Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:43:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080772.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_SRR3080772 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080772.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:43:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080772.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,690,357
Mapped reads	4,046,825 / 71.12%
Unmapped reads	1,643,532 / 28.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,942 / 0.53%
Read min/max/mean length	30 / 66 / 66.17
Duplicated reads (estimated)	388,236 / 6.82%
Duplication rate	7.4%
Clipped reads	774,202 / 13.61%

2.2. ACGT Content

Number/percentage of A's	77,020,152 / 30.19%
Number/percentage of C's	53,037,129 / 20.79%
Number/percentage of T's	65,475,153 / 25.66%
Number/percentage of G's	59,537,148 / 23.33%
Number/percentage of N's	87,212 / 0.03%
GC Percentage	44.12%

2.3. Coverage

Mean	0.0825

Standard Deviation	0.5462

2.4. Mapping Quality

Mean Mapping Quality	43.59

2.5. Mismatches and indels

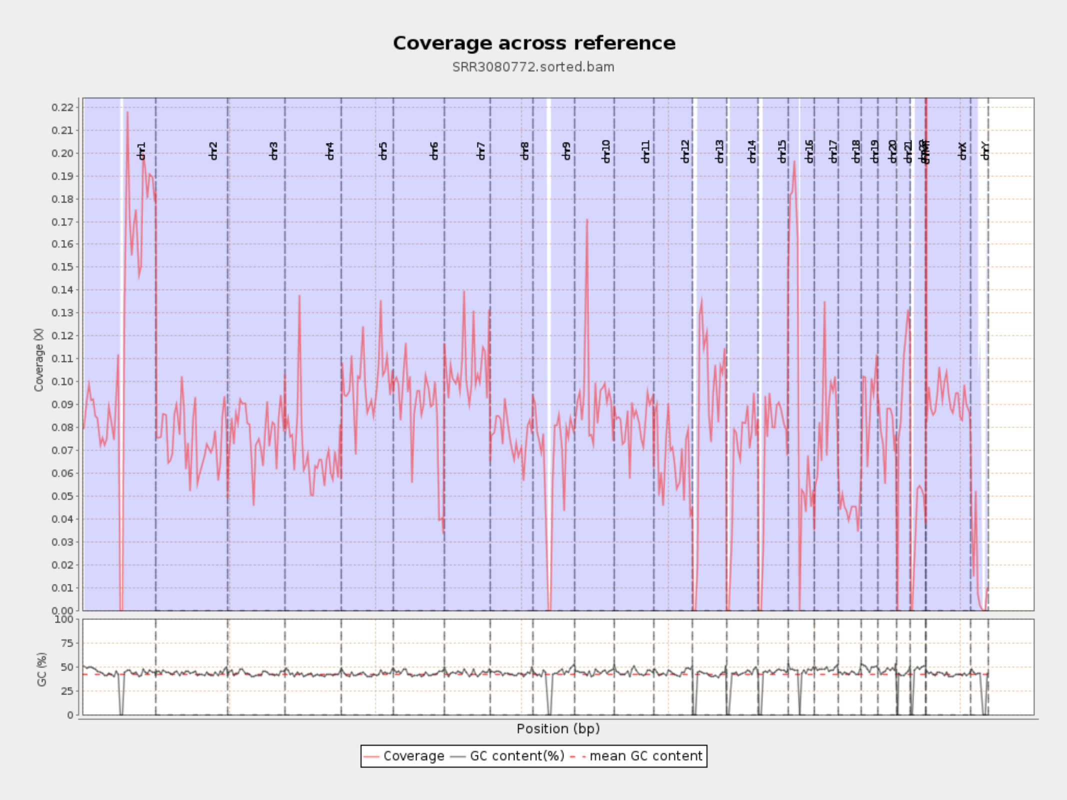
General error rate	0.79%
Mismatches	1,976,936
Insertions	19,052
Mapped reads with at least one insertion	0.47%
Deletions	46,951
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.14%

2.6. Chromosome stats

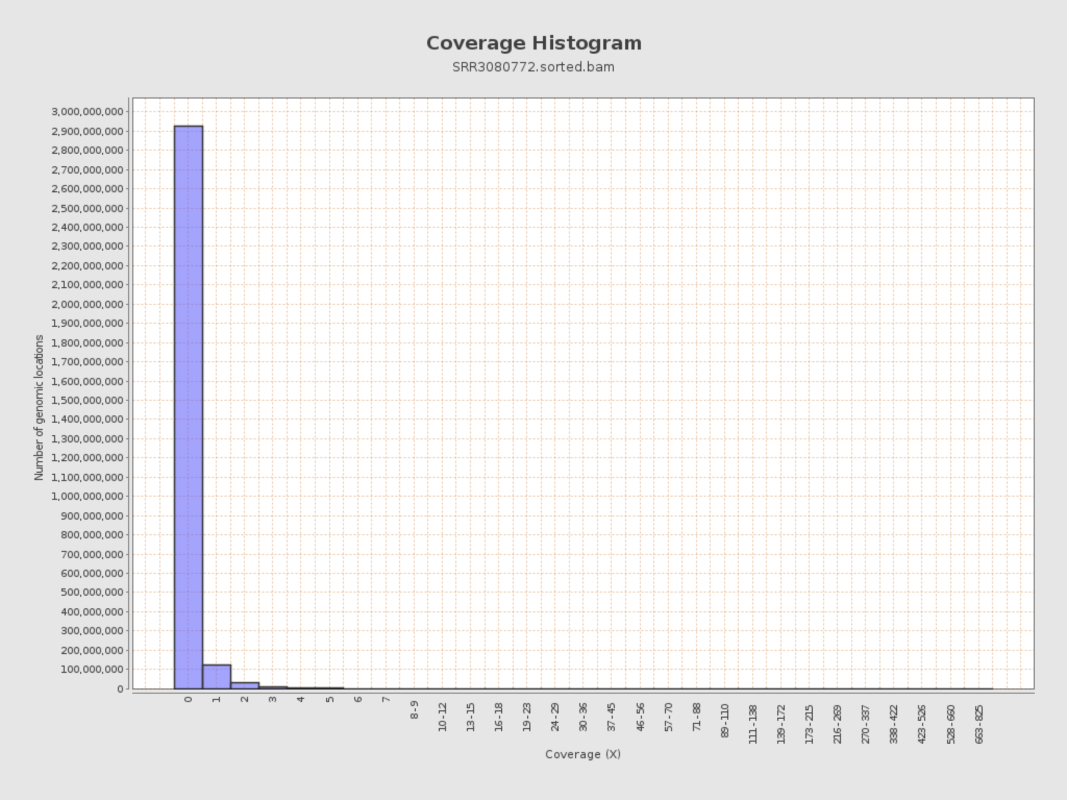
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29865439	0.1198	0.8019
chr2	243199373	18184535	0.0748	0.5203
chr3	198022430	15366126	0.0776	0.4001
chr4	191154276	13373358	0.07	0.4633
chr5	180915260	18040613	0.0997	0.4608
chr6	171115067	15030072	0.0878	0.5877
chr7	159138663	16974131	0.1067	0.6534

chr8	146364022	11139425	0.0761	0.5348
chr9	141213431	9237255	0.0654	0.4129
chr10	135534747	12670322	0.0935	0.8591
chr11	135006516	11100277	0.0822	0.4857
chr12	133851895	8828133	0.066	0.3705
chr13	115169878	10160656	0.0882	0.4317
chr14	107349540	7045758	0.0656	0.42
chr15	102531392	7008936	0.0684	0.3749
chr16	90354753	8773675	0.0971	0.5355
chr17	81195210	6905466	0.085	0.4487
chr18	78077248	3509658	0.045	0.5904
chr19	59128983	5427199	0.0918	0.8315
chr20	63025520	4913036	0.078	0.43
chr21	48129895	4630496	0.0962	0.5579
chr22	51304566	1869961	0.0364	0.2805
chrMT	16571	24417	1.4735	1.9259
chrX	155270560	14272028	0.0919	0.4492
chrY	59373566	894531	0.0151	0.4945

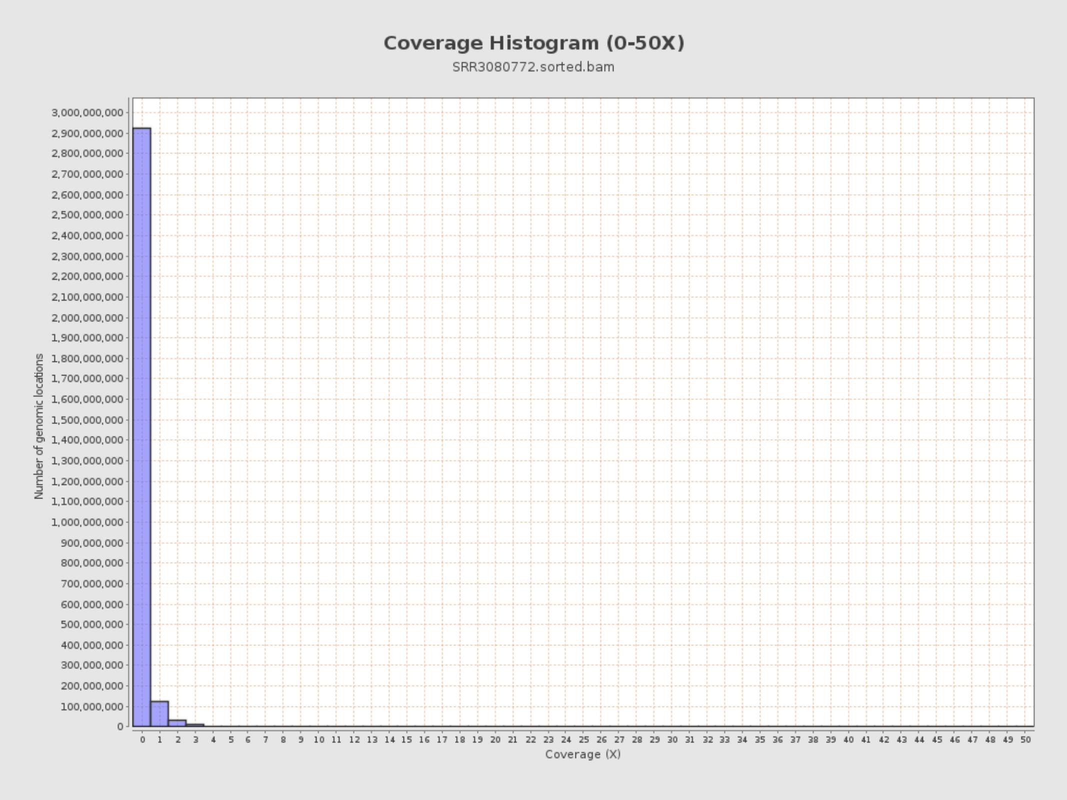
3. Results : Coverage across reference



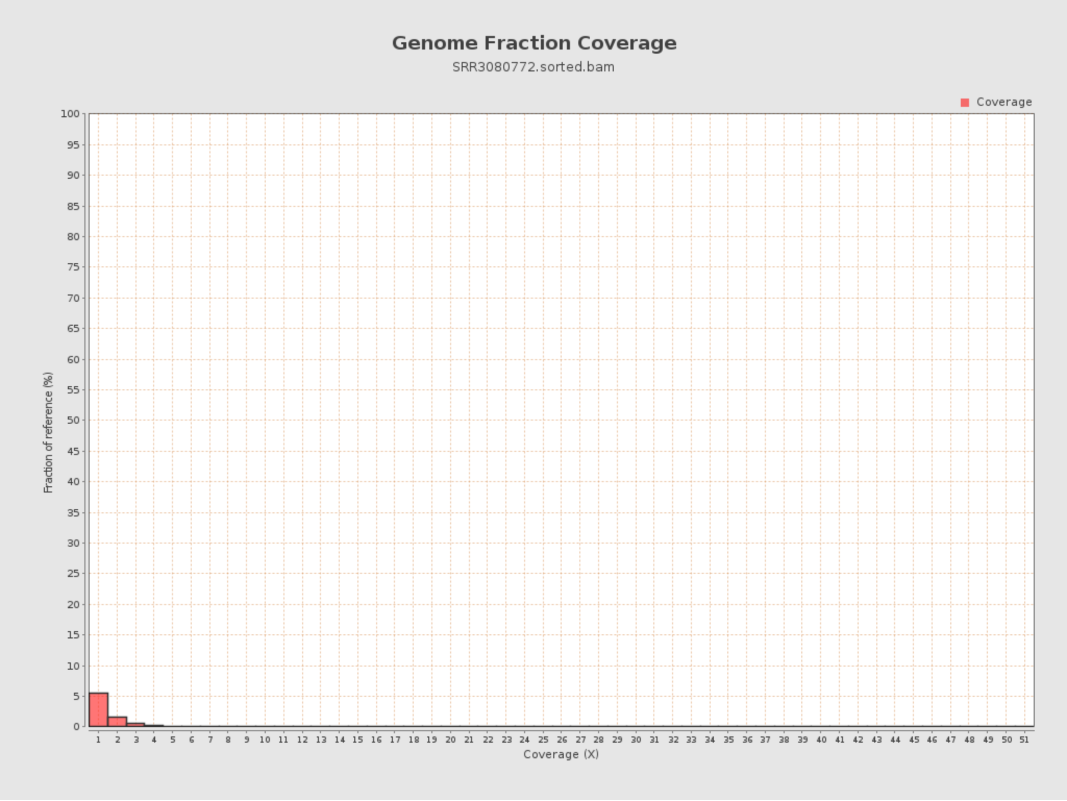
4. Results : Coverage Histogram



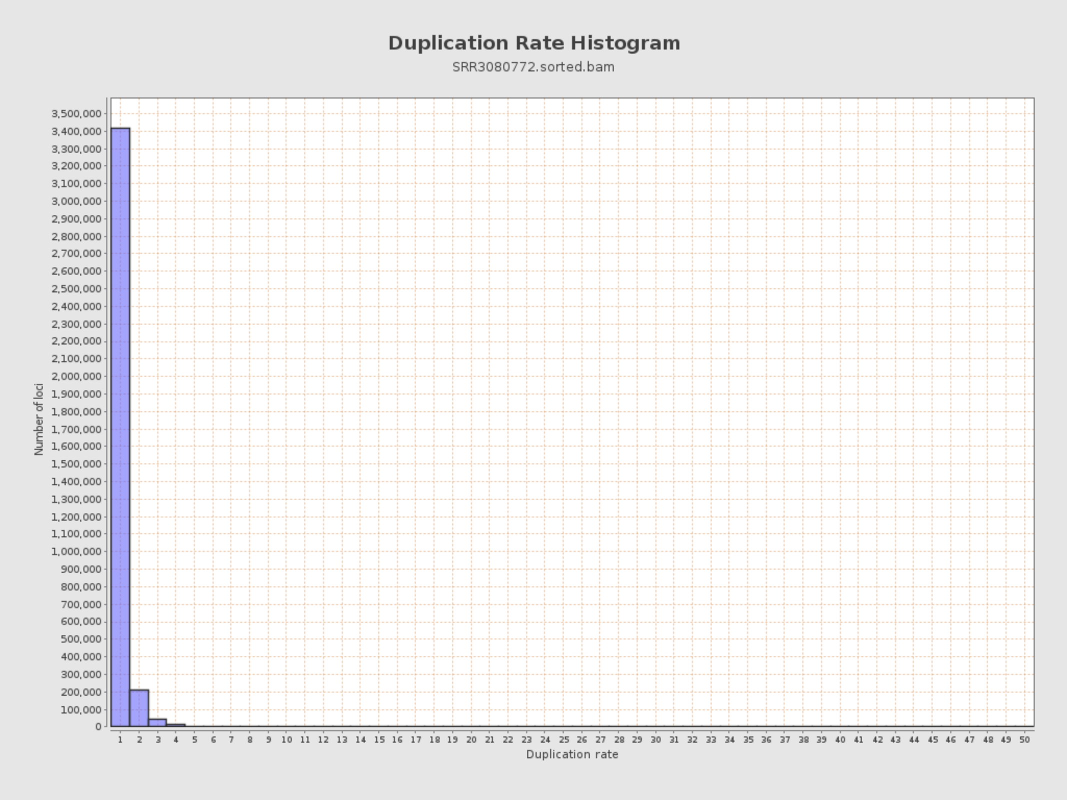
5. Results : Coverage Histogram (0-50X)



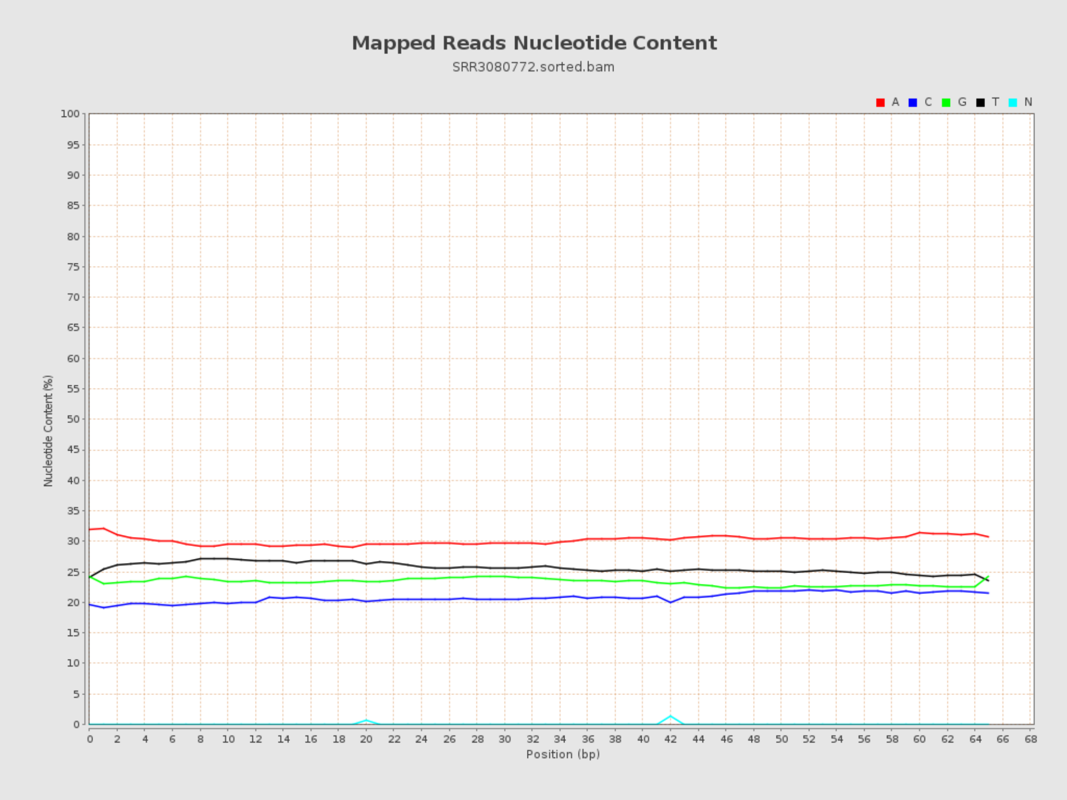
6. Results : Genome Fraction Coverage



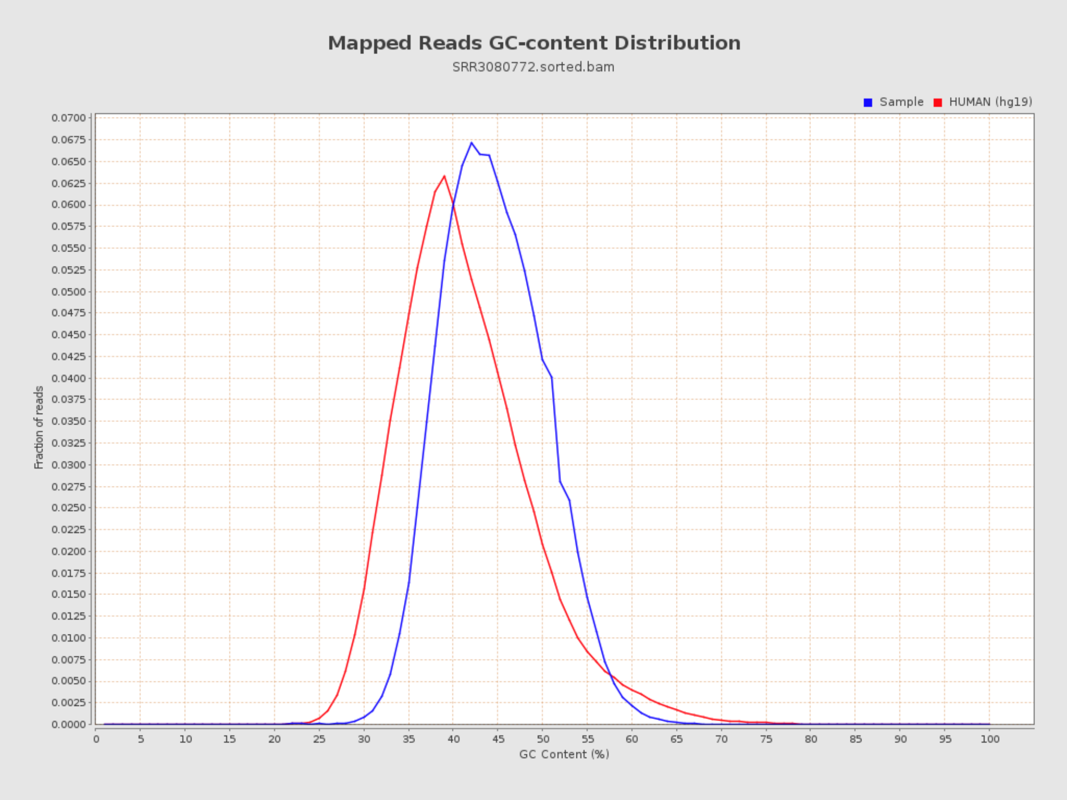
7. Results : Duplication Rate Histogram



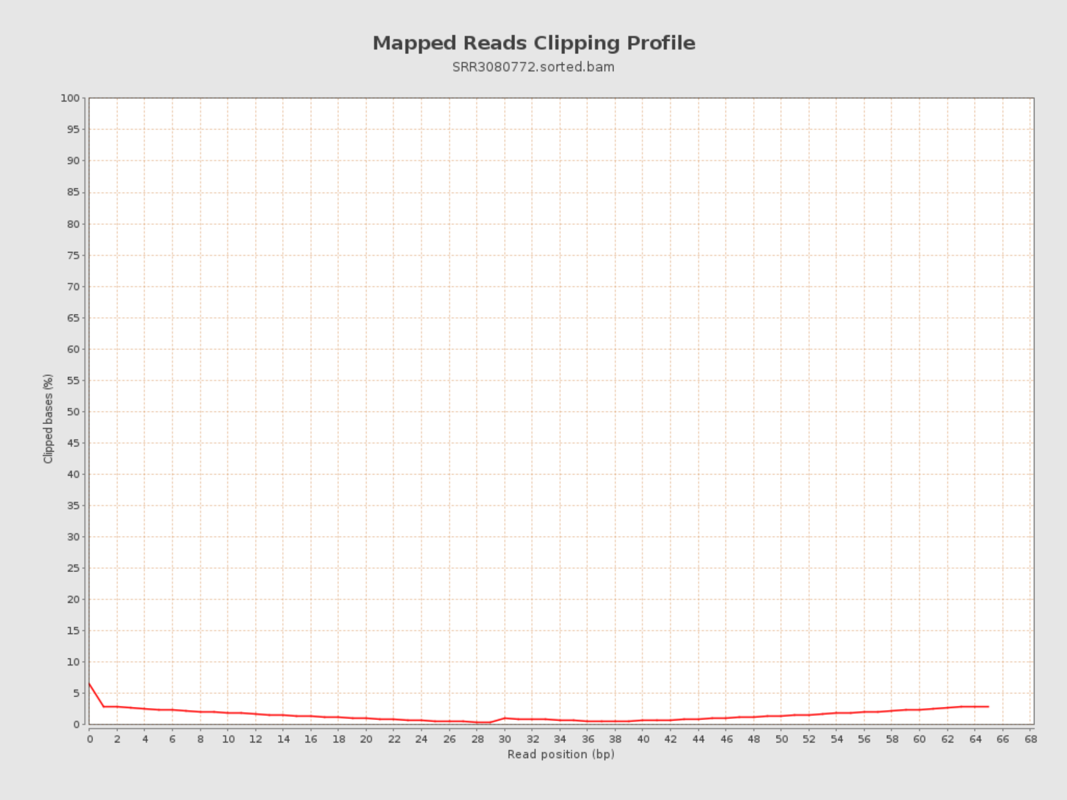
8. Results : Mapped Reads Nucleotide Content



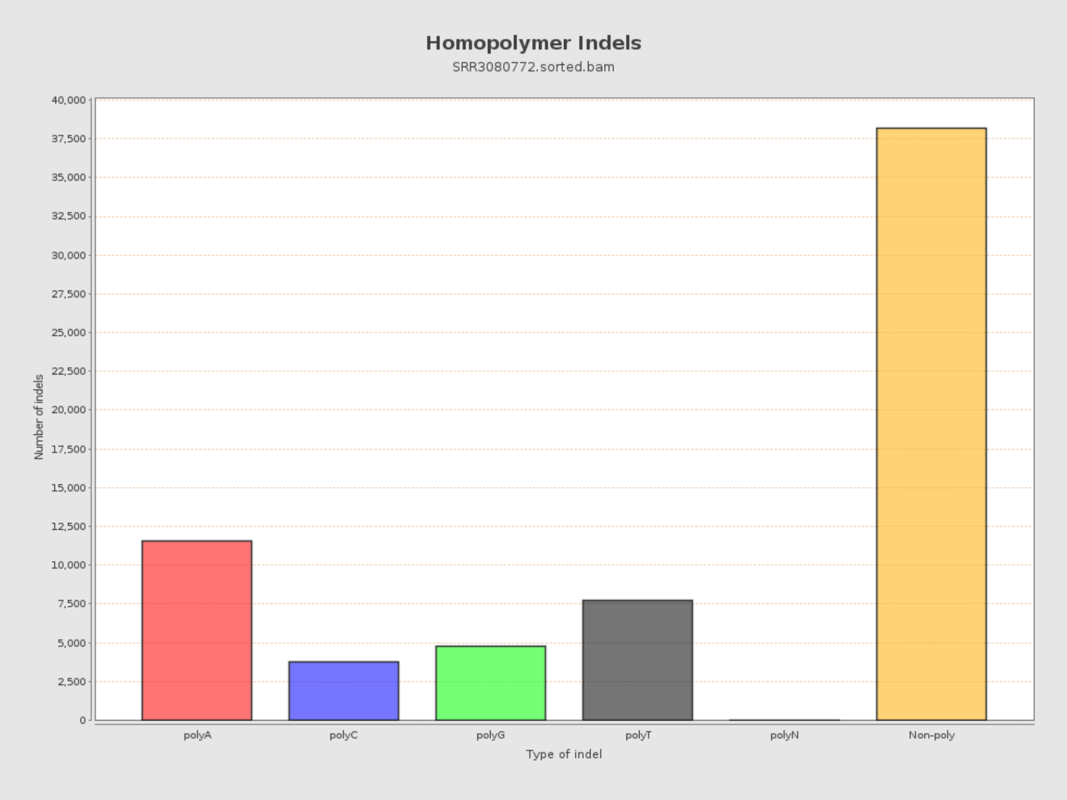
9. Results : Mapped Reads GC-content Distribution



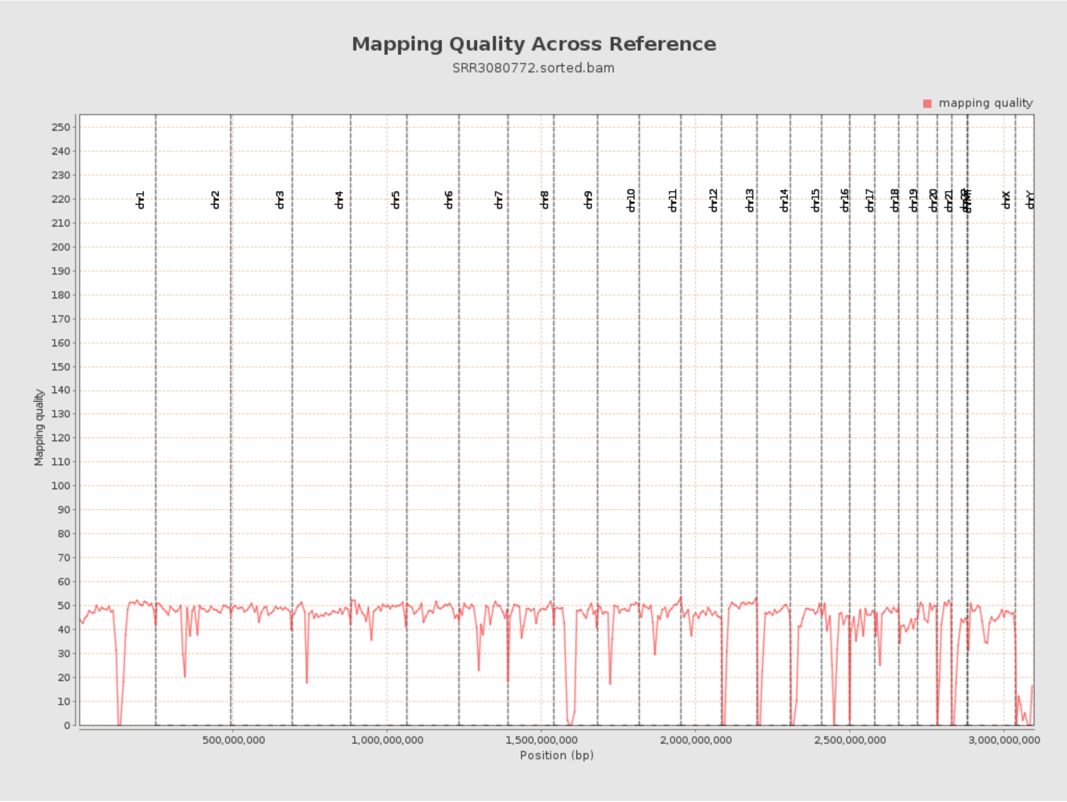
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram