Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:06:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084881.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_SRR3084881 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084881.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:06:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084881.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,577,963
Mapped reads	2,275,583 / 88.27%
Unmapped reads	302,380 / 11.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,211 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	102,301 / 3.97%
Duplication rate	3.53%
Clipped reads	740,990 / 28.74%

2.2. ACGT Content

Number/percentage of A's	46,384,100 / 29.3%
Number/percentage of C's	29,110,370 / 18.39%
Number/percentage of T's	50,603,036 / 31.97%
Number/percentage of G's	32,173,263 / 20.32%
Number/percentage of N's	24,844 / 0.02%
GC Percentage	38.71%

2.3. Coverage

Mean	0.0512

Standard Deviation	0.4675

2.4. Mapping Quality

Mean Mapping Quality	47.51

2.5. Mismatches and indels

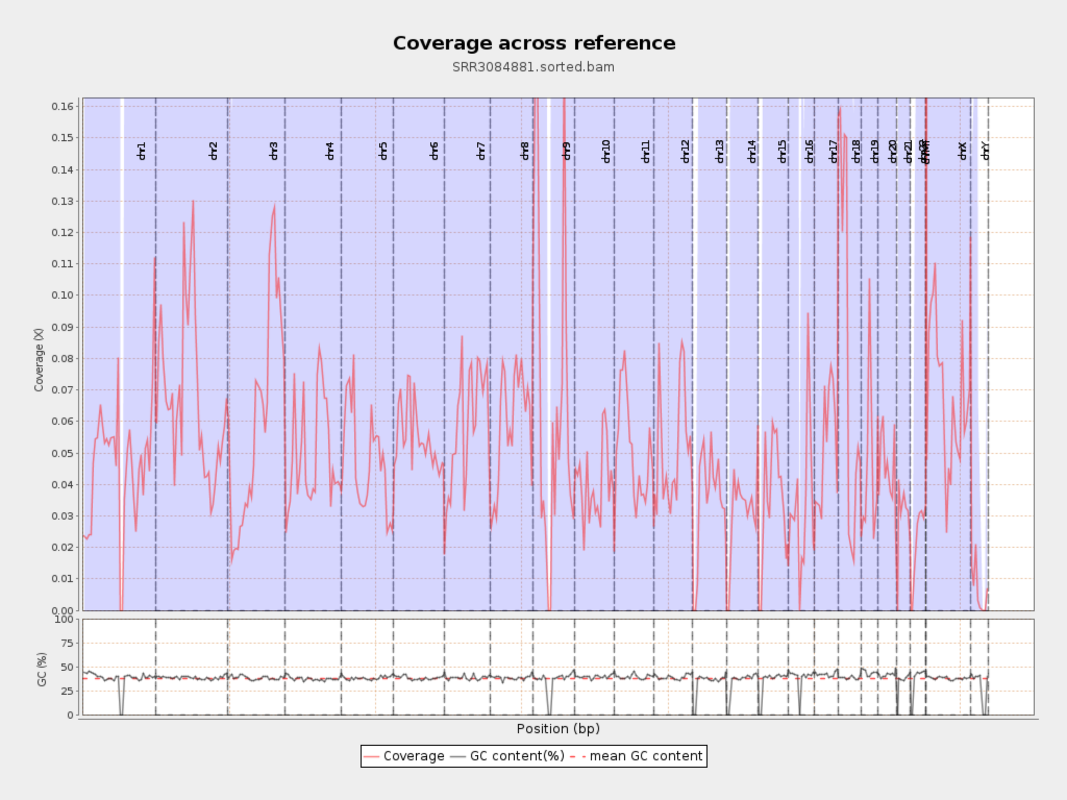
General error rate	0.85%
Mismatches	1,326,742
Insertions	12,702
Mapped reads with at least one insertion	0.55%
Deletions	35,134
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.54%

2.6. Chromosome stats

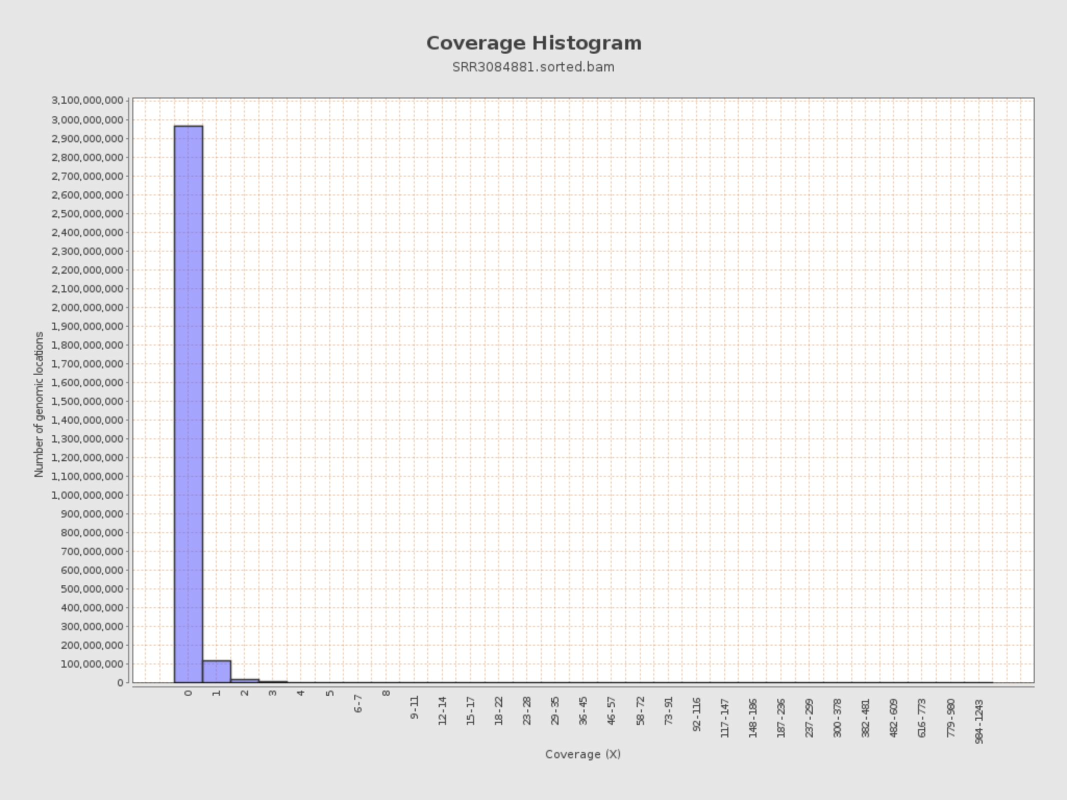
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11624446	0.0466	0.896
chr2	243199373	16317652	0.0671	0.5352
chr3	198022430	12070952	0.061	0.2845
chr4	191154276	9498654	0.0497	0.2598
chr5	180915260	8587755	0.0475	0.2612
chr6	171115067	9392351	0.0549	0.2775
chr7	159138663	9314874	0.0585	0.4581

chr8	146364022	8720139	0.0596	0.8655
chr9	141213431	9486719	0.0672	0.484
chr10	135534747	5523171	0.0408	0.3103
chr11	135006516	6845677	0.0507	0.3249
chr12	133851895	6929889	0.0518	0.2685
chr13	115169878	4057749	0.0352	0.2121
chr14	107349540	3252650	0.0303	0.2358
chr15	102531392	3560880	0.0347	0.2125
chr16	90354753	2902078	0.0321	0.2567
chr17	81195210	4320233	0.0532	0.2726
chr18	78077248	6474005	0.0829	0.8993
chr19	59128983	2780225	0.047	0.5098
chr20	63025520	2918825	0.0463	0.2634
chr21	48129895	1450384	0.0301	0.2229
chr22	51304566	1089926	0.0212	0.1625
chrMT	16571	256831	15.4988	8.2156
chrX	155270560	10596176	0.0682	0.3278
chrY	59373566	385985	0.0065	0.2054

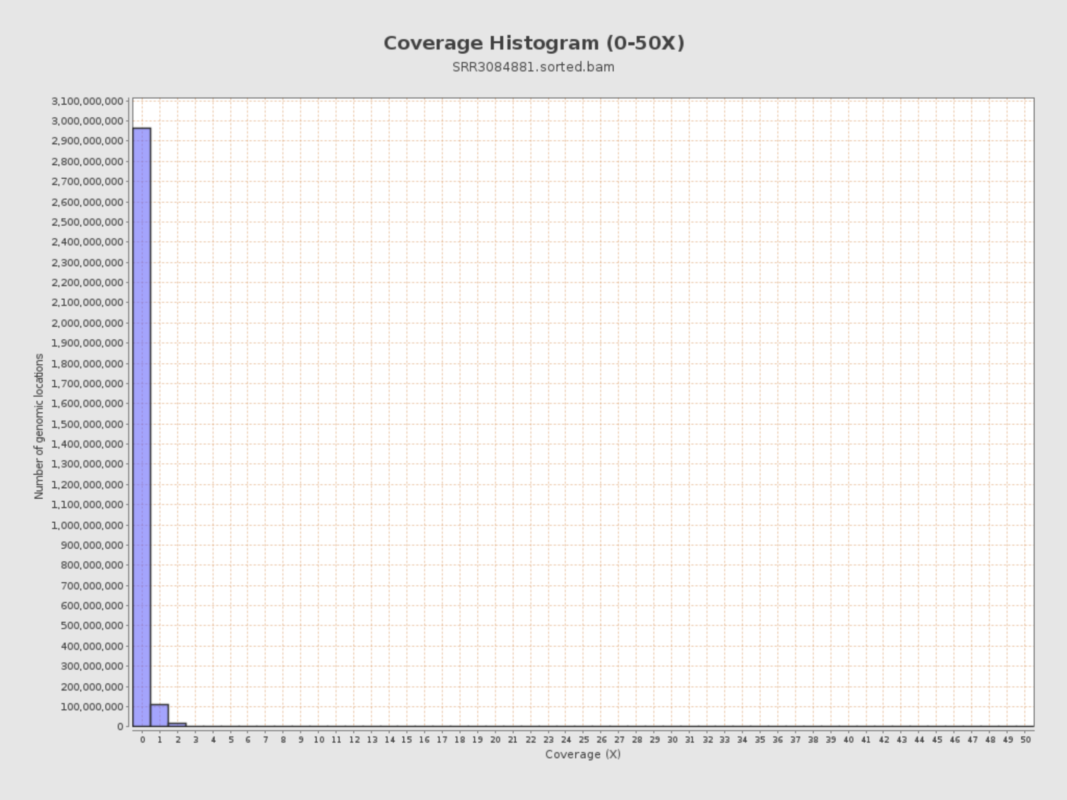
3. Results : Coverage across reference



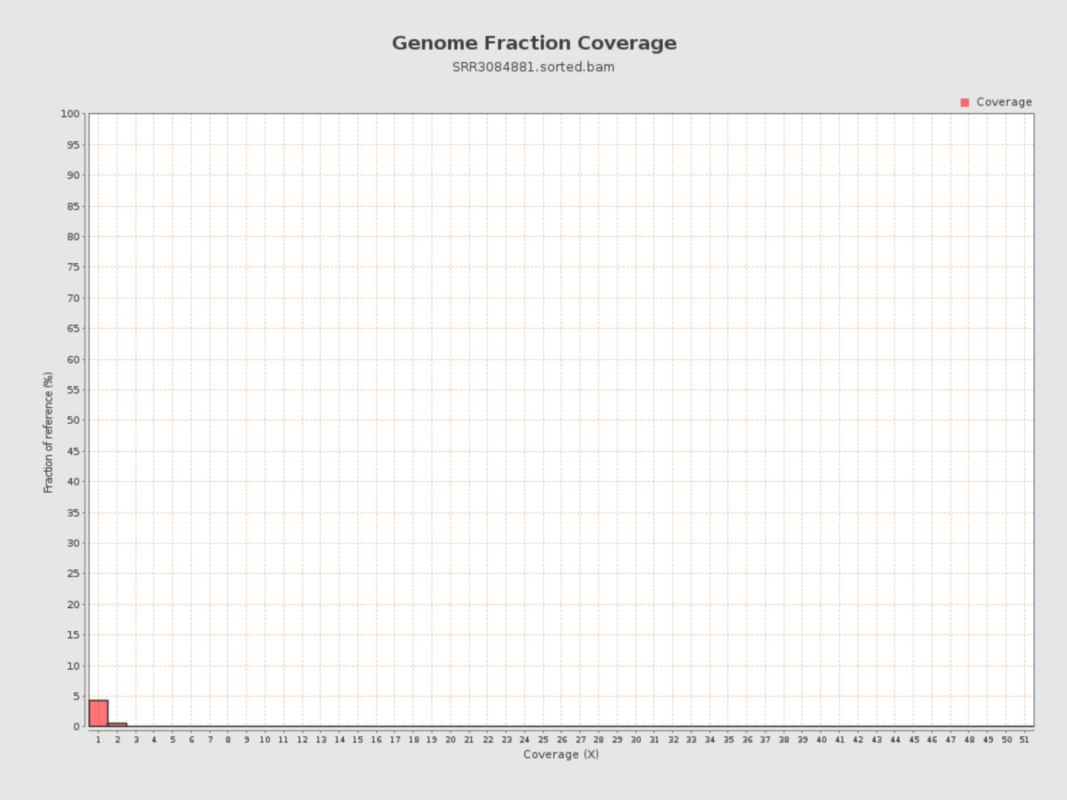
4. Results : Coverage Histogram



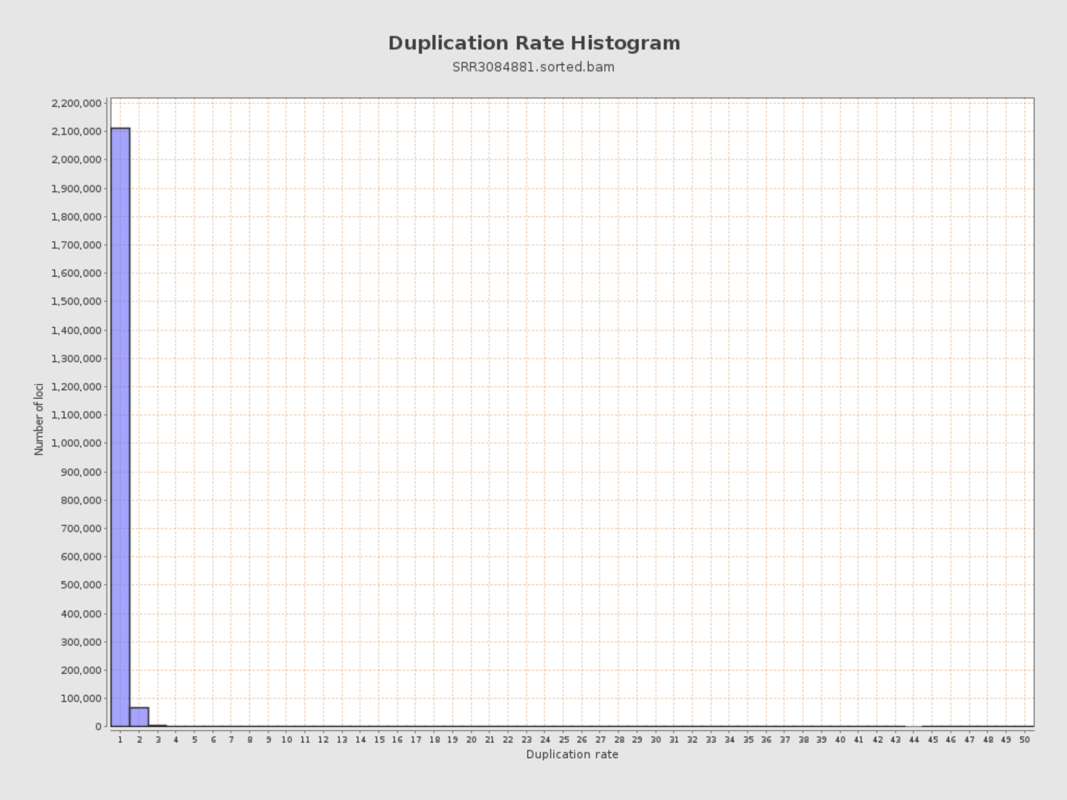
5. Results : Coverage Histogram (0-50X)



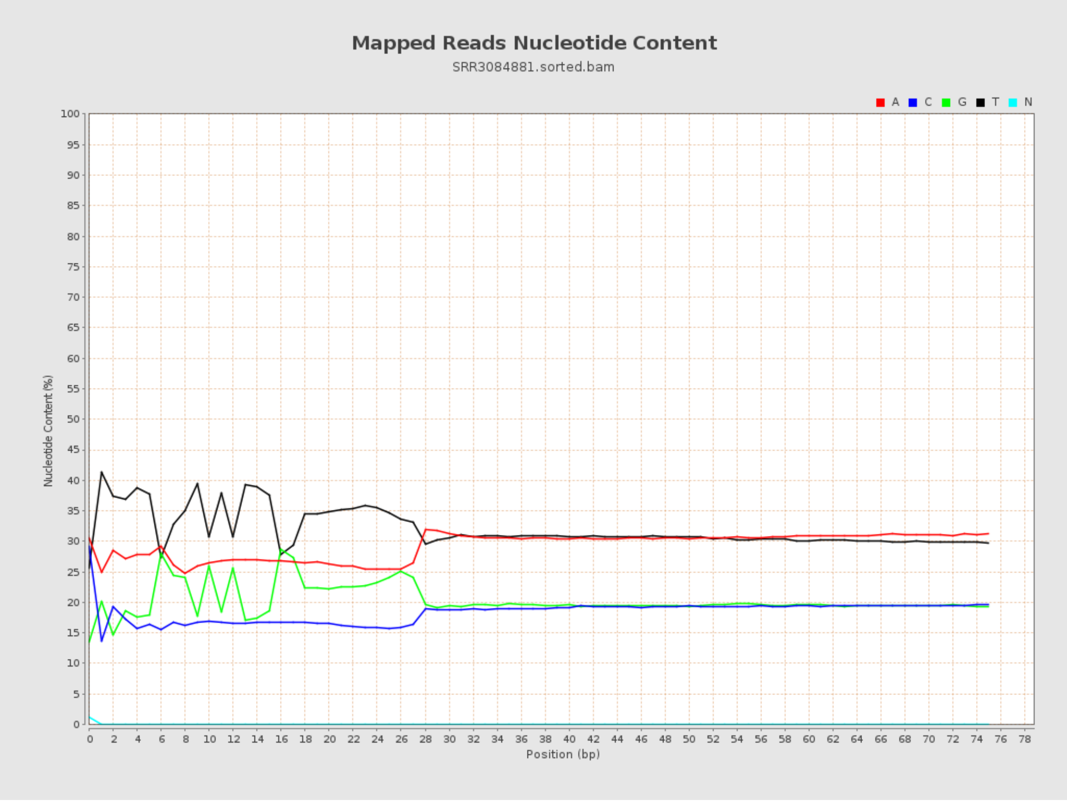
6. Results : Genome Fraction Coverage



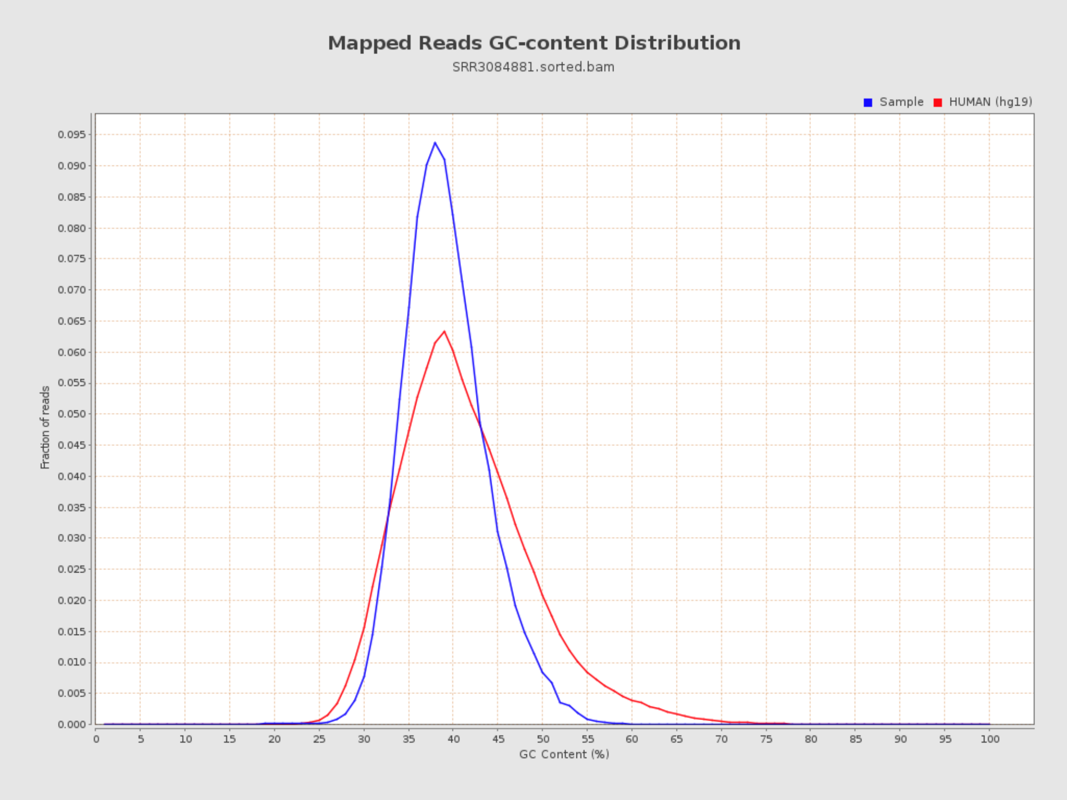
7. Results : Duplication Rate Histogram



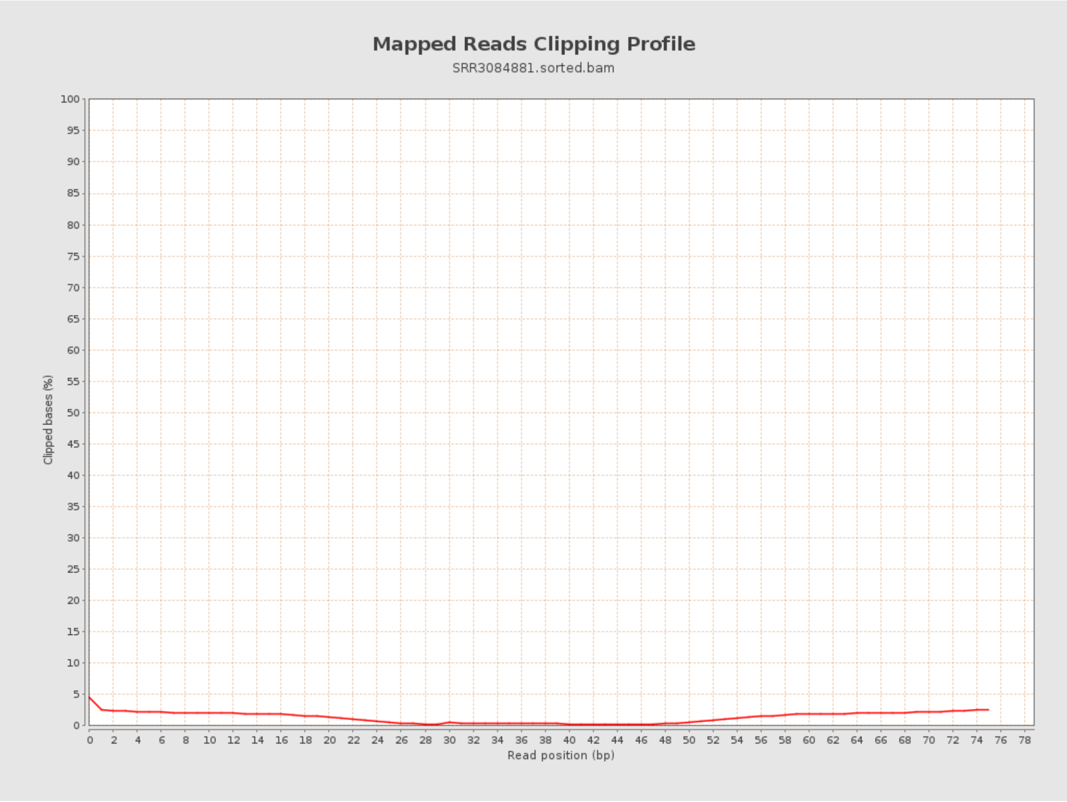
8. Results : Mapped Reads Nucleotide Content



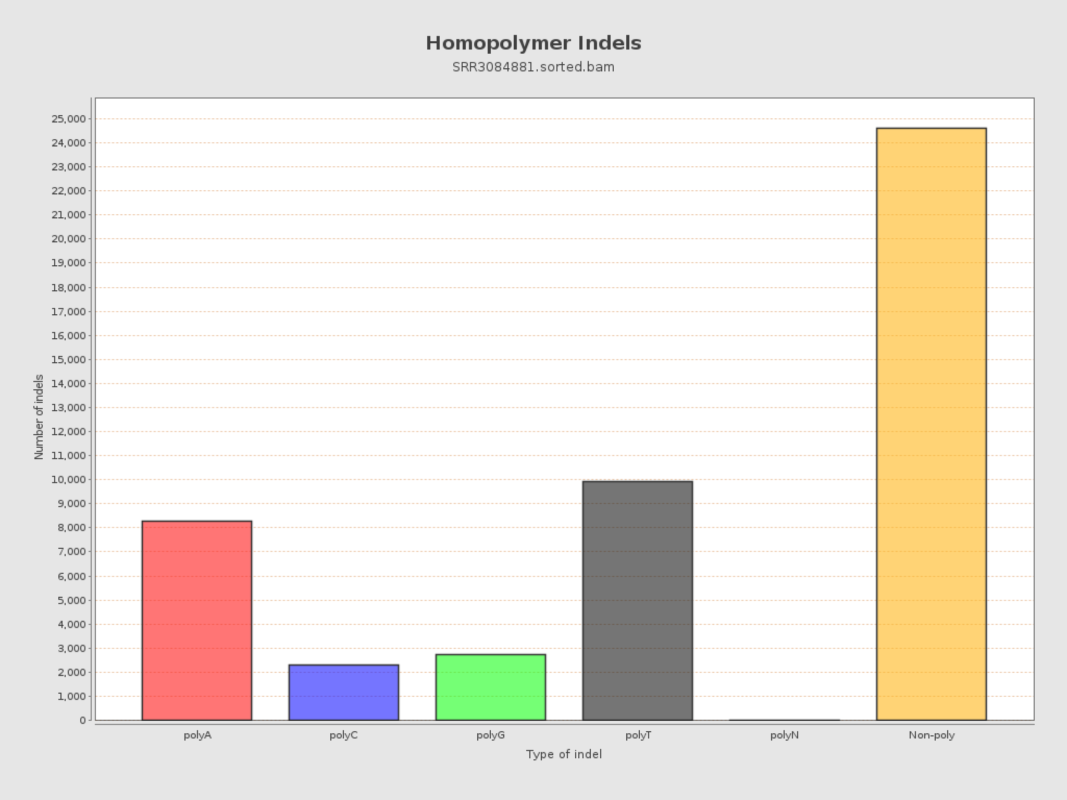
9. Results : Mapped Reads GC-content Distribution



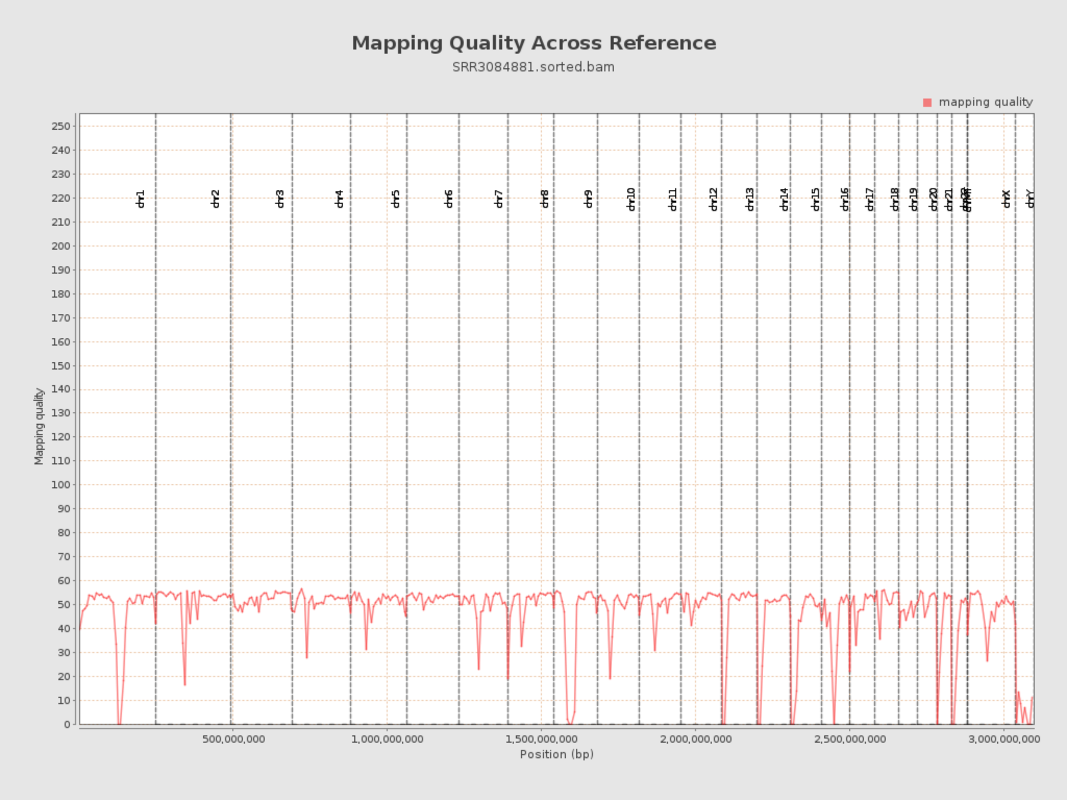
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram