Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:26:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080816.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_SRR3080816 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080816.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:26:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080816.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,619,551
Mapped reads	2,418,830 / 92.34%
Unmapped reads	200,721 / 7.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,788 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	136,028 / 5.19%
Duplication rate	4.69%
Clipped reads	862,260 / 32.92%

2.2. ACGT Content

Number/percentage of A's	47,759,283 / 28.68%
Number/percentage of C's	31,134,106 / 18.7%
Number/percentage of T's	52,526,682 / 31.55%
Number/percentage of G's	35,062,827 / 21.06%
Number/percentage of N's	23,949 / 0.01%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0538

Standard Deviation	0.4378

2.4. Mapping Quality

Mean Mapping Quality	46.89

2.5. Mismatches and indels

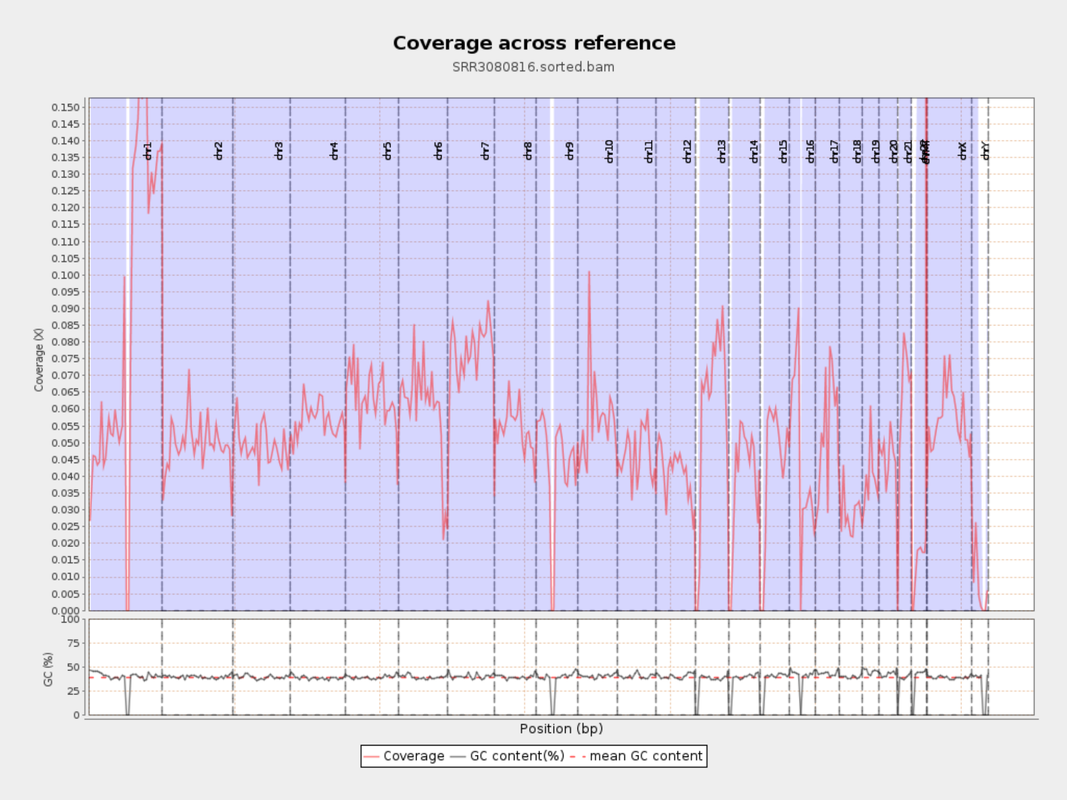
General error rate	0.82%
Mismatches	1,347,541
Insertions	12,399
Mapped reads with at least one insertion	0.51%
Deletions	36,687
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.72%

2.6. Chromosome stats

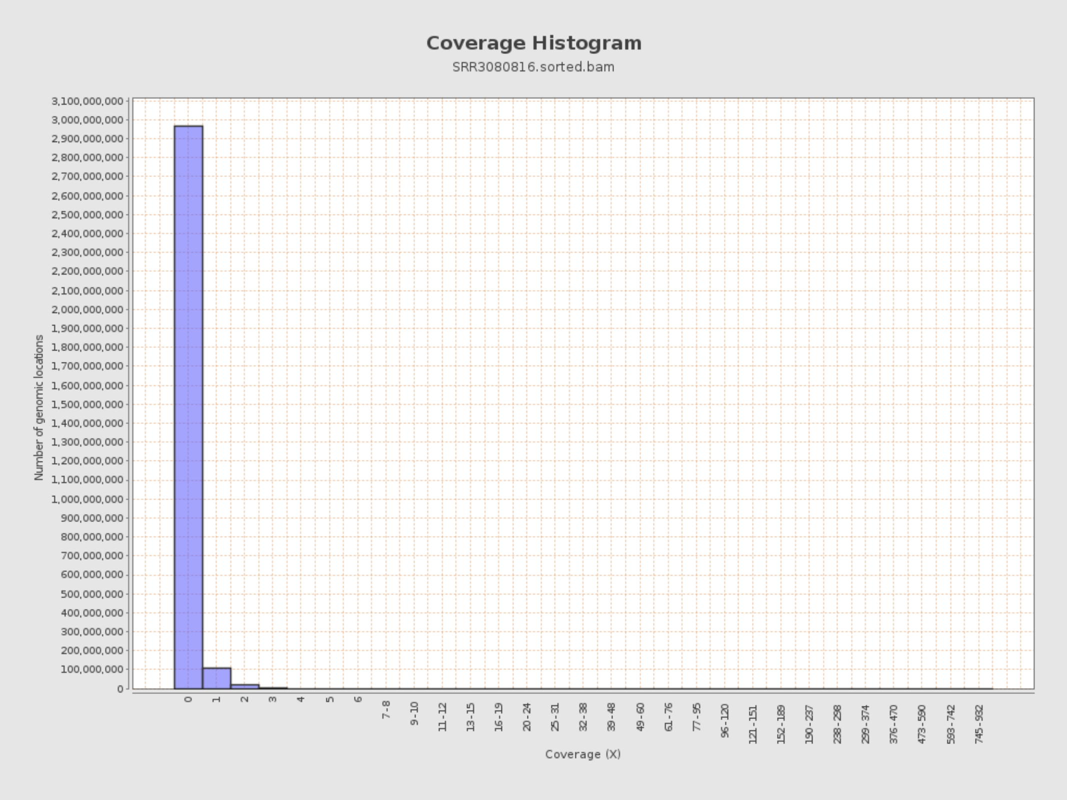
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21537318	0.0864	0.918
chr2	243199373	12092216	0.0497	0.3884
chr3	198022430	9718983	0.0491	0.2749
chr4	191154276	10841148	0.0567	0.3139
chr5	180915260	11578483	0.064	0.3039
chr6	171115067	10360304	0.0605	0.3835
chr7	159138663	12409610	0.078	0.4951

chr8	146364022	7937267	0.0542	0.5927
chr9	141213431	6172410	0.0437	0.3033
chr10	135534747	7750177	0.0572	0.5319
chr11	135006516	6278383	0.0465	0.2809
chr12	133851895	5525089	0.0413	0.2484
chr13	115169878	6916064	0.0601	0.2943
chr14	107349540	4142143	0.0386	0.2531
chr15	102531392	4393899	0.0429	0.2478
chr16	90354753	4104900	0.0454	0.2965
chr17	81195210	4382518	0.054	0.291
chr18	78077248	2285436	0.0293	0.5126
chr19	59128983	2348447	0.0397	0.6367
chr20	63025520	2853287	0.0453	0.266
chr21	48129895	2963181	0.0616	0.317
chr22	51304566	668561	0.013	0.1352
chrMT	16571	26247	1.5839	1.7476
chrX	155270560	8841186	0.0569	0.3013
chrY	59373566	444600	0.0075	0.2086

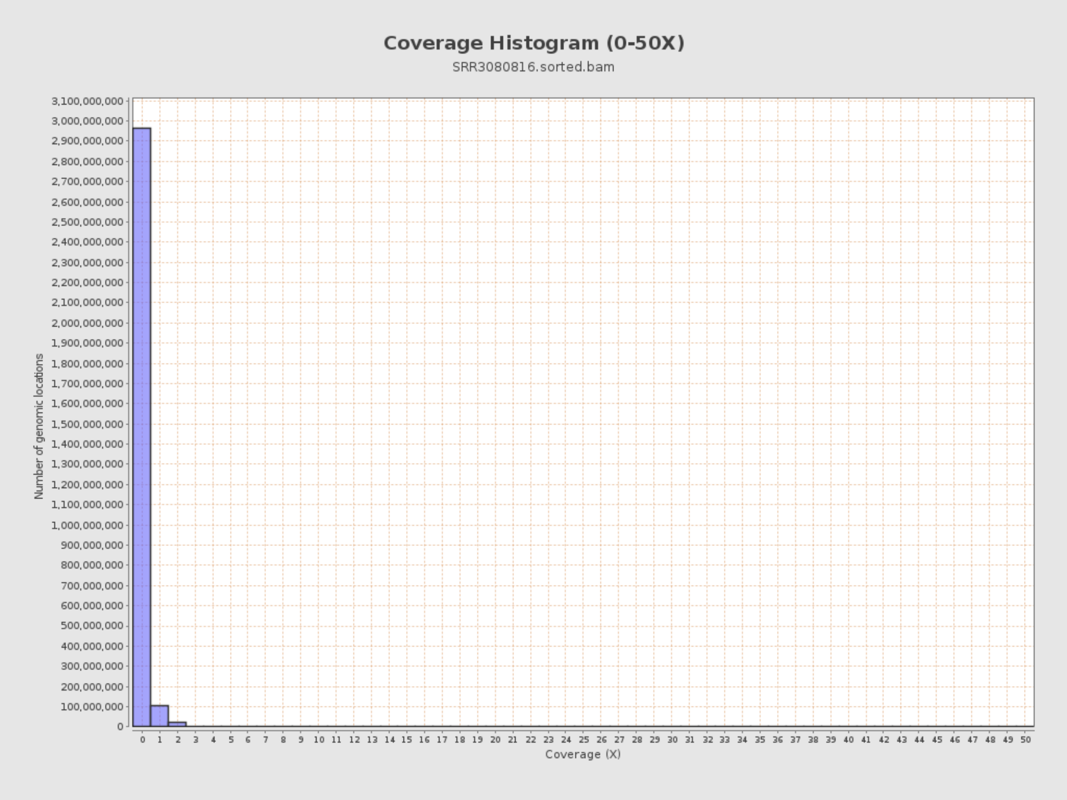
3. Results : Coverage across reference



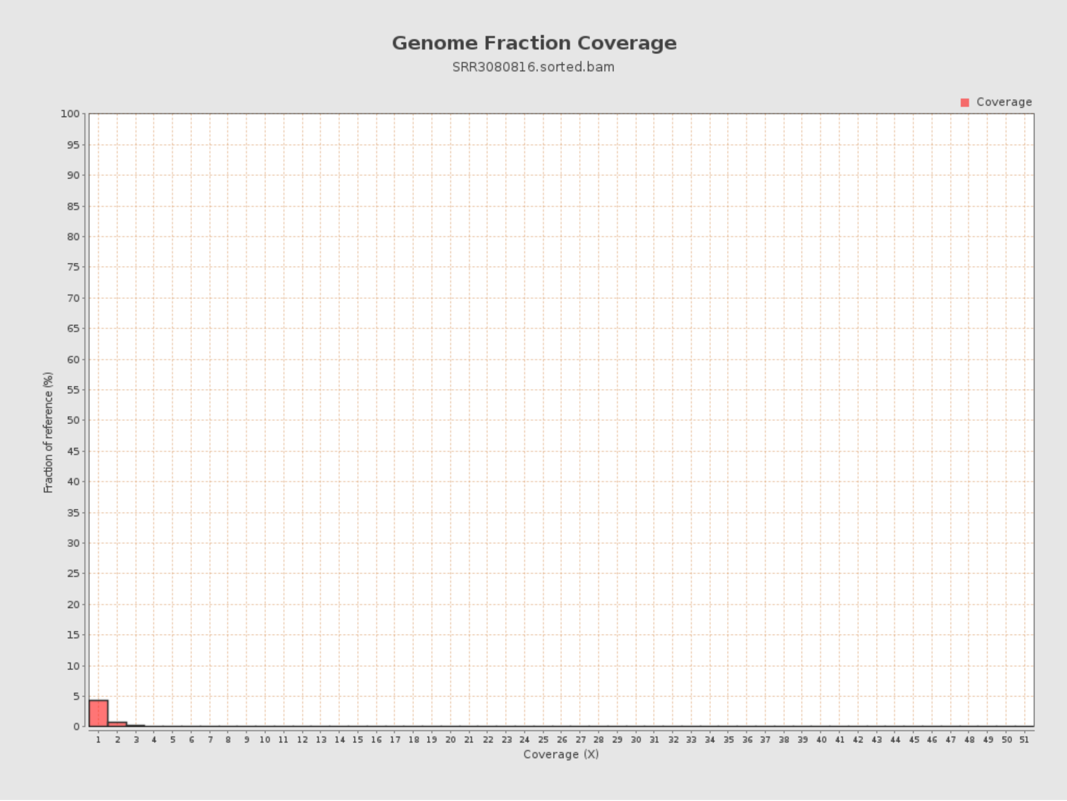
4. Results : Coverage Histogram



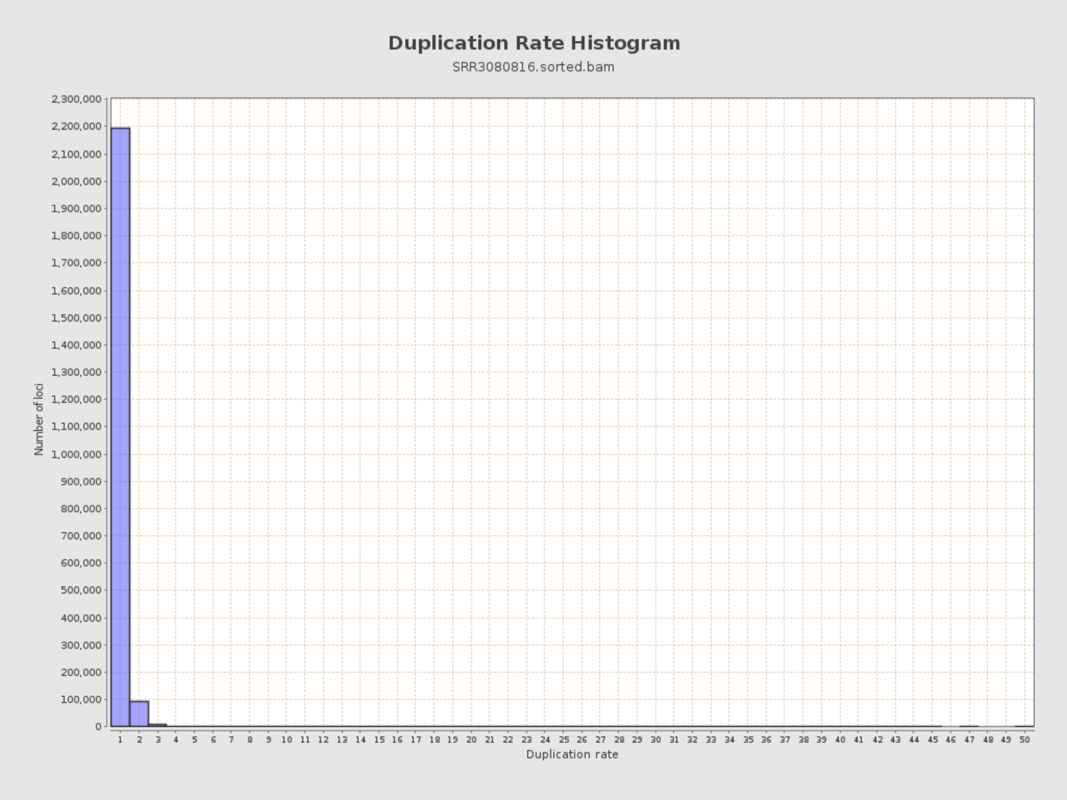
5. Results : Coverage Histogram (0-50X)



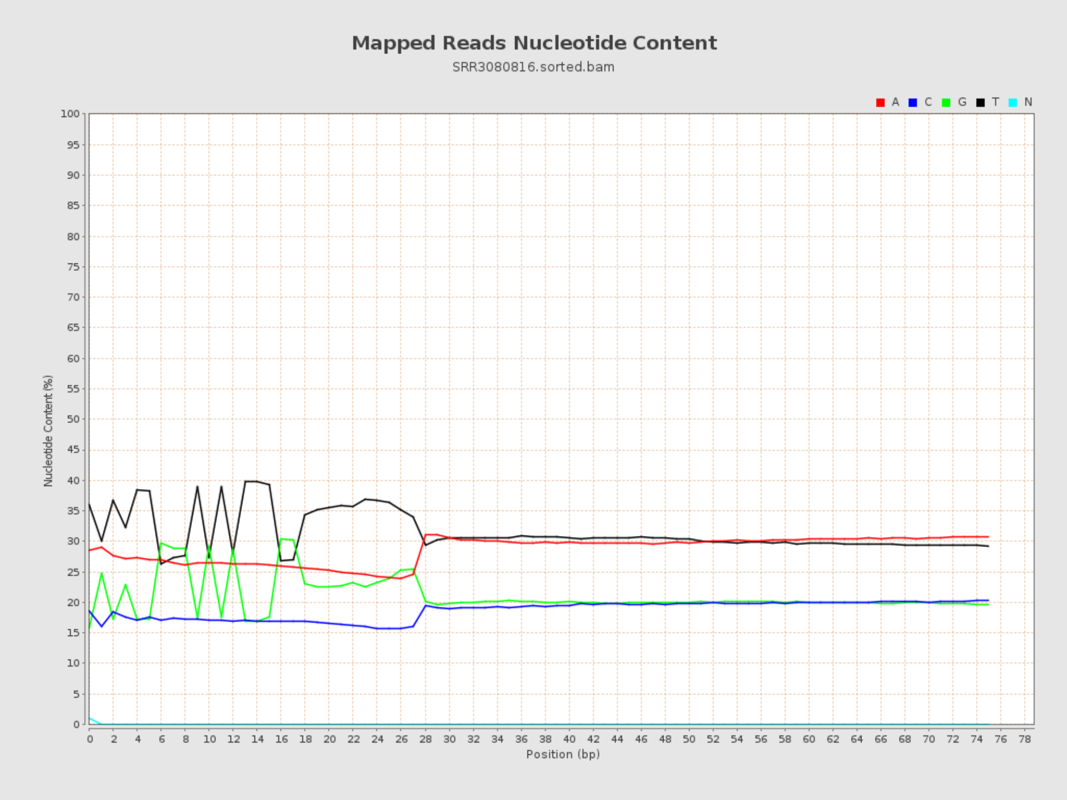
6. Results : Genome Fraction Coverage



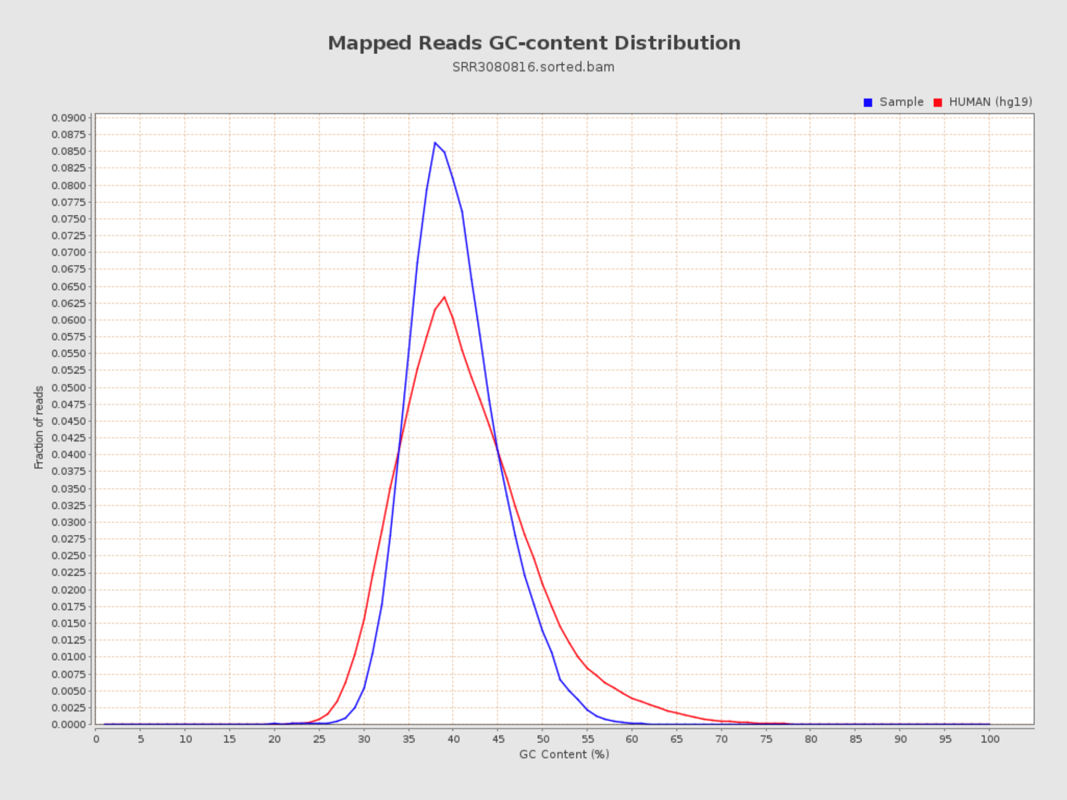
7. Results : Duplication Rate Histogram



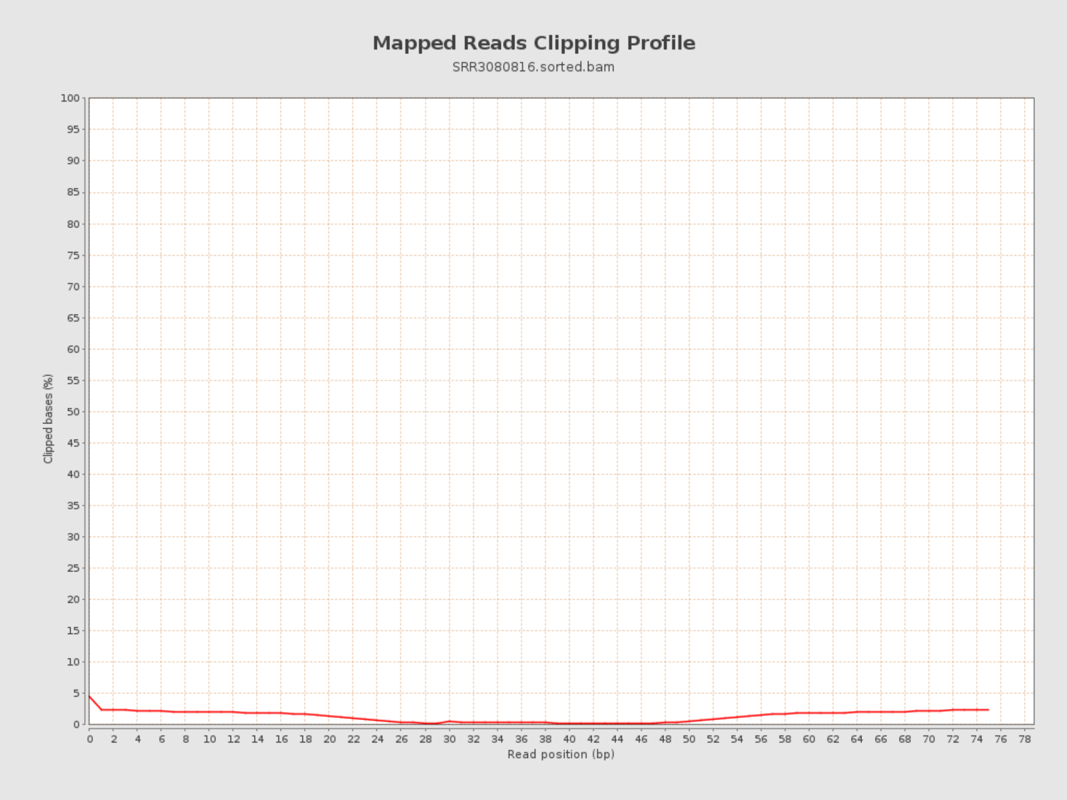
8. Results : Mapped Reads Nucleotide Content



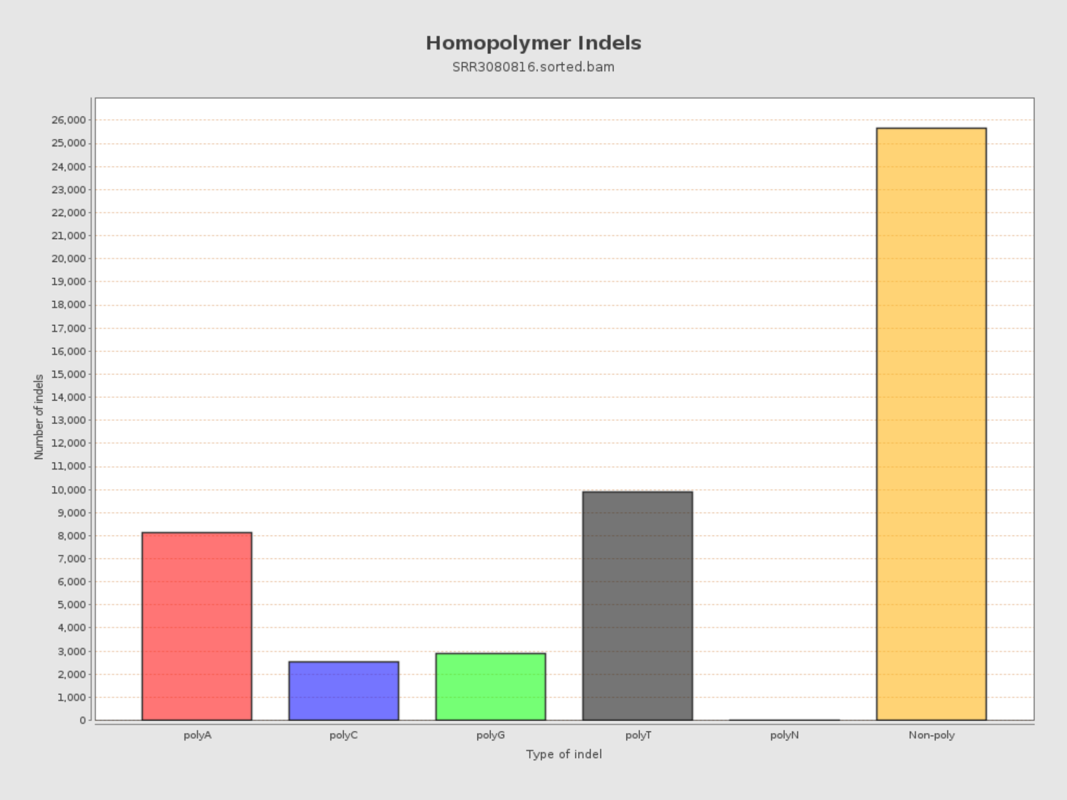
9. Results : Mapped Reads GC-content Distribution



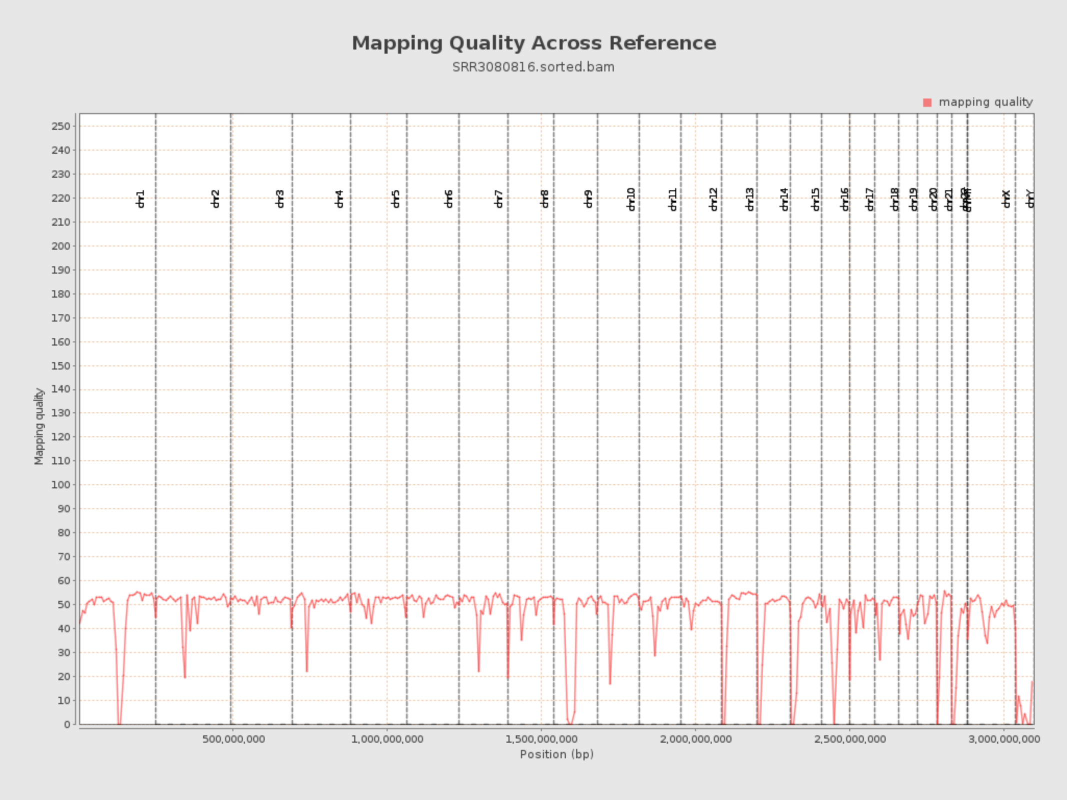
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram