Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:31:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708583.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_SRR1708583 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708583.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:31:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708583.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,106,023
Mapped reads	5,011,347 / 98.15%
Unmapped reads	94,676 / 1.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	134 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	48,943 / 0.96%
Duplication rate	0.98%
Clipped reads	67,228 / 1.32%

2.2. ACGT Content

Number/percentage of A's	77,334,355 / 30.94%
Number/percentage of C's	47,530,742 / 19.02%
Number/percentage of T's	76,895,878 / 30.77%
Number/percentage of G's	48,162,676 / 19.27%
Number/percentage of N's	8,905 / 0%
GC Percentage	38.29%

2.3. Coverage

Mean	0.0807

Standard Deviation	0.296

2.4. Mapping Quality

Mean Mapping Quality	46.69

2.5. Mismatches and indels

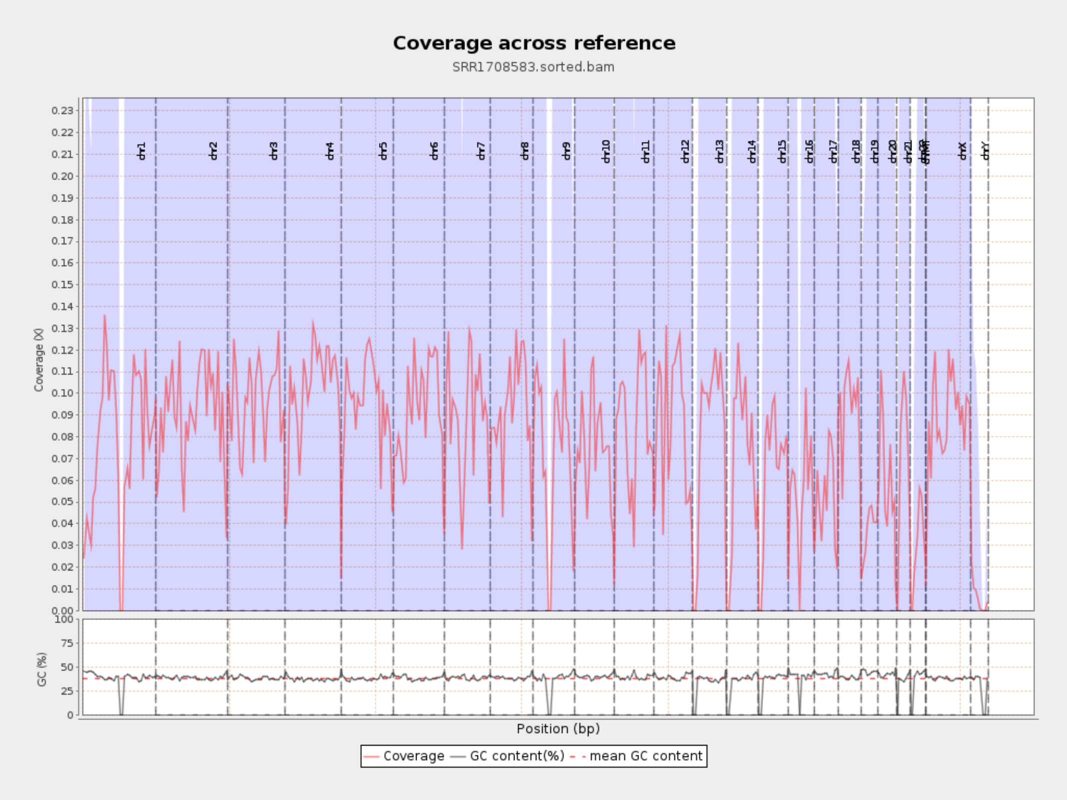
General error rate	0.15%
Mismatches	361,212
Insertions	15,671
Mapped reads with at least one insertion	0.31%
Deletions	12,568
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.66%

2.6. Chromosome stats

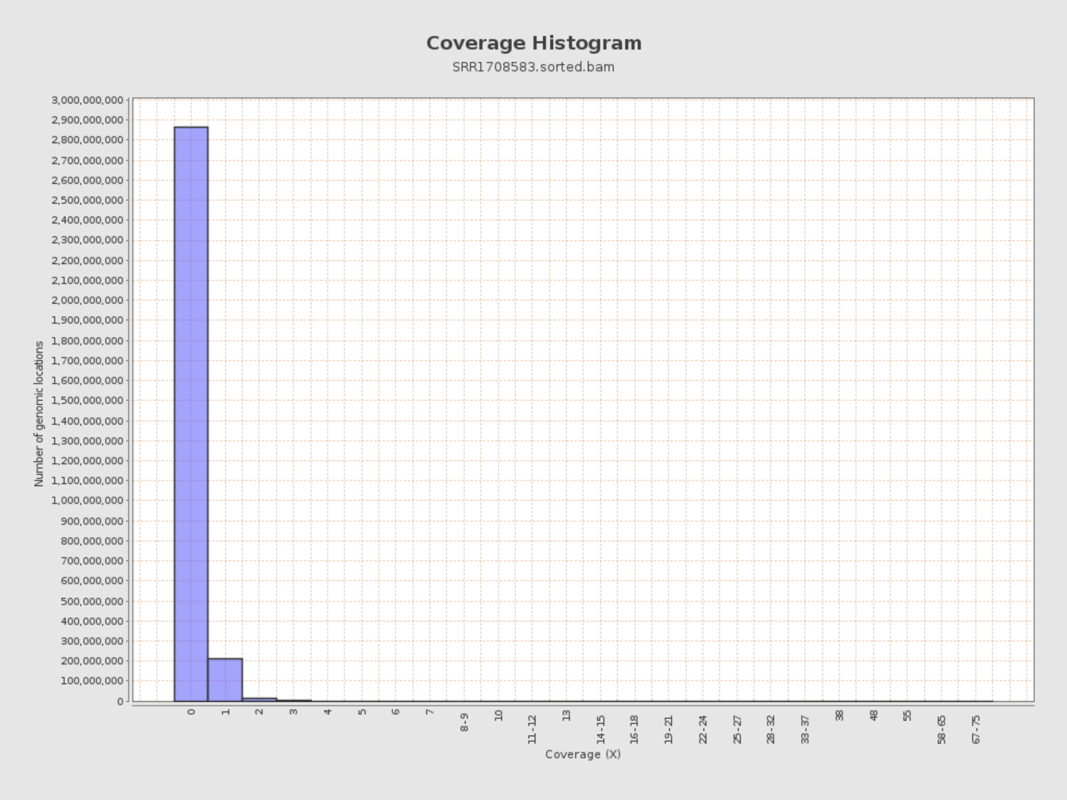
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19323665	0.0775	0.2919
chr2	243199373	22147386	0.0911	0.313
chr3	198022430	19206218	0.097	0.3227
chr4	191154276	19555880	0.1023	0.3313
chr5	180915260	17074171	0.0944	0.3181
chr6	171115067	16087824	0.094	0.3182
chr7	159138663	13930599	0.0875	0.3077

chr8	146364022	13547580	0.0926	0.3154
chr9	141213431	10468818	0.0741	0.2843
chr10	135534747	10236672	0.0755	0.285
chr11	135006516	11474762	0.085	0.3044
chr12	133851895	11560140	0.0864	0.3057
chr13	115169878	9563401	0.083	0.3
chr14	107349540	7608462	0.0709	0.2778
chr15	102531392	6565518	0.064	0.2641
chr16	90354753	4785433	0.053	0.239
chr17	81195210	4335656	0.0534	0.2416
chr18	78077248	7395445	0.0947	0.3184
chr19	59128983	2192897	0.0371	0.199
chr20	63025520	3908013	0.062	0.2591
chr21	48129895	3255498	0.0676	0.2741
chr22	51304566	1556958	0.0303	0.181
chrMT	16571	200	0.0121	0.1092
chrX	155270560	13825765	0.089	0.3105
chrY	59373566	346794	0.0058	0.0801

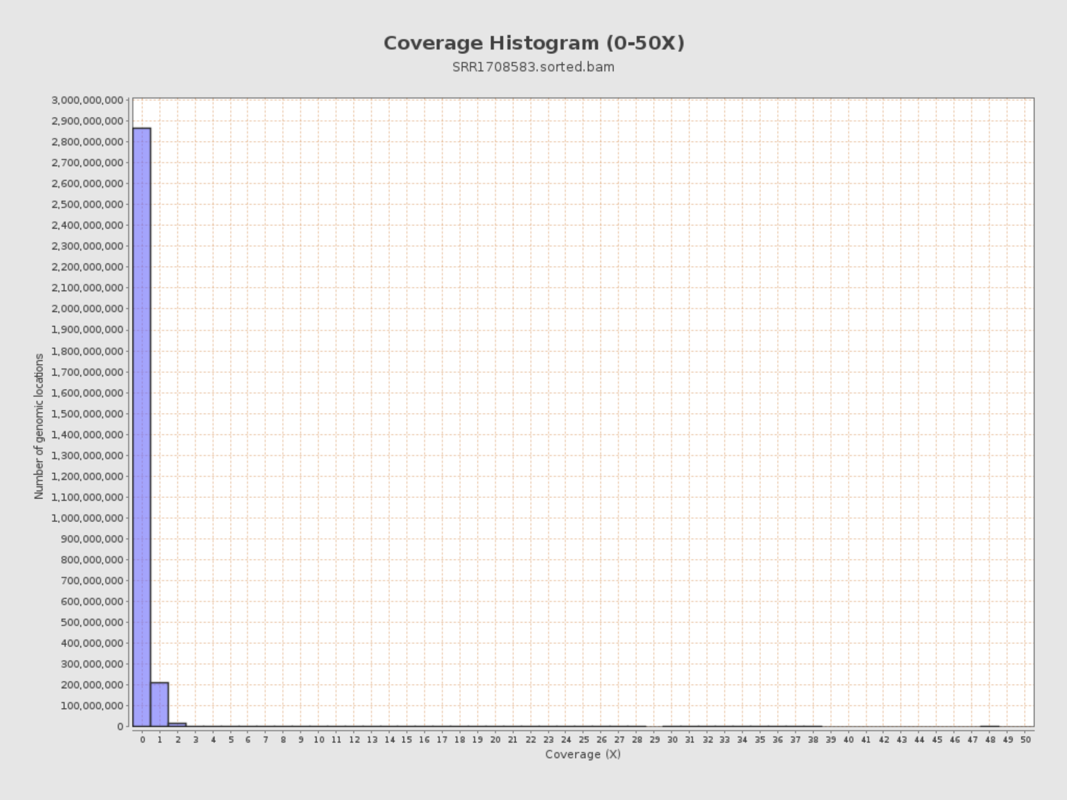
3. Results : Coverage across reference



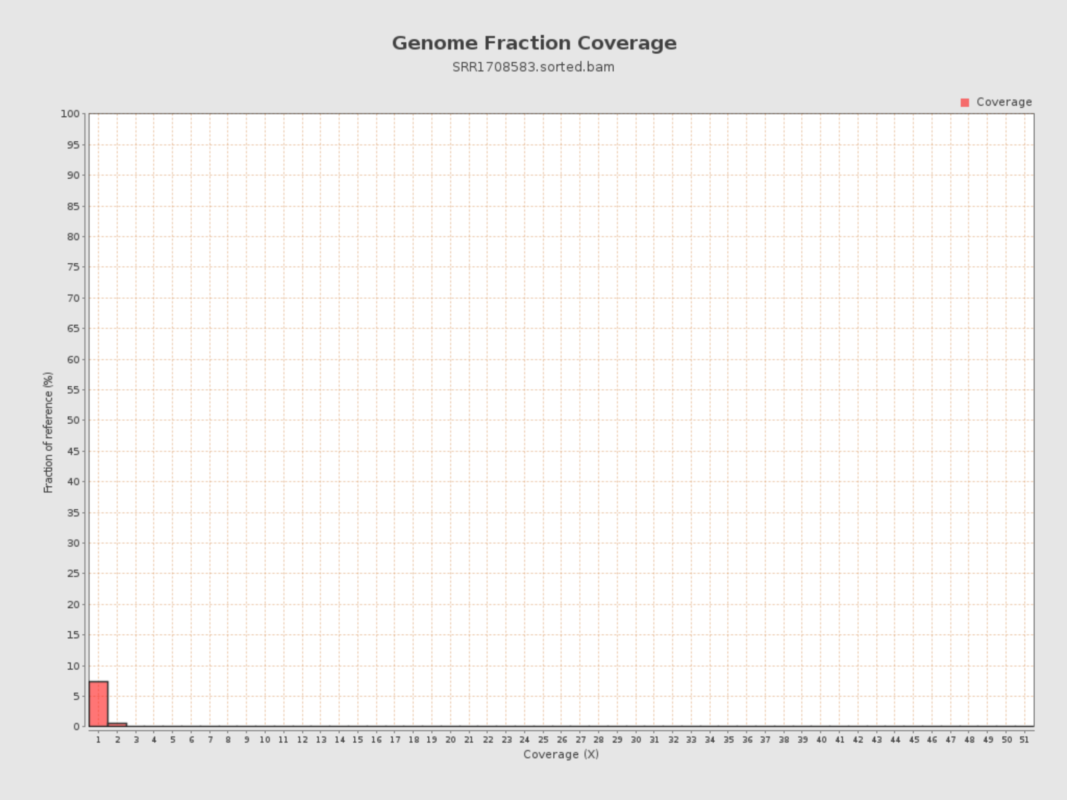
4. Results : Coverage Histogram



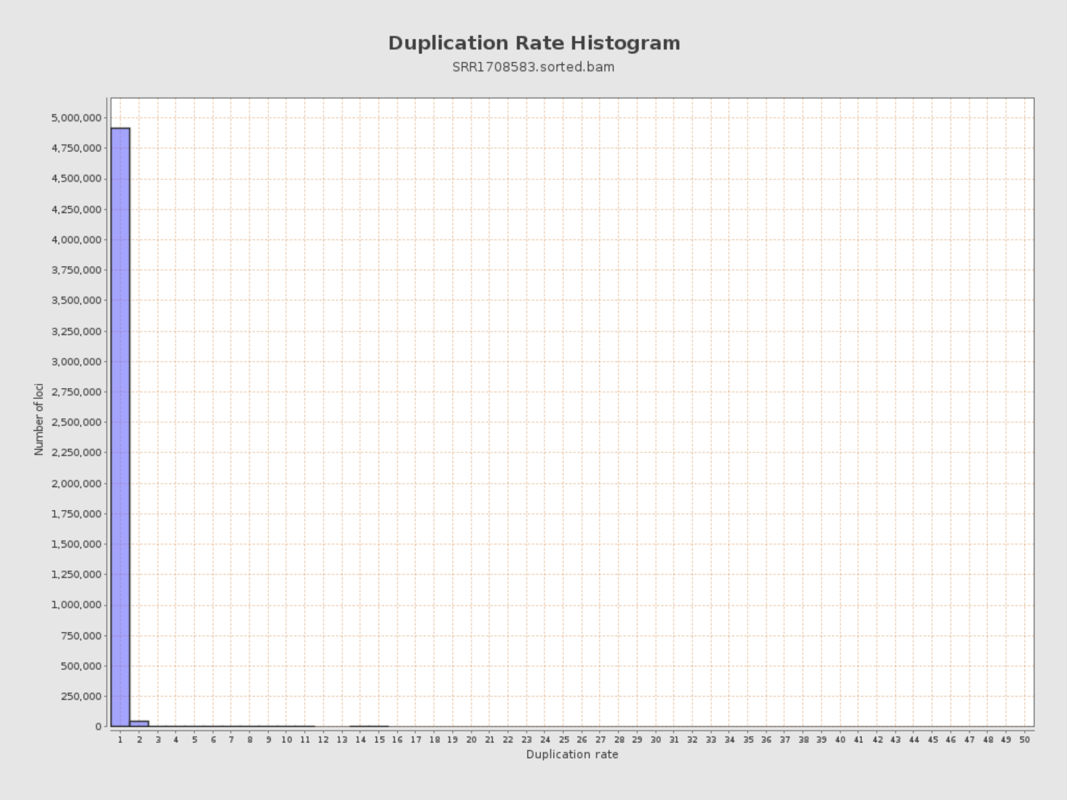
5. Results : Coverage Histogram (0-50X)



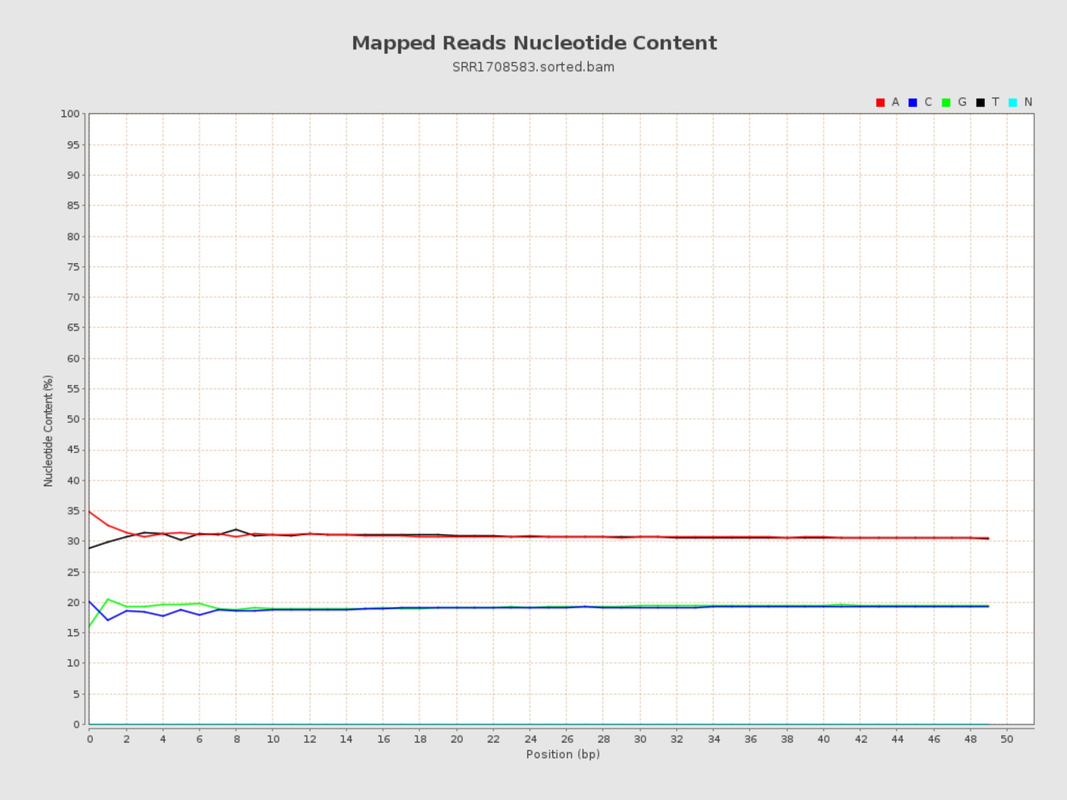
6. Results : Genome Fraction Coverage



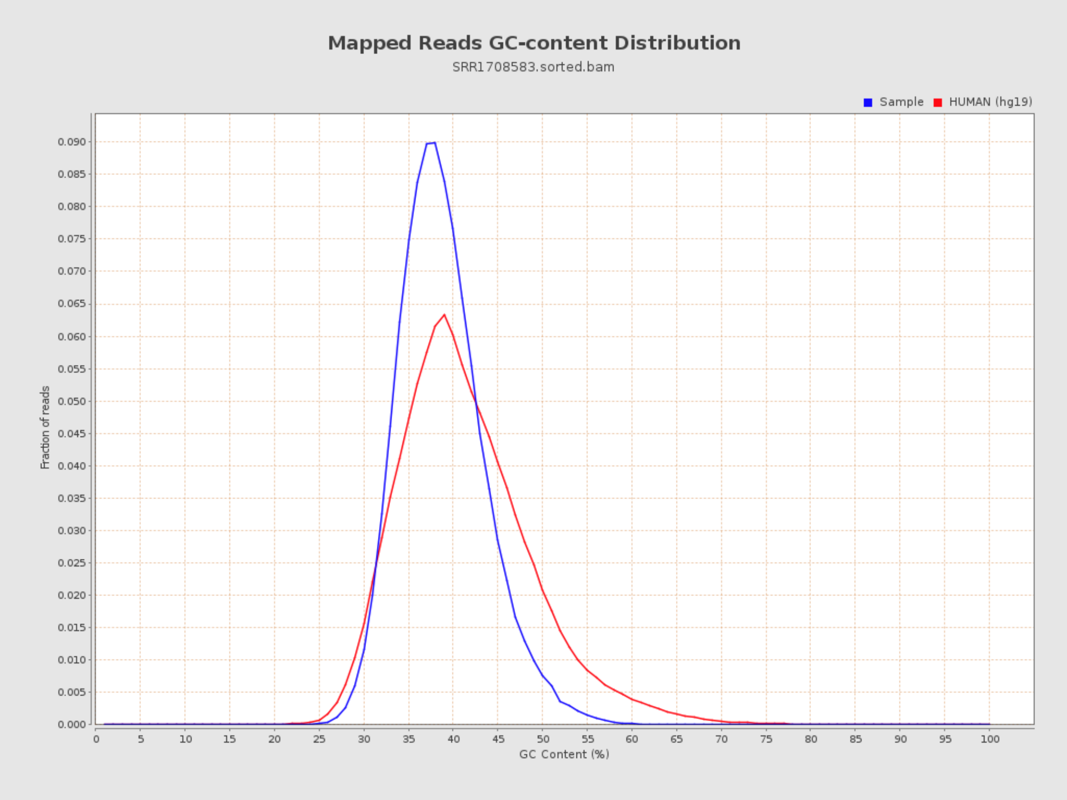
7. Results : Duplication Rate Histogram



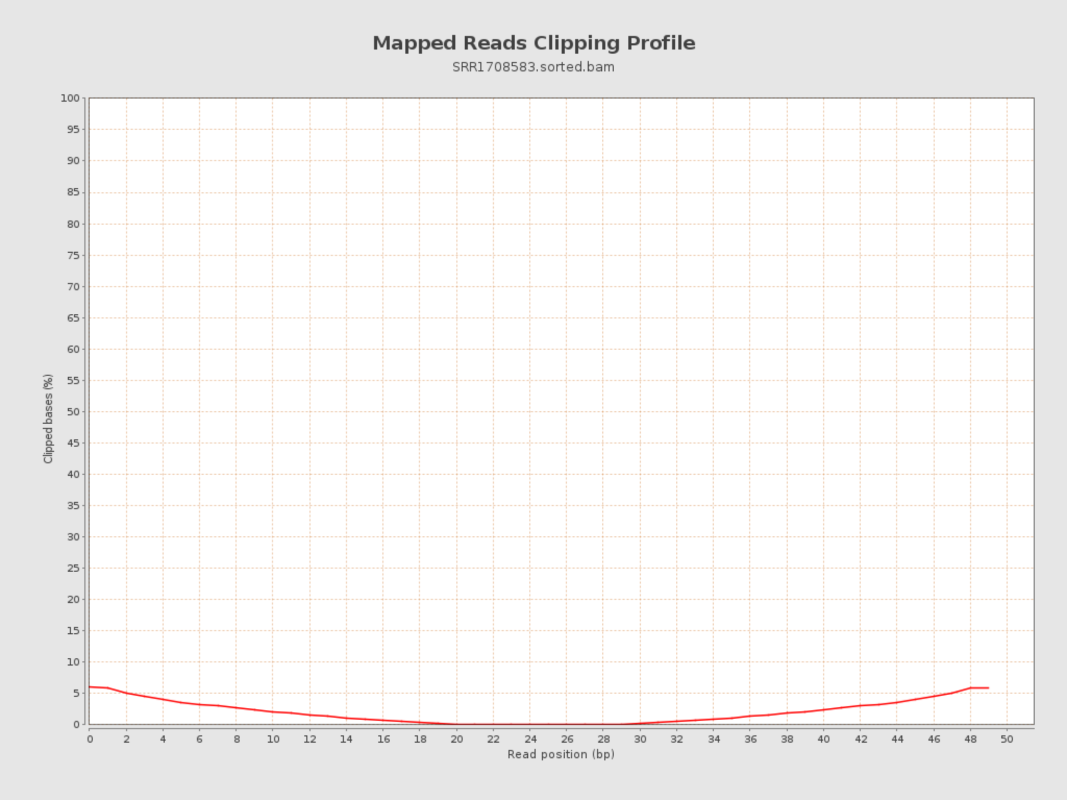
8. Results : Mapped Reads Nucleotide Content



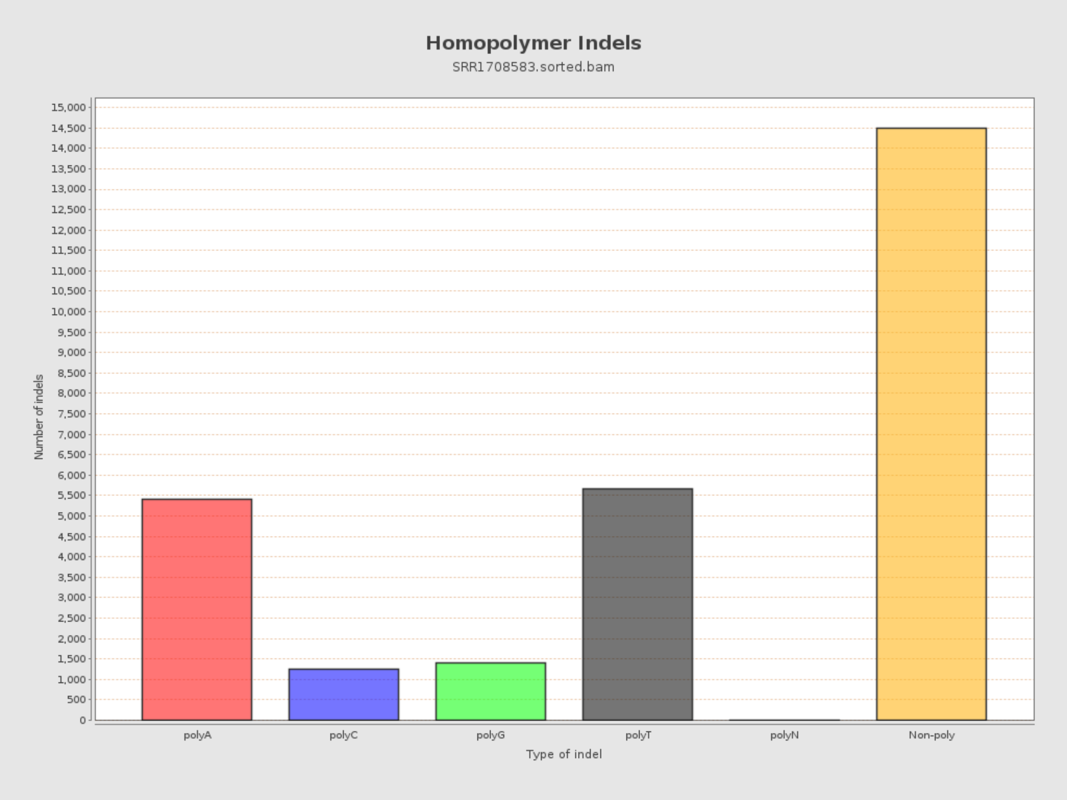
9. Results : Mapped Reads GC-content Distribution



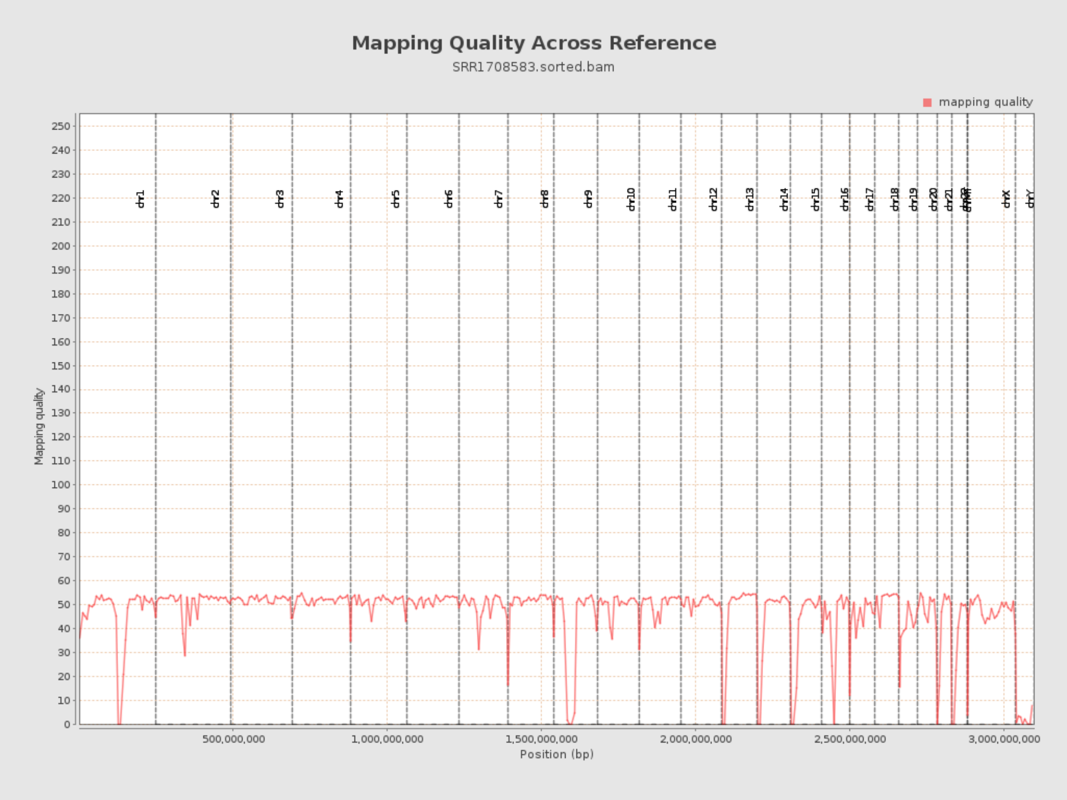
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram