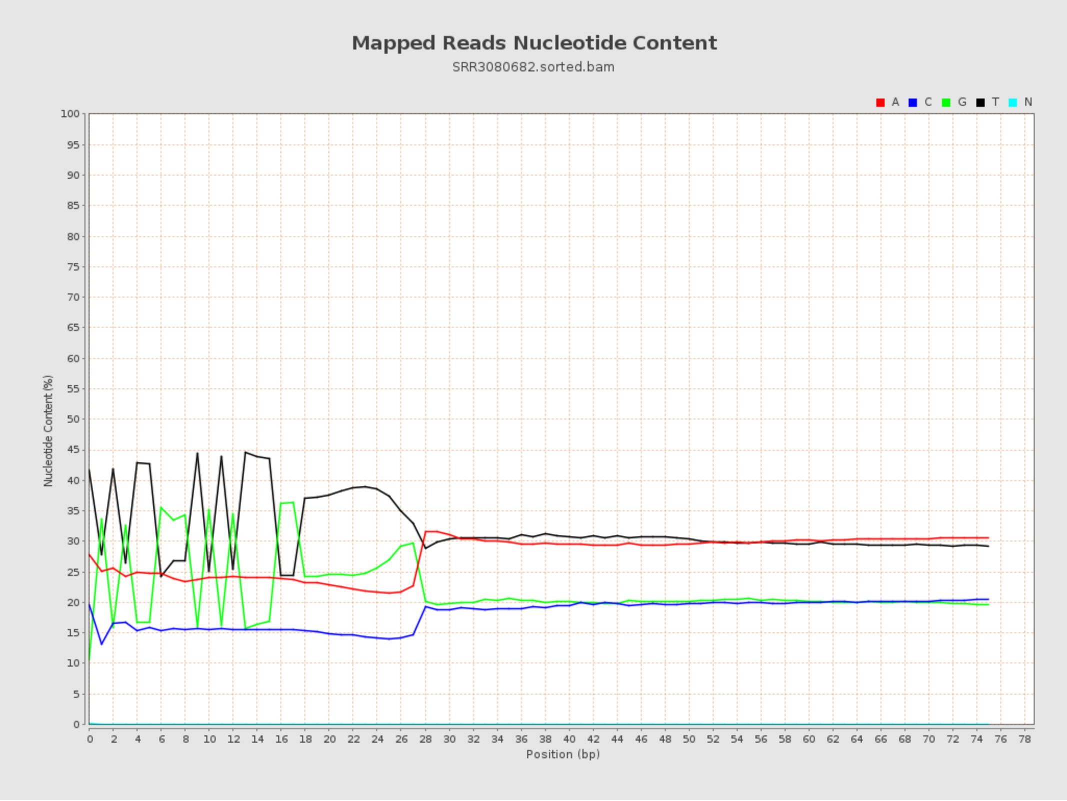
6. Results : Genome Fraction Coverage



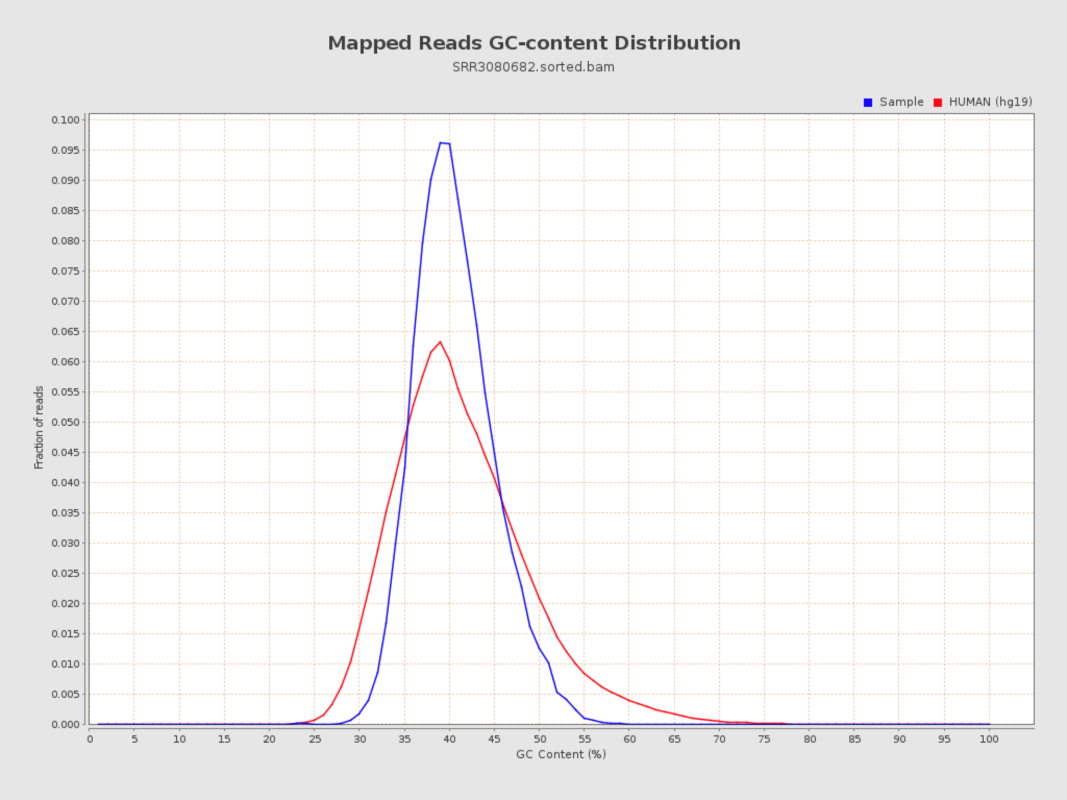
7. Results : Duplication Rate Histogram



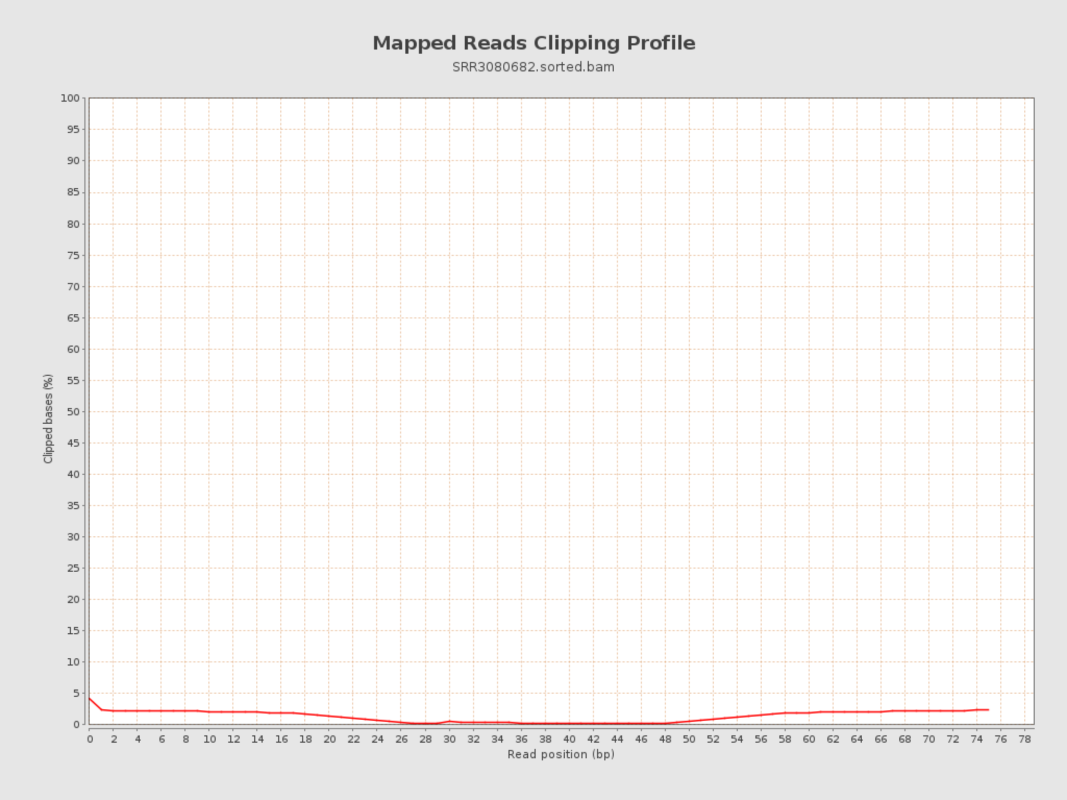
8. Results : Mapped Reads Nucleotide Content



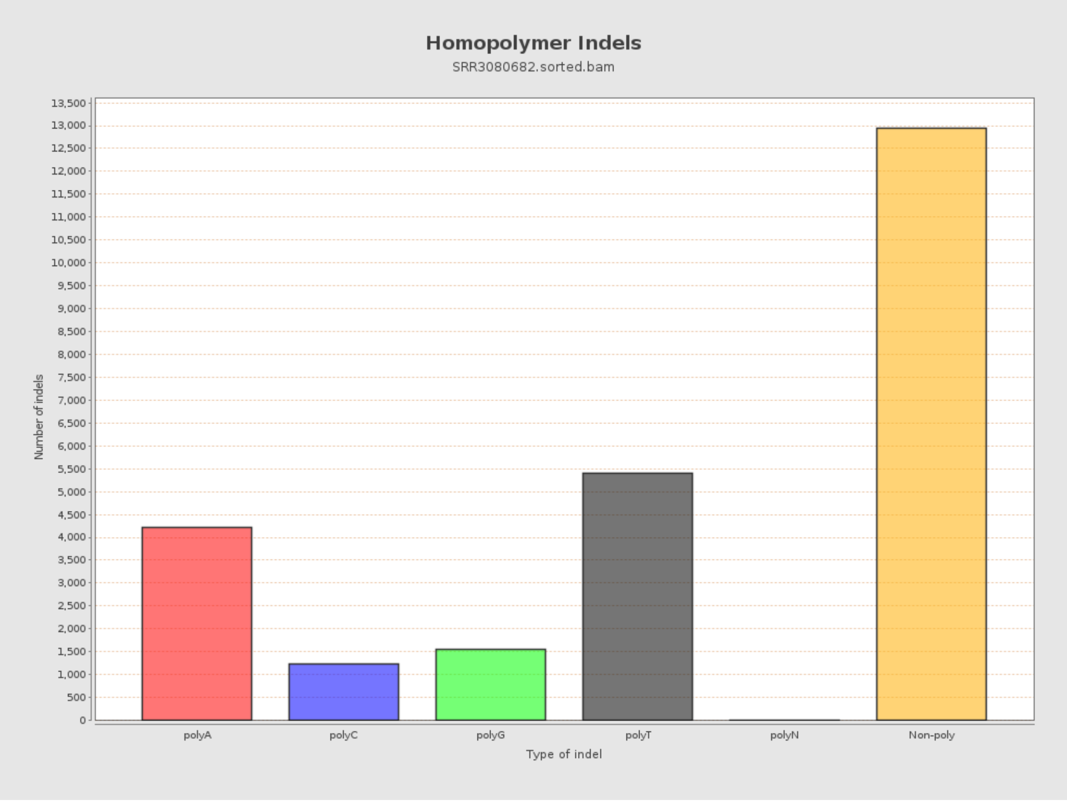
9. Results : Mapped Reads GC-content Distribution



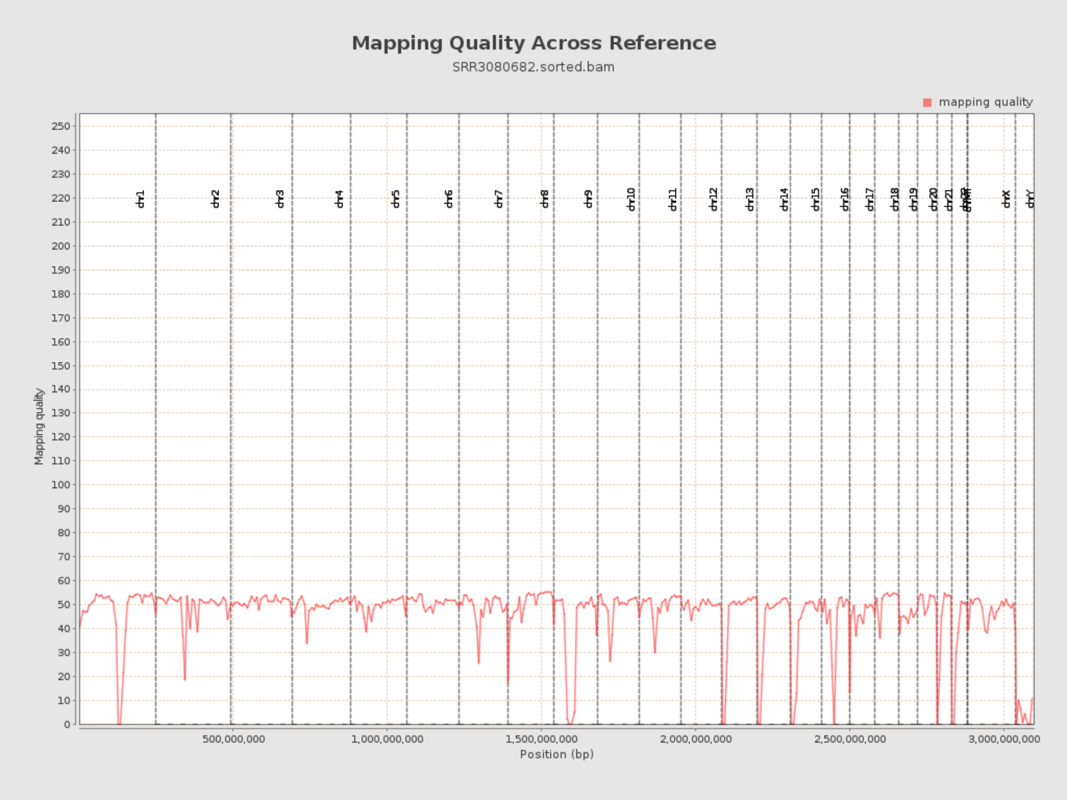
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram