Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:19:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008830.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_SRR6008830 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008830.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:19:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008830.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,215,324
Mapped reads	1,921,638 / 86.74%
Unmapped reads	293,686 / 13.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,741 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	80,597 / 3.64%
Duplication rate	3.06%
Clipped reads	928,563 / 41.92%

2.2. ACGT Content

Number/percentage of A's	35,039,476 / 27.81%
Number/percentage of C's	24,260,936 / 19.25%
Number/percentage of T's	38,580,860 / 30.62%
Number/percentage of G's	27,950,204 / 22.18%
Number/percentage of N's	173,028 / 0.14%
GC Percentage	41.44%

2.3. Coverage

Mean	0.0407

Standard Deviation	0.3964

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

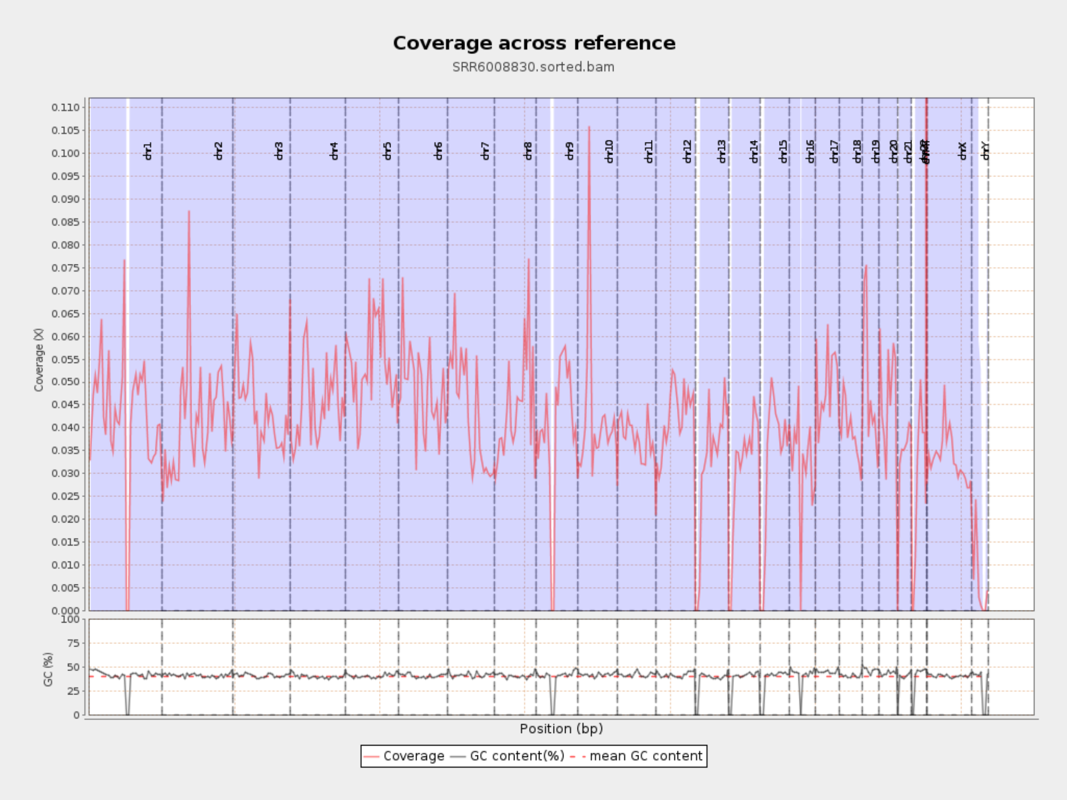
General error rate	0.89%
Mismatches	1,101,226
Insertions	9,508
Mapped reads with at least one insertion	0.49%
Deletions	40,322
Mapped reads with at least one deletion	2.07%
Homopolymer indels	44.88%

2.6. Chromosome stats

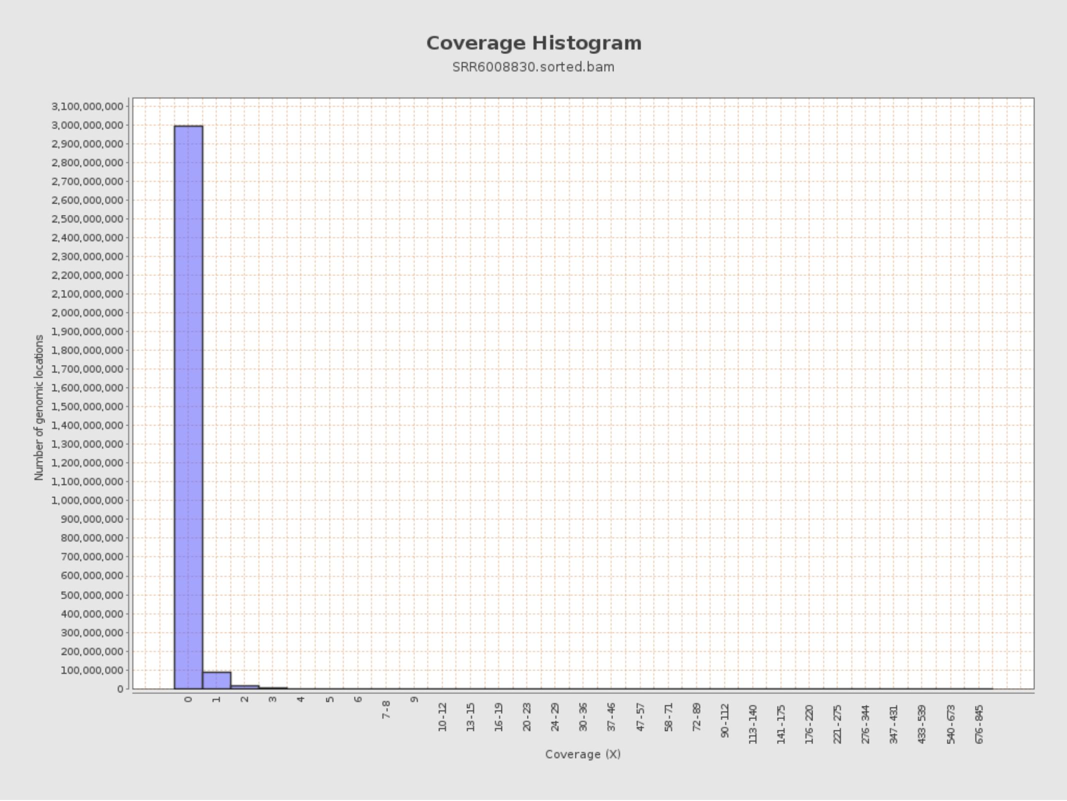
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10604715	0.0425	0.7326
chr2	243199373	10131879	0.0417	0.4701
chr3	198022430	8664767	0.0438	0.26
chr4	191154276	8571619	0.0448	0.278
chr5	180915260	9768735	0.054	0.2726
chr6	171115067	8237193	0.0481	0.2896
chr7	159138663	6832887	0.0429	0.3789

chr8	146364022	6476086	0.0442	0.5372
chr9	141213431	5627604	0.0399	0.3459
chr10	135534747	5706130	0.0421	0.6117
chr11	135006516	5050014	0.0374	0.2935
chr12	133851895	5639987	0.0421	0.2424
chr13	115169878	3675797	0.0319	0.2055
chr14	107349540	3326054	0.031	0.2326
chr15	102531392	3404968	0.0332	0.2108
chr16	90354753	2867233	0.0317	0.2662
chr17	81195210	4069298	0.0501	0.2794
chr18	78077248	3051735	0.0391	0.5801
chr19	59128983	2877976	0.0487	0.5114
chr20	63025520	2941940	0.0467	0.2632
chr21	48129895	1592556	0.0331	0.2503
chr22	51304566	1386601	0.027	0.1889
chrMT	16571	11809	0.7126	0.945
chrX	155270560	5181810	0.0334	0.2352
chrY	59373566	376844	0.0063	0.2213

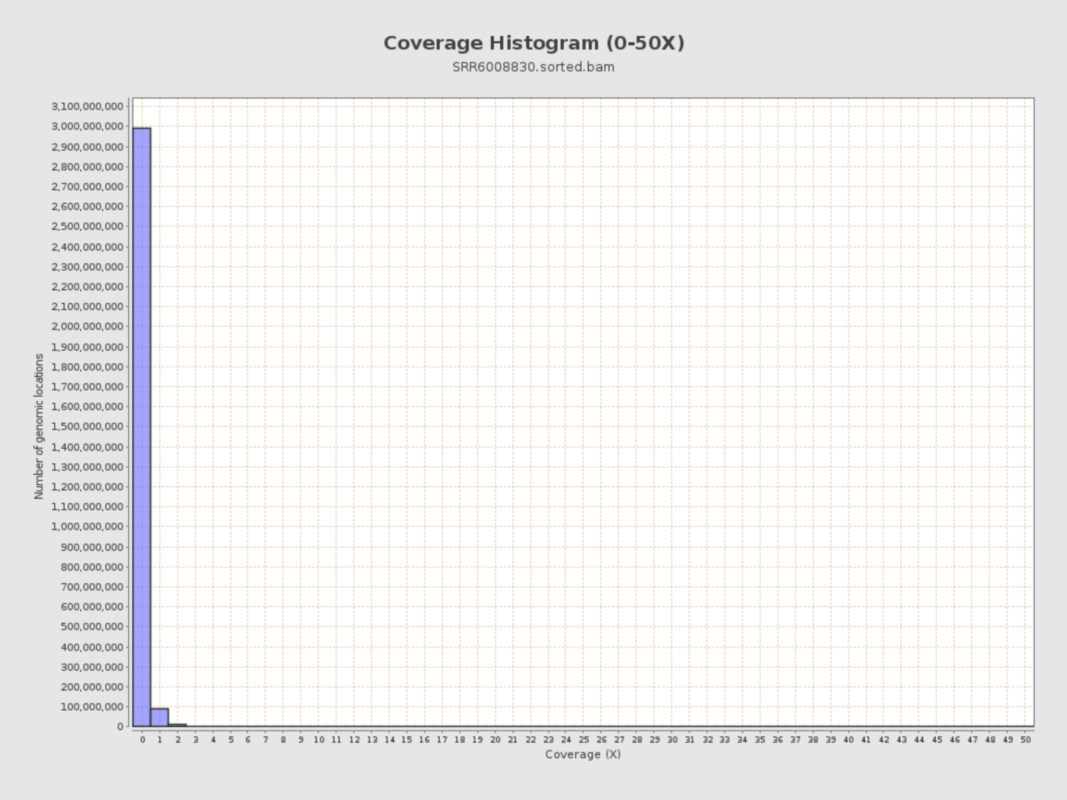
3. Results : Coverage across reference



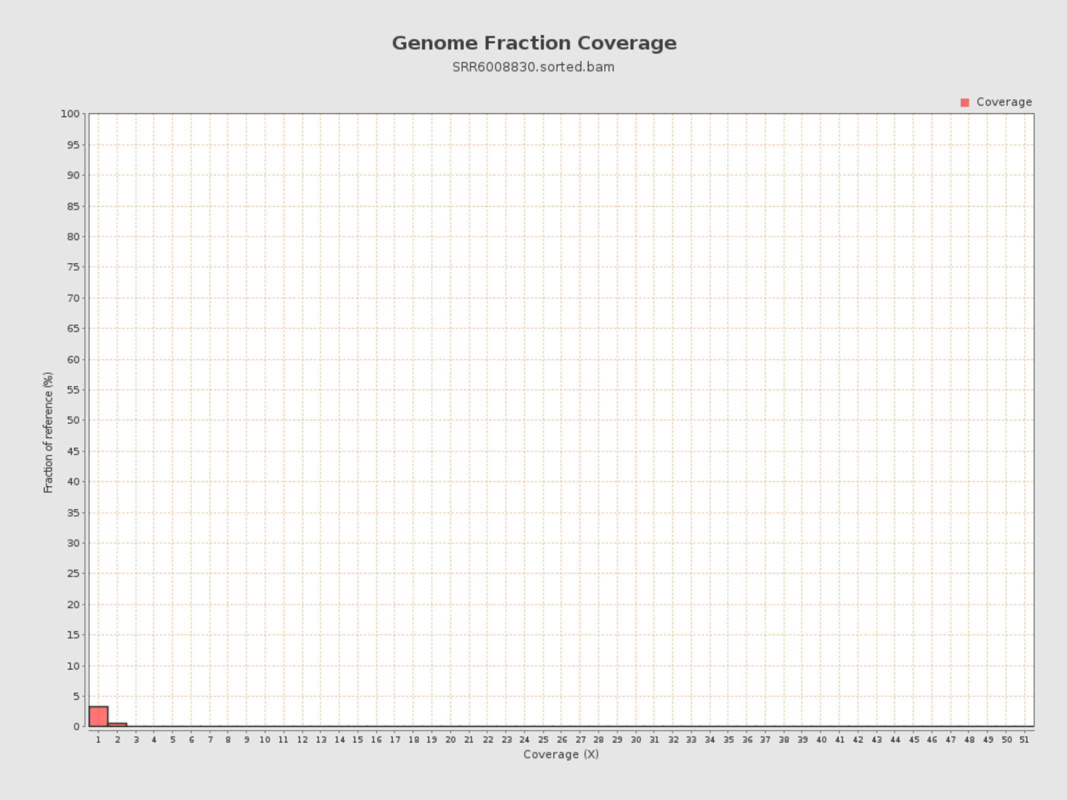
4. Results : Coverage Histogram



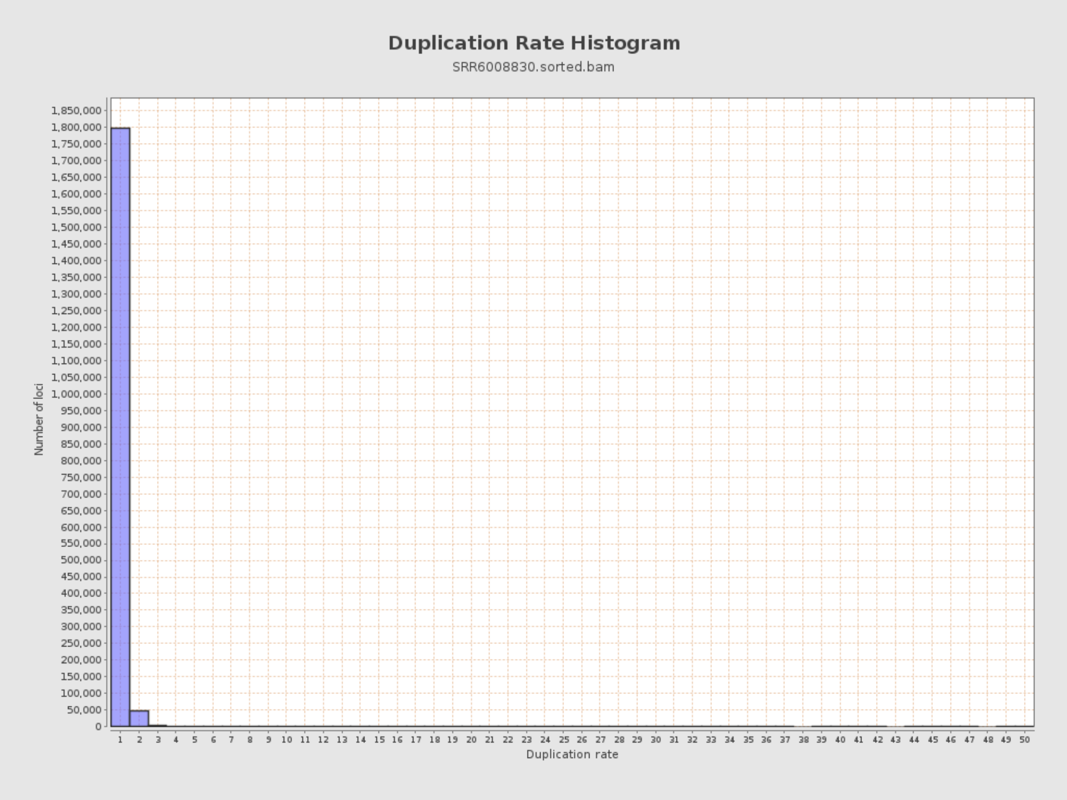
5. Results : Coverage Histogram (0-50X)



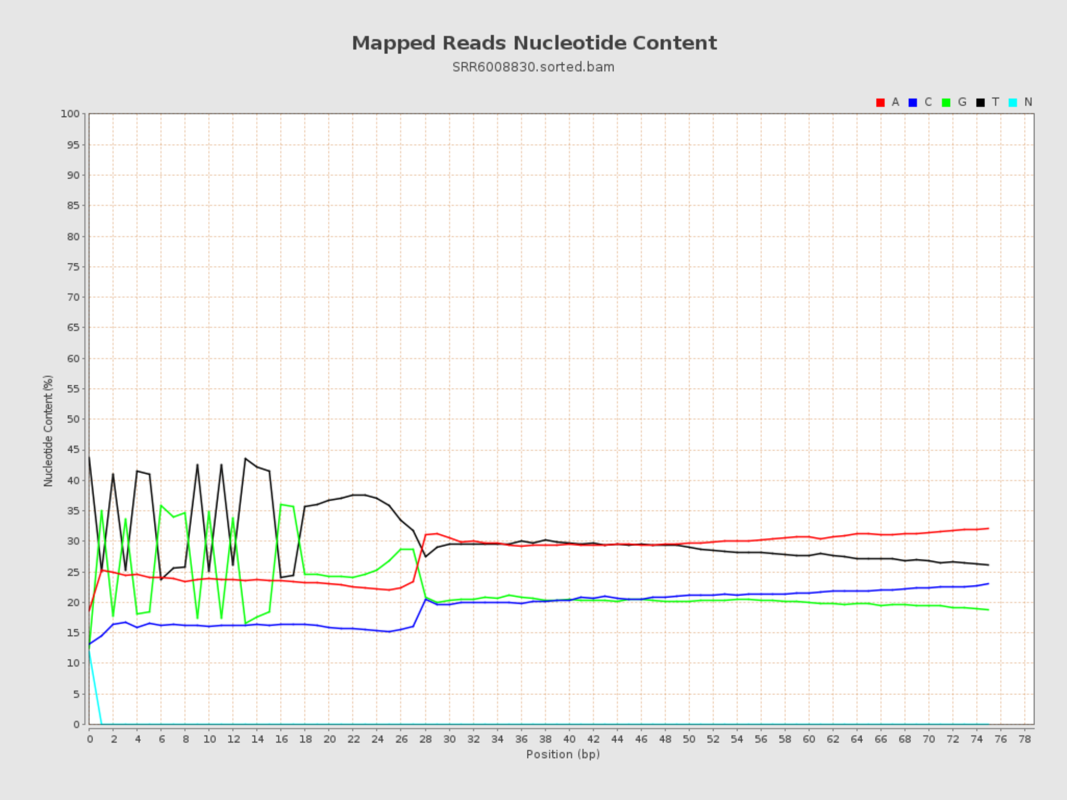
6. Results : Genome Fraction Coverage



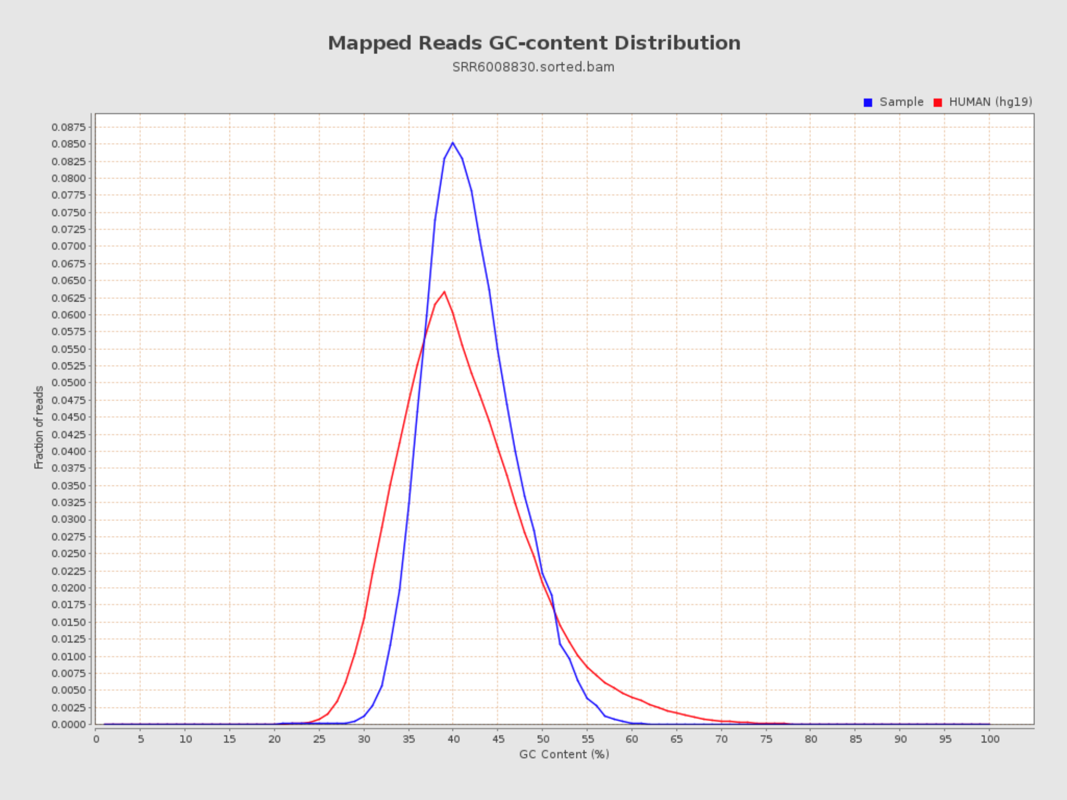
7. Results : Duplication Rate Histogram



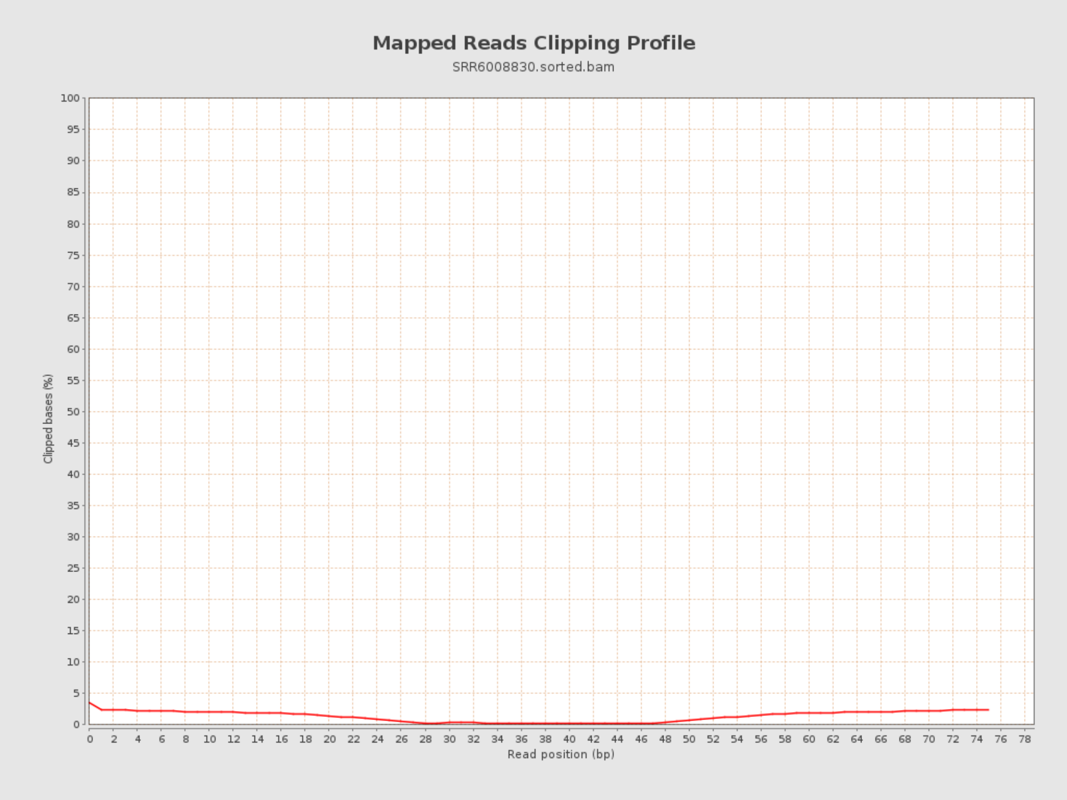
8. Results : Mapped Reads Nucleotide Content



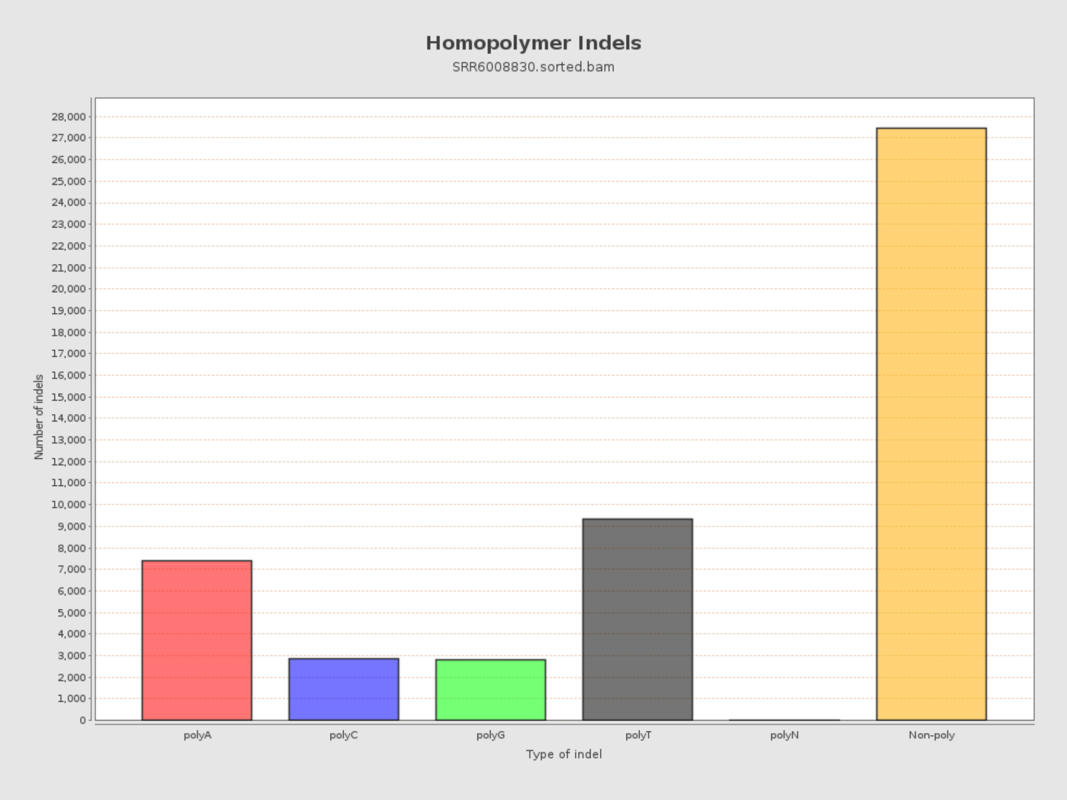
9. Results : Mapped Reads GC-content Distribution



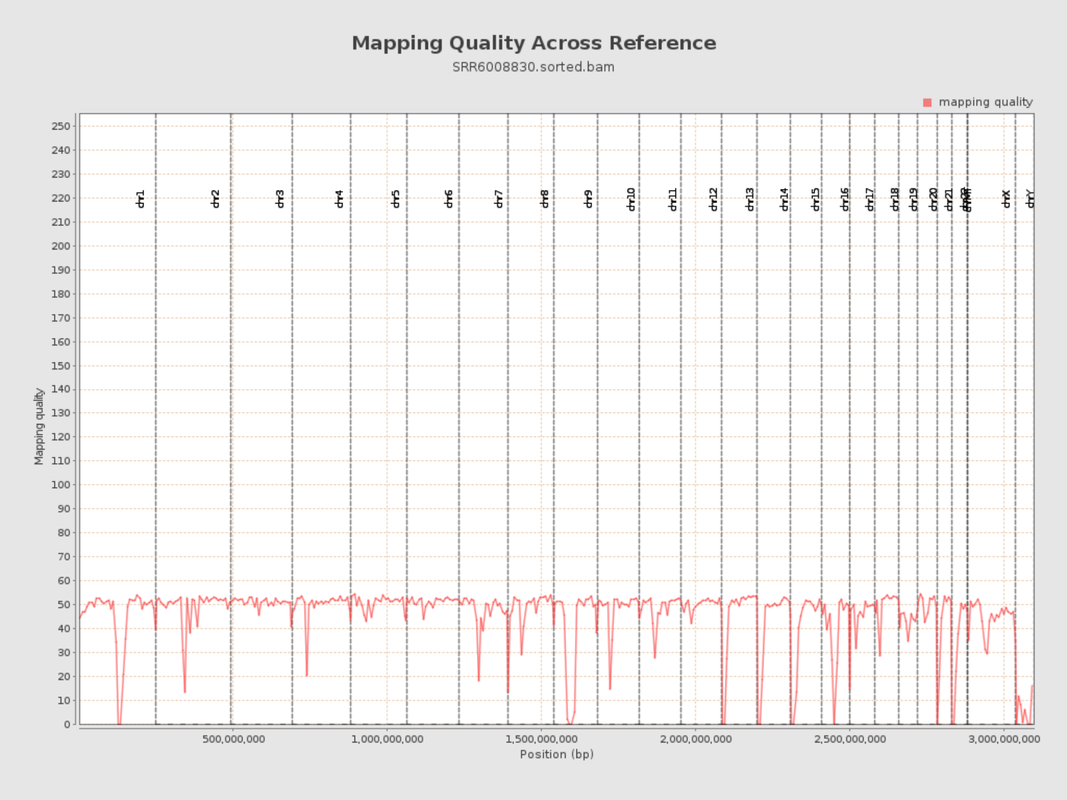
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram