Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 05:42:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083771.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_SRR3083771 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083771.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 05:42:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083771.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,958,803
Mapped reads	1,516,269 / 77.41%
Unmapped reads	442,534 / 22.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,717 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	48,505 / 2.48%
Duplication rate	2.64%
Clipped reads	801,406 / 40.91%

2.2. ACGT Content

Number/percentage of A's	27,840,505 / 28.56%
Number/percentage of C's	17,814,261 / 18.27%
Number/percentage of T's	30,259,997 / 31.04%
Number/percentage of G's	21,566,888 / 22.12%
Number/percentage of N's	1,098 / 0%
GC Percentage	40.4%

2.3. Coverage

Mean	0.0315

Standard Deviation	0.2485

2.4. Mapping Quality

Mean Mapping Quality	46.3

2.5. Mismatches and indels

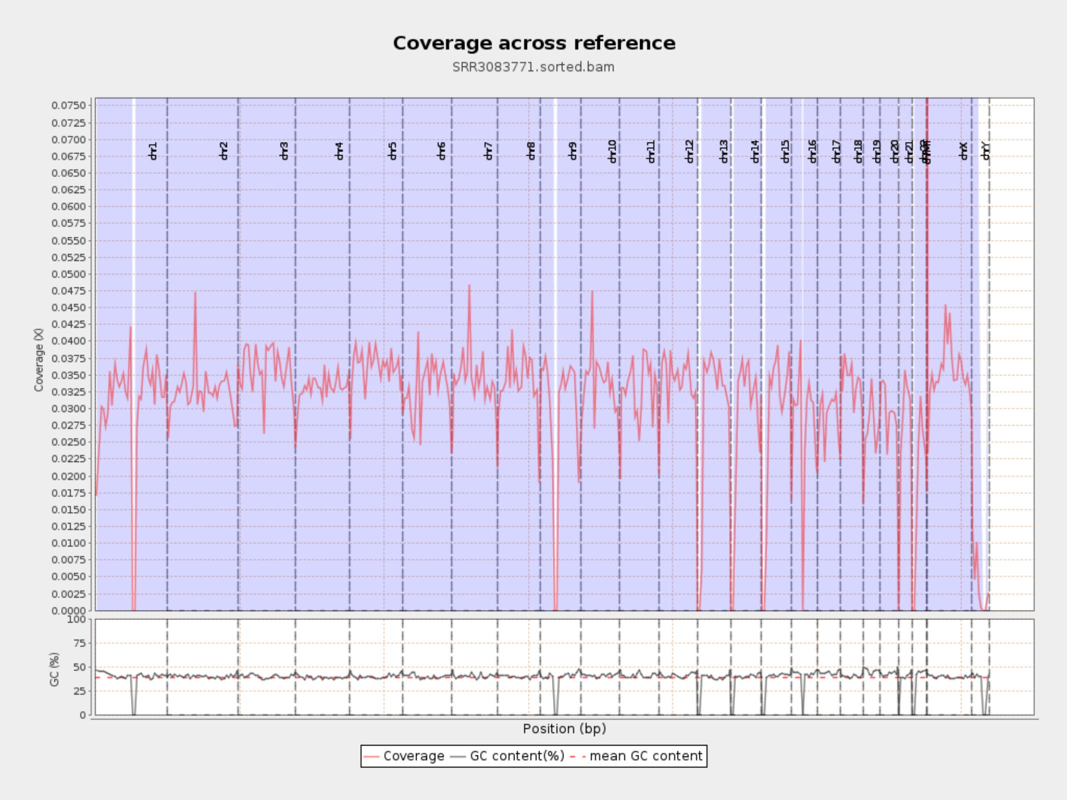
General error rate	0.84%
Mismatches	805,530
Insertions	7,052
Mapped reads with at least one insertion	0.46%
Deletions	20,856
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.94%

2.6. Chromosome stats

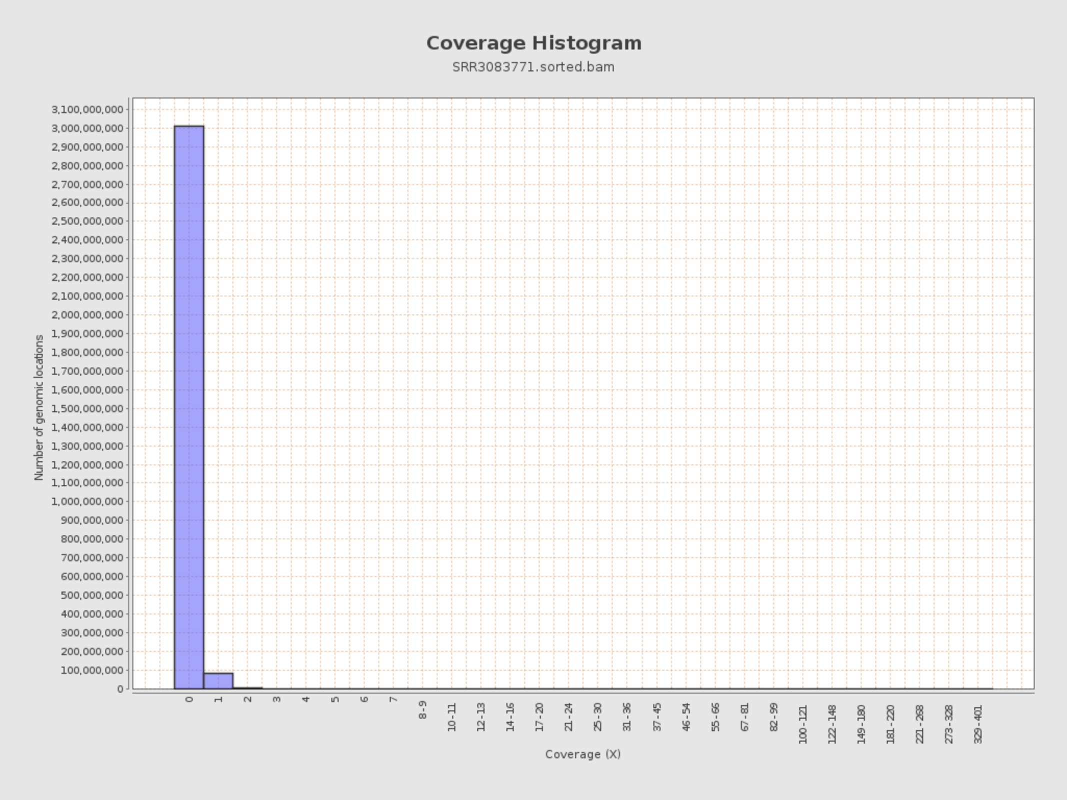
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7615073	0.0306	0.3422
chr2	243199373	7911824	0.0325	0.2927
chr3	198022430	7125947	0.036	0.2463
chr4	191154276	6305133	0.033	0.201
chr5	180915260	6599653	0.0365	0.2068
chr6	171115067	5652110	0.033	0.2225
chr7	159138663	5512485	0.0346	0.2909

chr8	146364022	5010131	0.0342	0.2793
chr9	141213431	4101637	0.029	0.2261
chr10	135534747	4588838	0.0339	0.2496
chr11	135006516	4438239	0.0329	0.2228
chr12	133851895	4585399	0.0343	0.2033
chr13	115169878	3331181	0.0289	0.1844
chr14	107349540	2951568	0.0275	0.1883
chr15	102531392	2868777	0.028	0.1865
chr16	90354753	2452805	0.0271	0.1902
chr17	81195210	2337983	0.0288	0.2011
chr18	78077248	2666449	0.0342	0.4158
chr19	59128983	1615705	0.0273	0.2611
chr20	63025520	1841196	0.0292	0.1905
chr21	48129895	1299425	0.027	0.1831
chr22	51304566	955293	0.0186	0.3166
chrMT	16571	5947	0.3589	0.6412
chrX	155270560	5525938	0.0356	0.2201
chrY	59373566	217215	0.0037	0.078

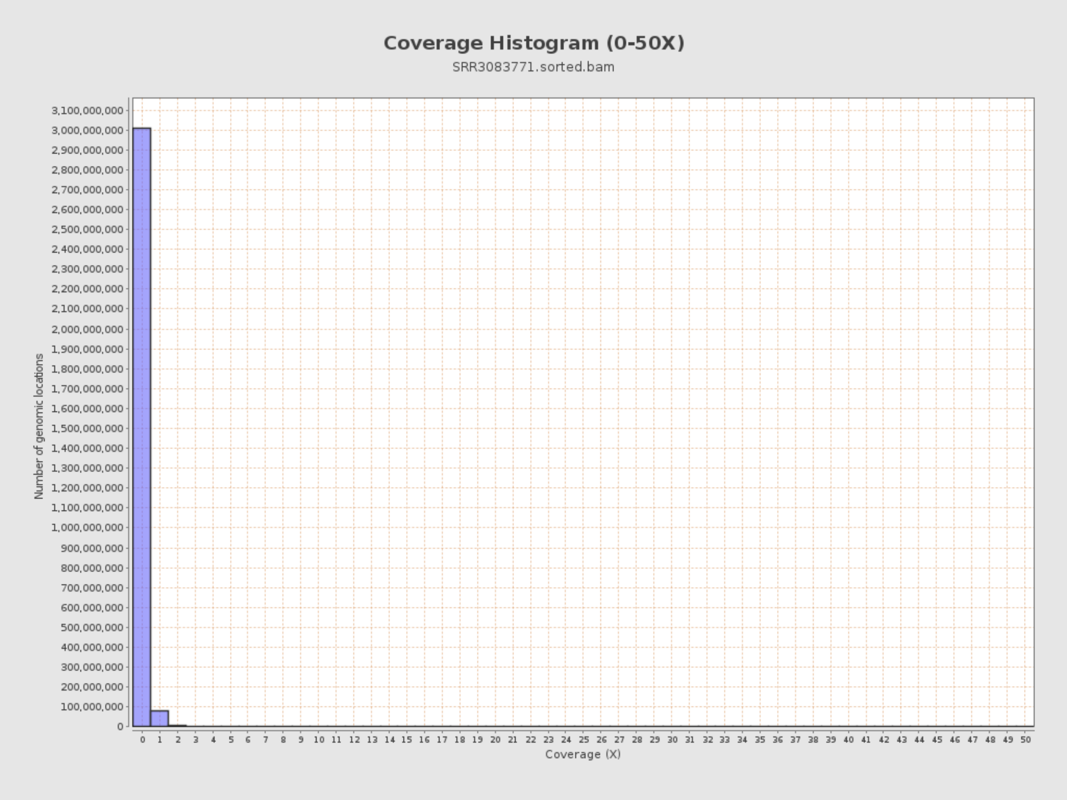
3. Results : Coverage across reference



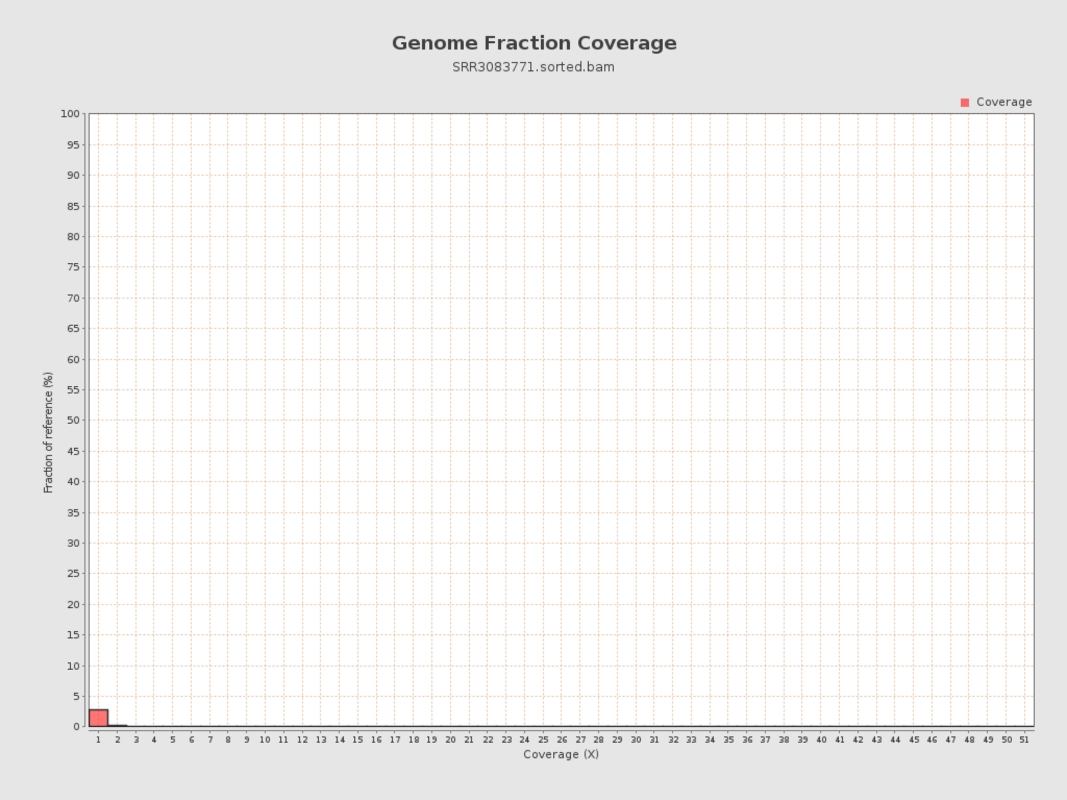
4. Results : Coverage Histogram



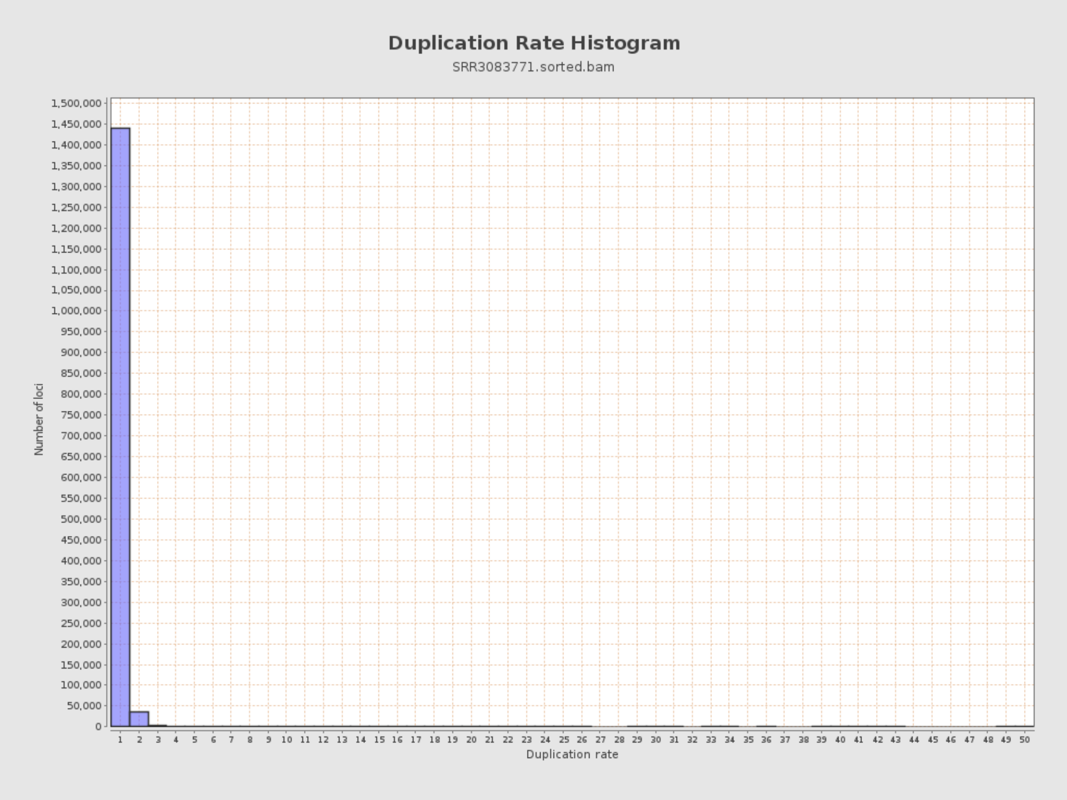
5. Results : Coverage Histogram (0-50X)



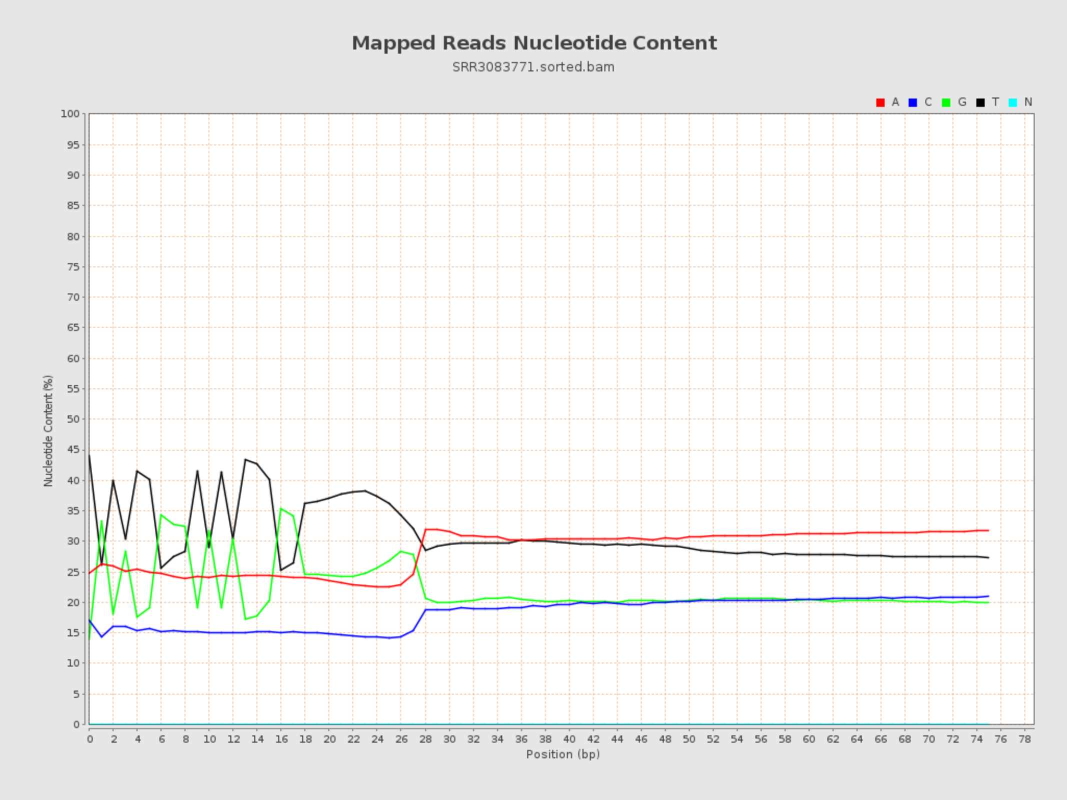
6. Results : Genome Fraction Coverage



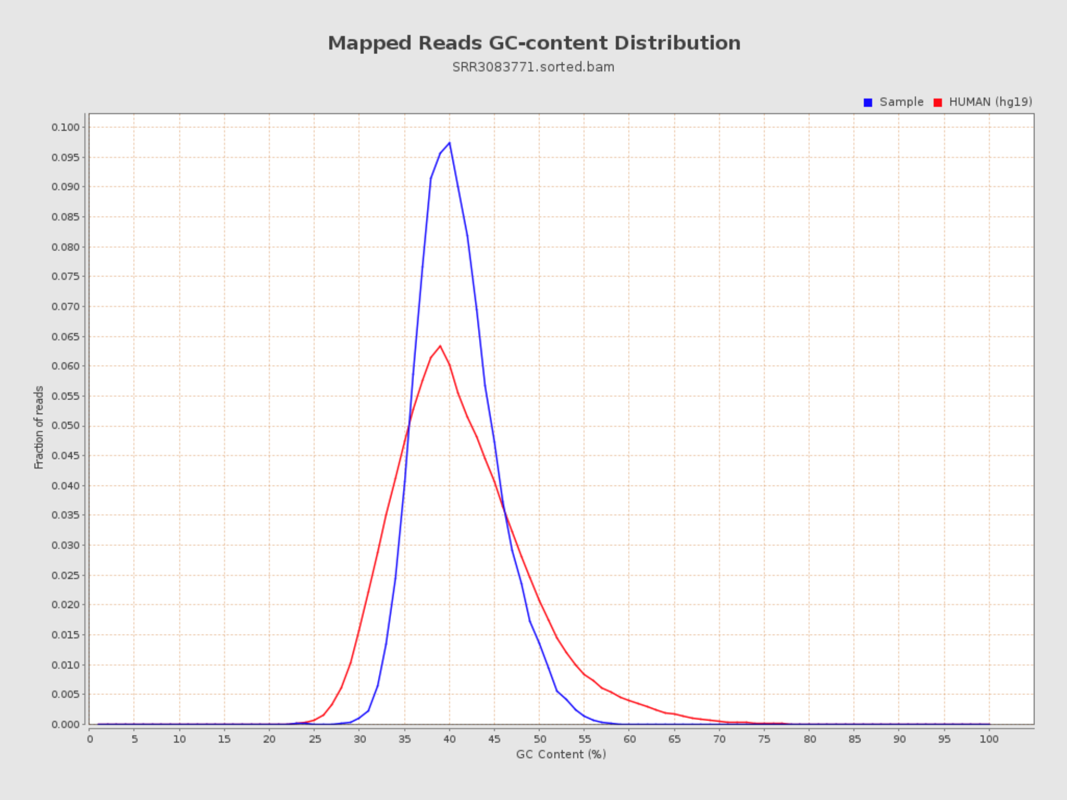
7. Results : Duplication Rate Histogram



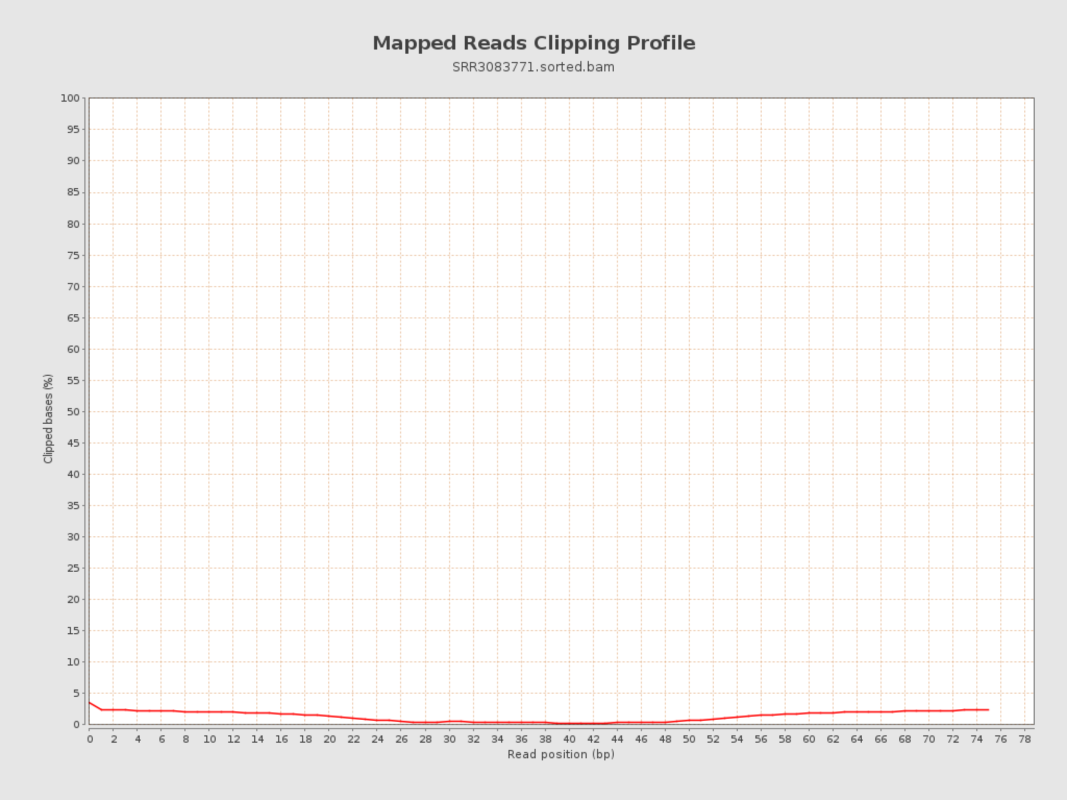
8. Results : Mapped Reads Nucleotide Content



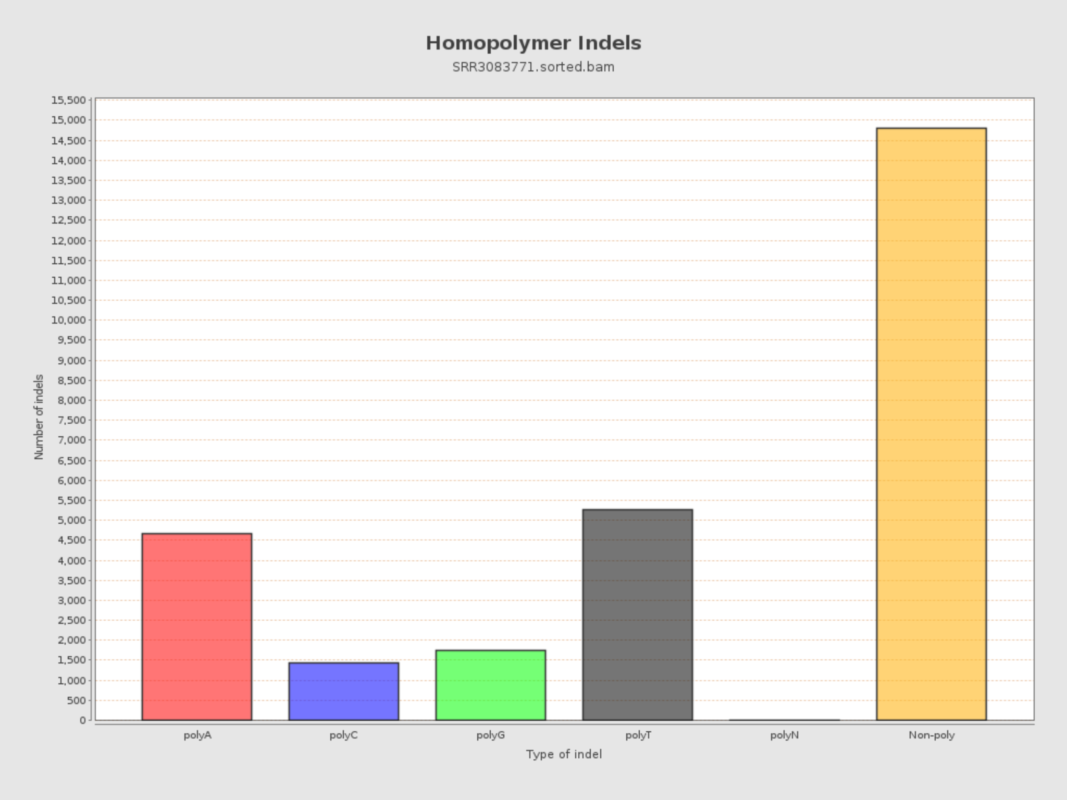
9. Results : Mapped Reads GC-content Distribution



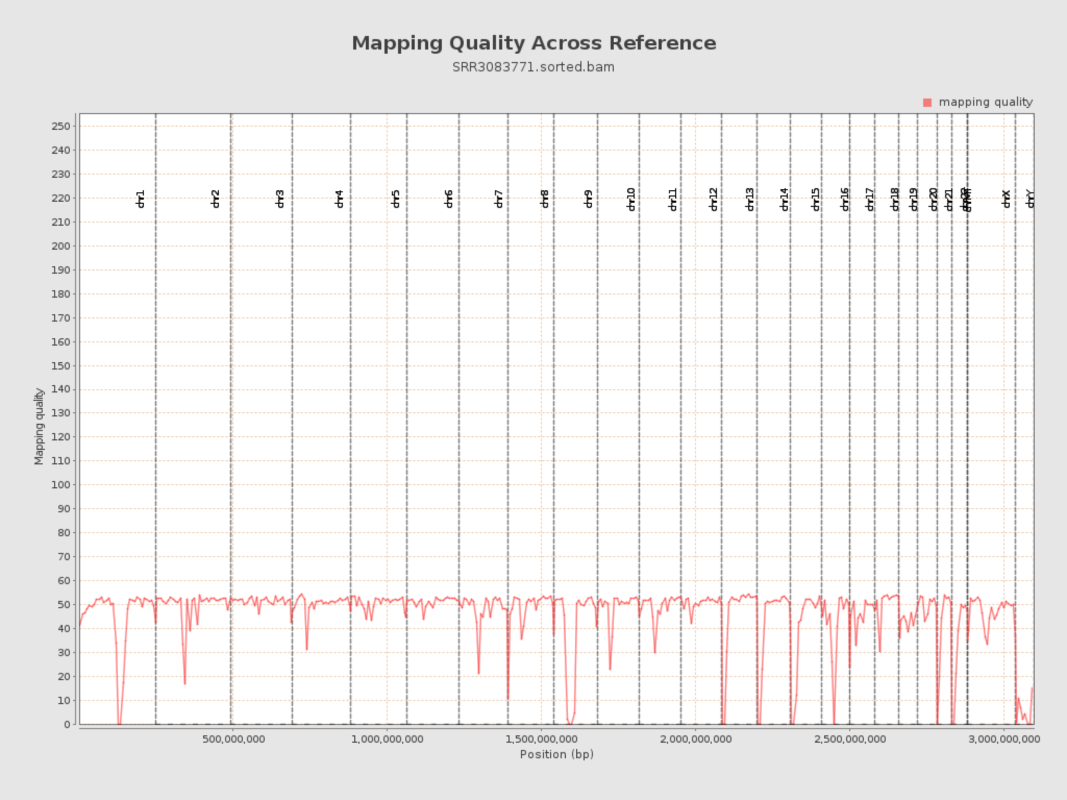
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram