Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:48:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084788.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_SRR3084788 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084788.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:48:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084788.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,837,008
Mapped reads	1,665,038 / 90.64%
Unmapped reads	171,970 / 9.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,164 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	65,612 / 3.57%
Duplication rate	3.21%
Clipped reads	653,063 / 35.55%

2.2. ACGT Content

Number/percentage of A's	32,054,116 / 28.31%
Number/percentage of C's	20,960,894 / 18.51%
Number/percentage of T's	35,718,374 / 31.54%
Number/percentage of G's	24,452,061 / 21.59%
Number/percentage of N's	47,924 / 0.04%
GC Percentage	40.11%

2.3. Coverage

Mean	0.0366

Standard Deviation	0.296

2.4. Mapping Quality

Mean Mapping Quality	47.46

2.5. Mismatches and indels

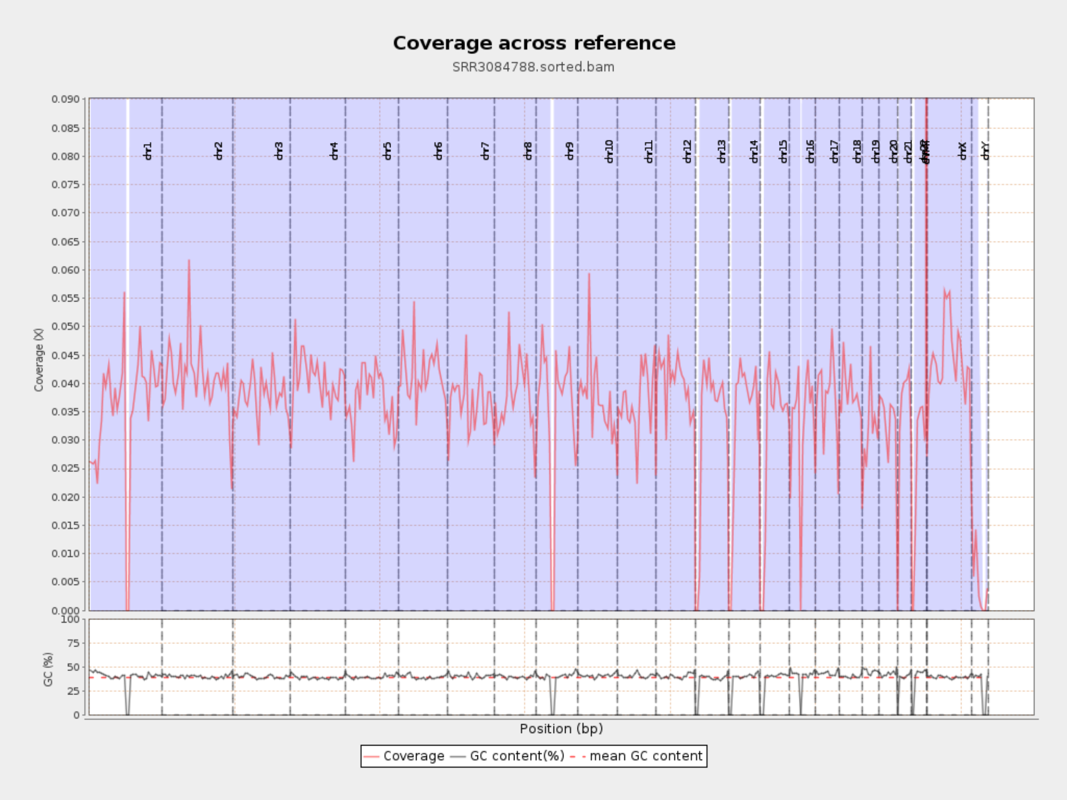
General error rate	0.85%
Mismatches	942,825
Insertions	8,927
Mapped reads with at least one insertion	0.53%
Deletions	26,402
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.97%

2.6. Chromosome stats

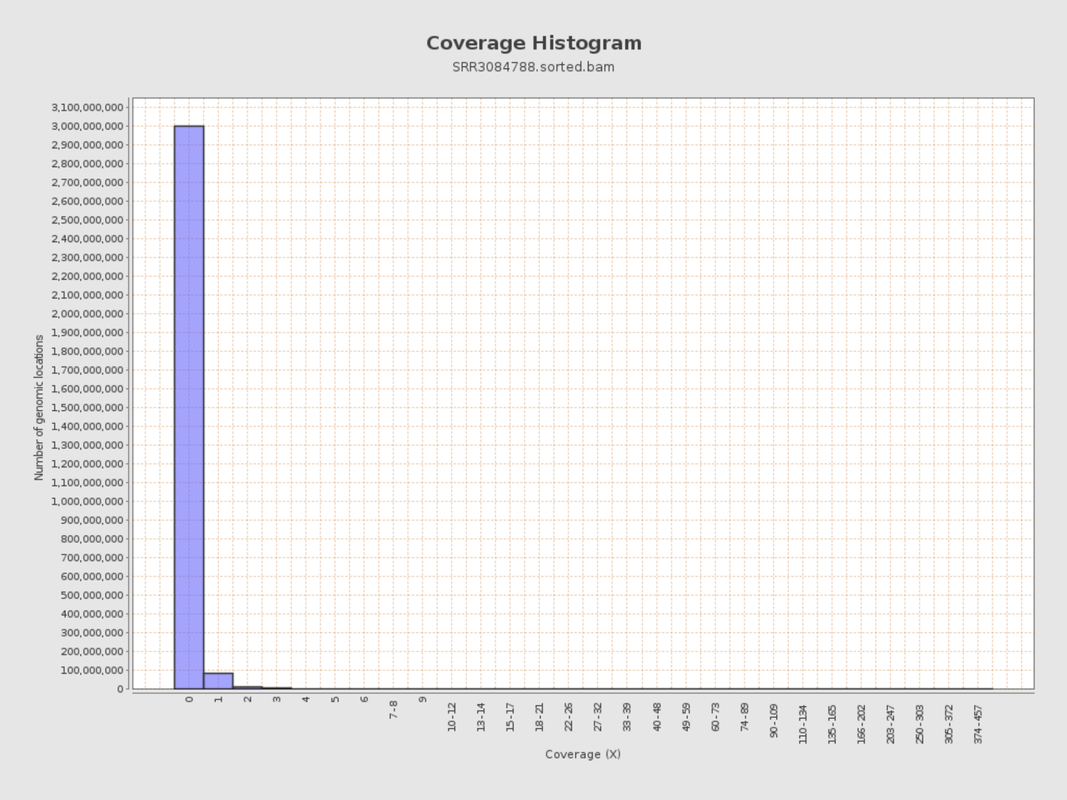
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8887628	0.0357	0.4517
chr2	243199373	10027027	0.0412	0.3496
chr3	198022430	7527417	0.038	0.2212
chr4	191154276	7786131	0.0407	0.2371
chr5	180915260	6707898	0.0371	0.2198
chr6	171115067	7135491	0.0417	0.2684
chr7	159138663	5856500	0.0368	0.3108

chr8	146364022	5519084	0.0377	0.365
chr9	141213431	4983988	0.0353	0.2866
chr10	135534747	5092383	0.0376	0.3095
chr11	135006516	4979701	0.0369	0.2758
chr12	133851895	5404203	0.0404	0.2299
chr13	115169878	3727365	0.0324	0.2065
chr14	107349540	3518633	0.0328	0.2225
chr15	102531392	3164660	0.0309	0.2045
chr16	90354753	2984581	0.033	0.2259
chr17	81195210	3023348	0.0372	0.2372
chr18	78077248	3014827	0.0386	0.558
chr19	59128983	1896233	0.0321	0.3349
chr20	63025520	2092212	0.0332	0.2146
chr21	48129895	1645279	0.0342	0.2188
chr22	51304566	1221591	0.0238	0.1737
chrMT	16571	7889	0.4761	0.8453
chrX	155270560	6799480	0.0438	0.2546
chrY	59373566	272794	0.0046	0.1084

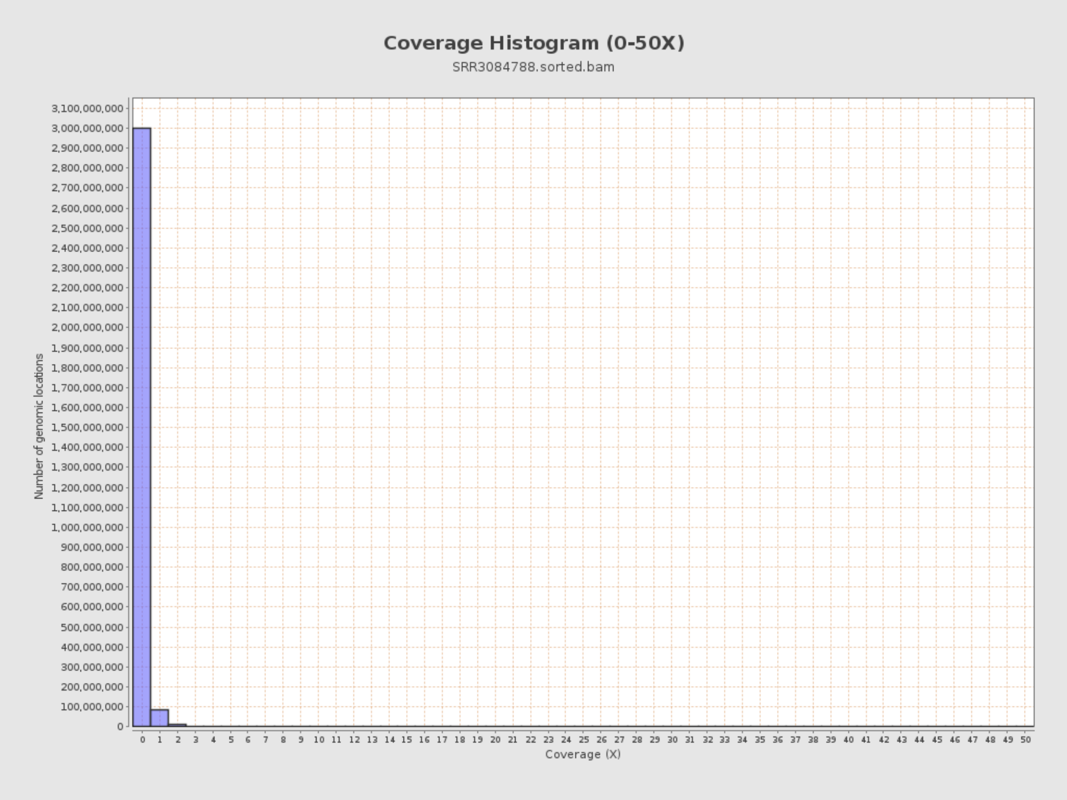
3. Results : Coverage across reference



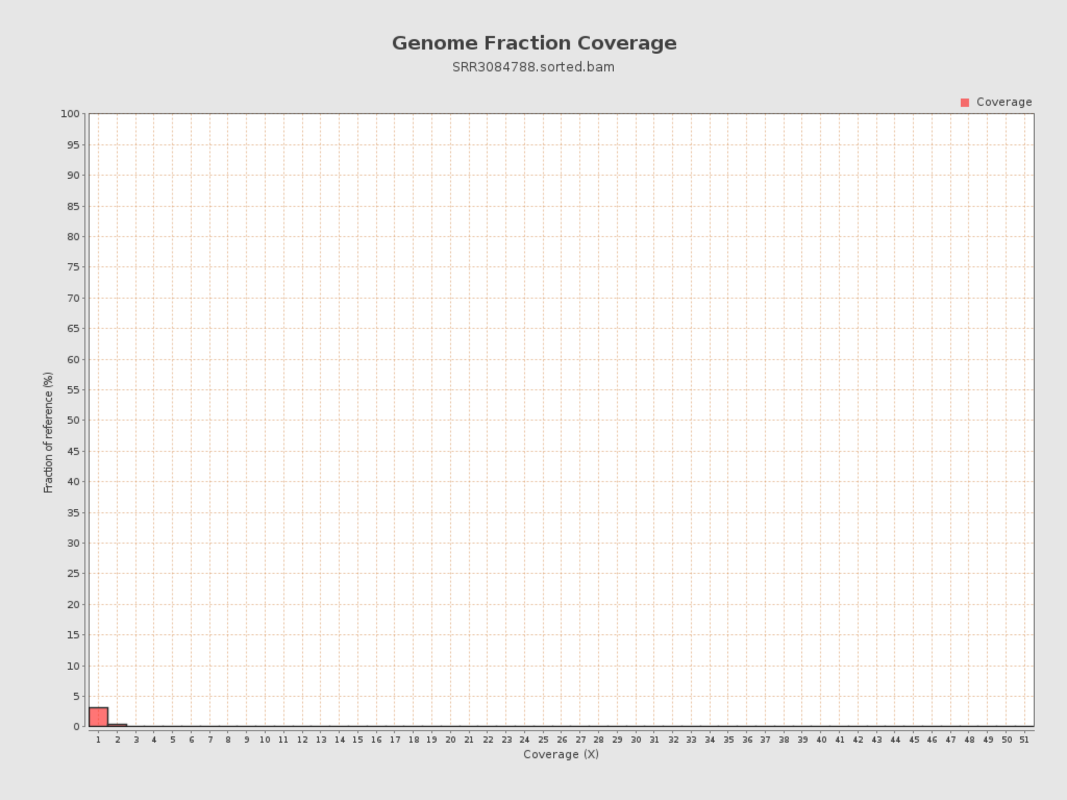
4. Results : Coverage Histogram



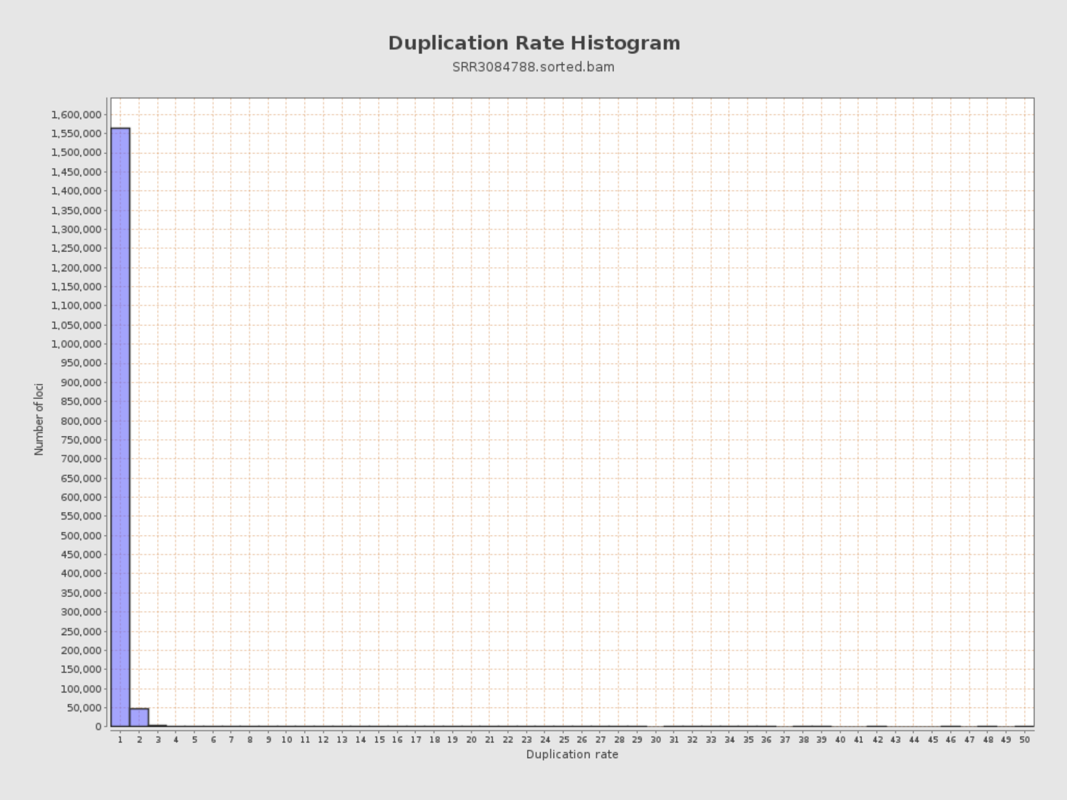
5. Results : Coverage Histogram (0-50X)



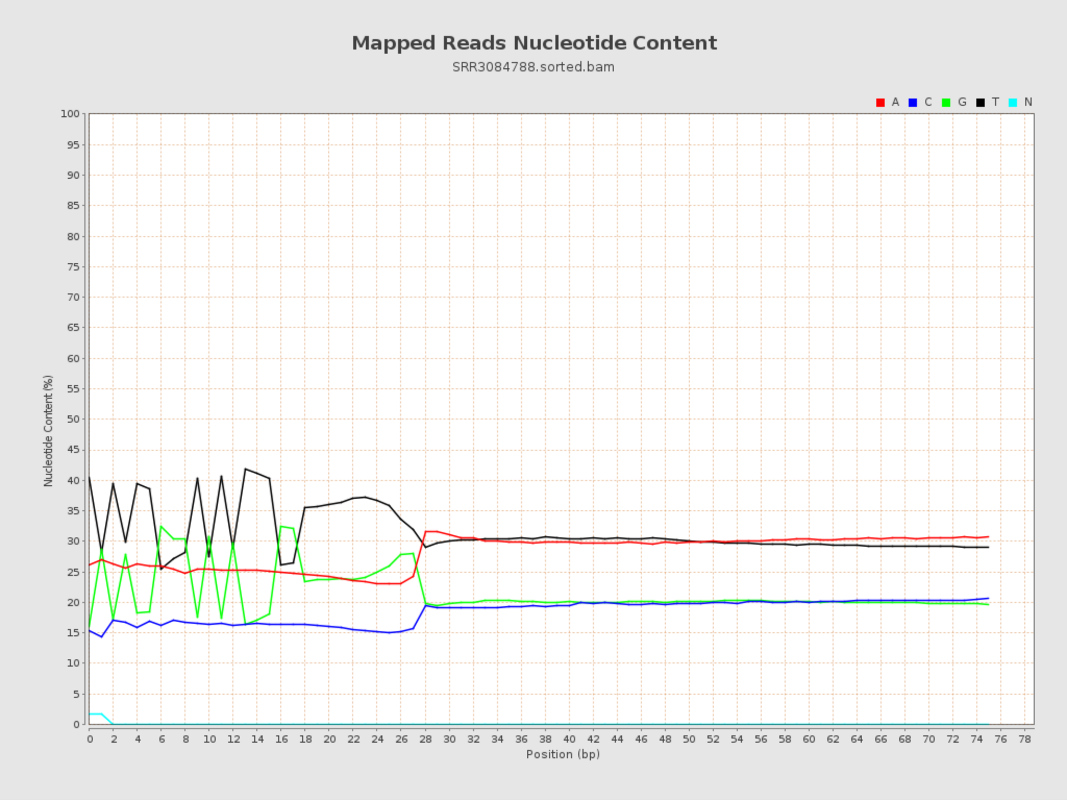
6. Results : Genome Fraction Coverage



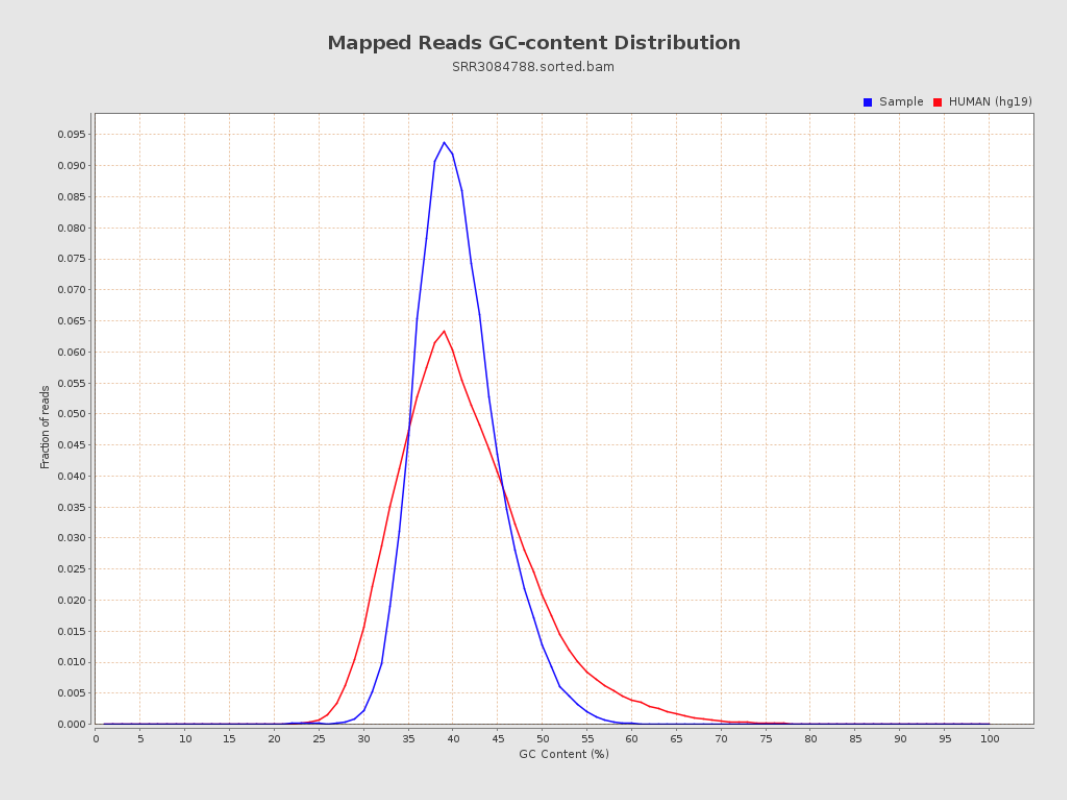
7. Results : Duplication Rate Histogram



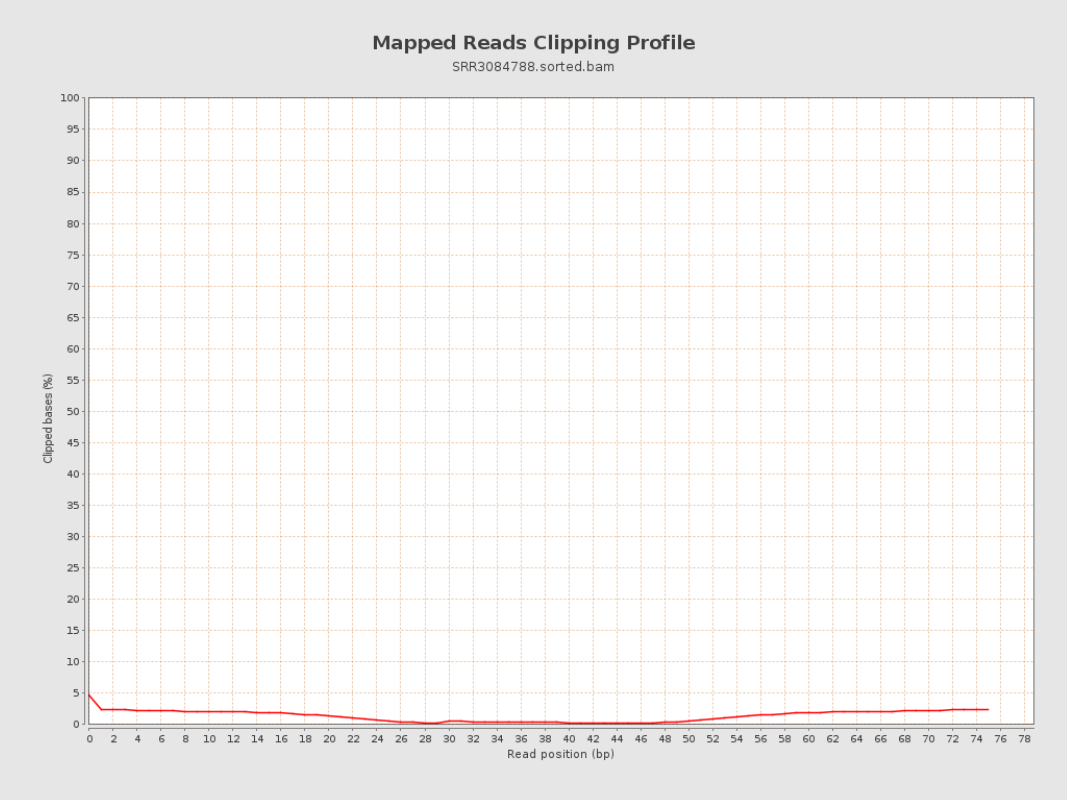
8. Results : Mapped Reads Nucleotide Content



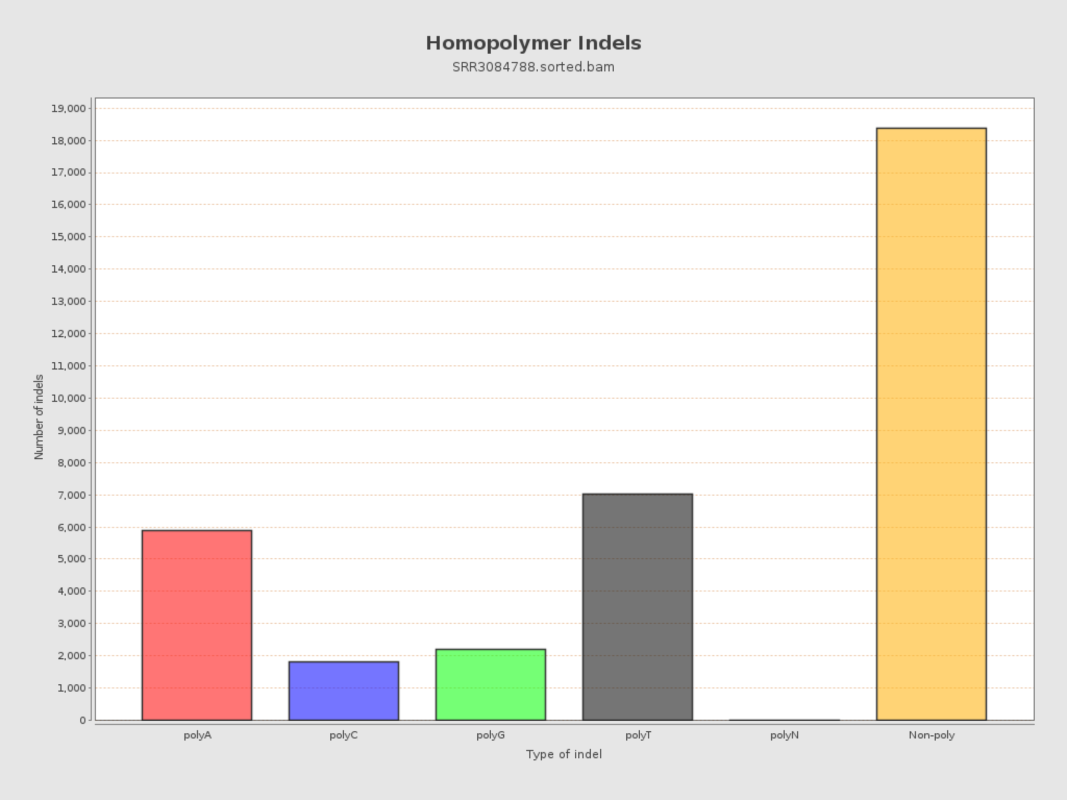
9. Results : Mapped Reads GC-content Distribution



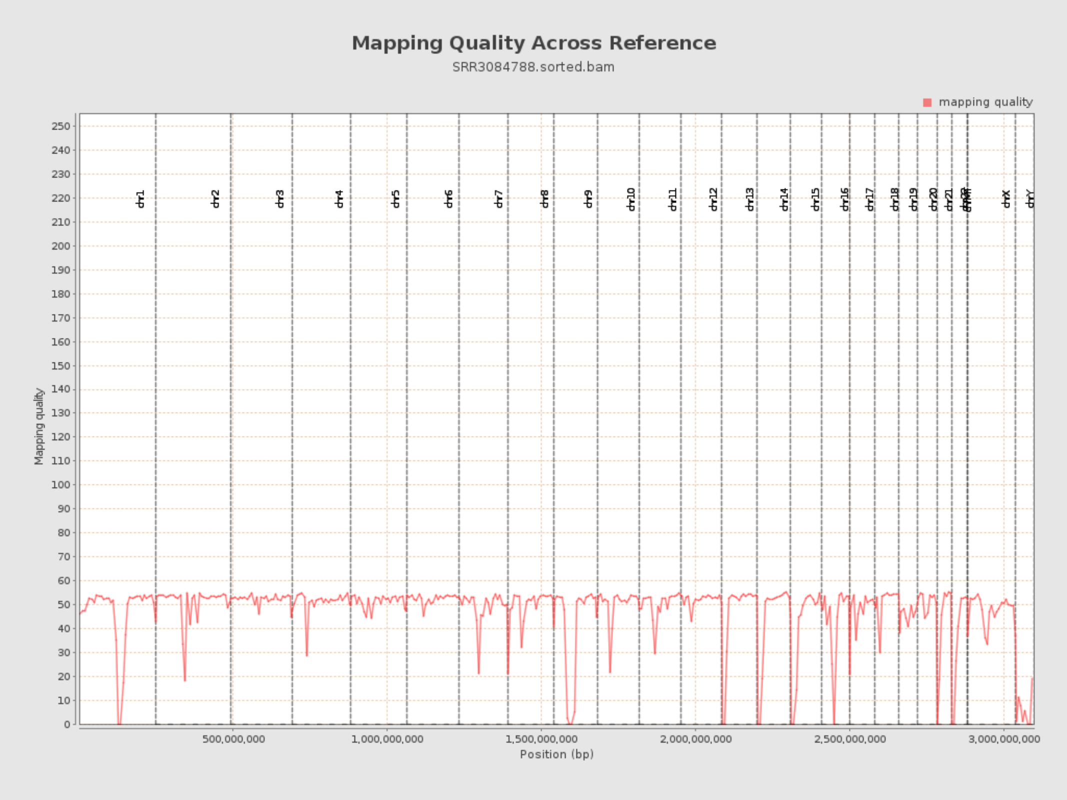
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram