Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 00:32:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089714.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_SRR089714 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089714.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 00:32:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089714.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,545,931
Mapped reads	20,769,502 / 88.21%
Unmapped reads	2,776,429 / 11.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	994 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,597,778 / 15.28%
Duplication rate	11.08%
Clipped reads	1,431,120 / 6.08%

2.2. ACGT Content

Number/percentage of A's	293,906,678 / 29.88%
Number/percentage of C's	199,663,841 / 20.3%
Number/percentage of T's	285,600,170 / 29.04%
Number/percentage of G's	204,312,107 / 20.77%
Number/percentage of N's	43,795 / 0%
GC Percentage	41.07%

2.3. Coverage

Mean	0.3178

Standard Deviation	2.3482

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

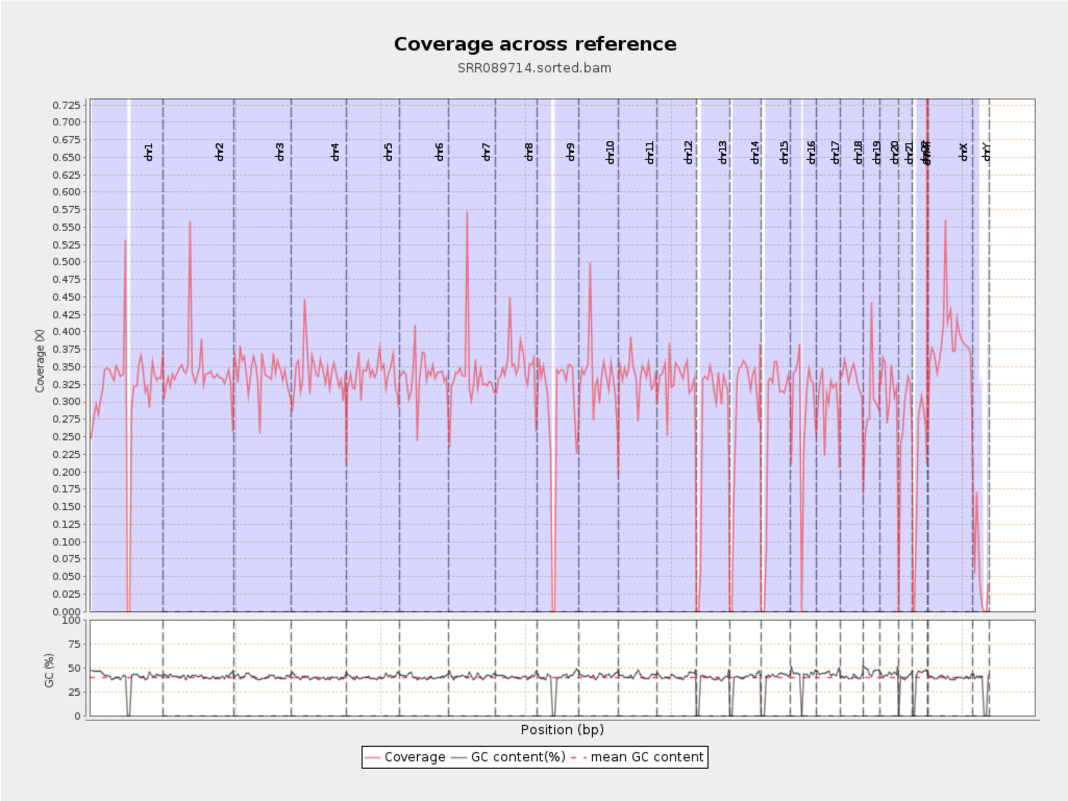
General error rate	0.42%
Mismatches	4,046,862
Insertions	39,025
Mapped reads with at least one insertion	0.19%
Deletions	133,320
Mapped reads with at least one deletion	0.64%
Homopolymer indels	48.19%

2.6. Chromosome stats

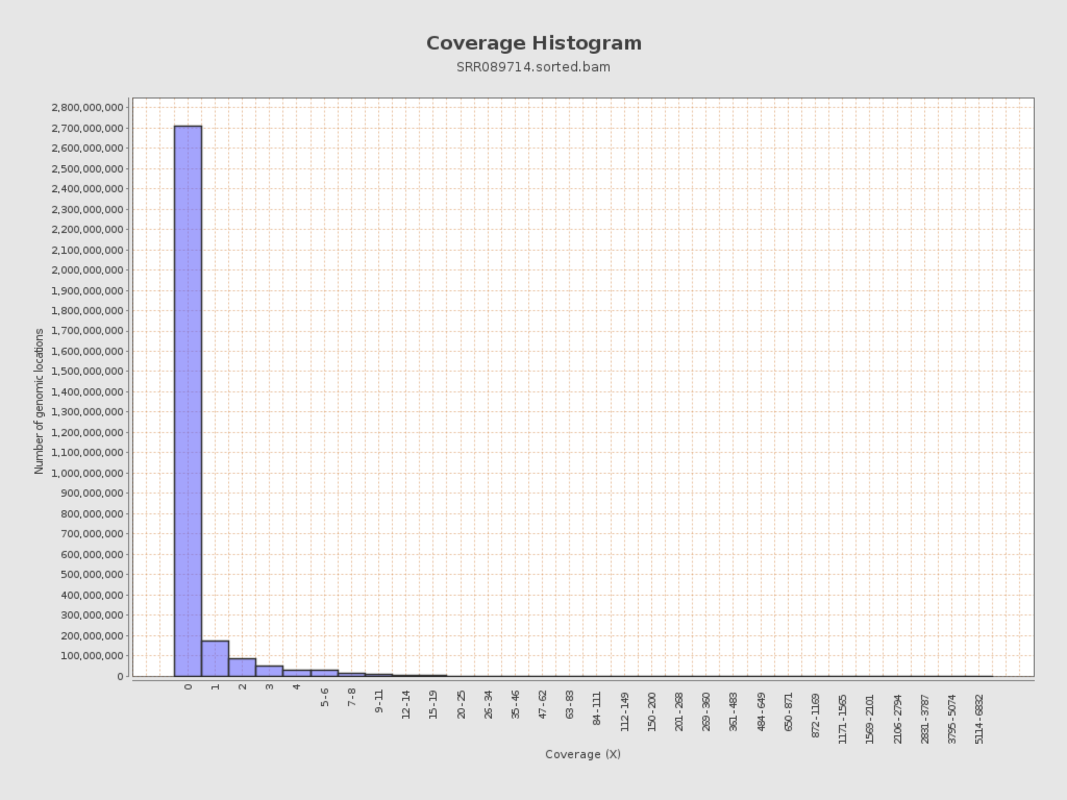
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	77684504	0.3117	4.8561
chr2	243199373	83584991	0.3437	2.3197
chr3	198022430	67607547	0.3414	1.2215
chr4	191154276	65122202	0.3407	1.3615
chr5	180915260	61190819	0.3382	1.2448
chr6	171115067	57680654	0.3371	1.5284
chr7	159138663	53972140	0.3392	3.5537

chr8	146364022	51063570	0.3489	2.3859
chr9	141213431	40803500	0.2889	2.0403
chr10	135534747	45736529	0.3375	1.9599
chr11	135006516	45444091	0.3366	2.2301
chr12	133851895	44482724	0.3323	1.3523
chr13	115169878	31237199	0.2712	1.0782
chr14	107349540	30129578	0.2807	1.3753
chr15	102531392	27229442	0.2656	1.0837
chr16	90354753	26228070	0.2903	1.2706
chr17	81195210	24284768	0.2991	1.5063
chr18	78077248	26316241	0.3371	4.0162
chr19	59128983	17750121	0.3002	3.7776
chr20	63025520	20006401	0.3174	1.3003
chr21	48129895	12531878	0.2604	1.3257
chr22	51304566	10129851	0.1974	0.905
chrMT	16571	474575	28.6389	17.3144
chrX	155270560	59929430	0.386	1.7139
chrY	59373566	3105086	0.0523	1.1602

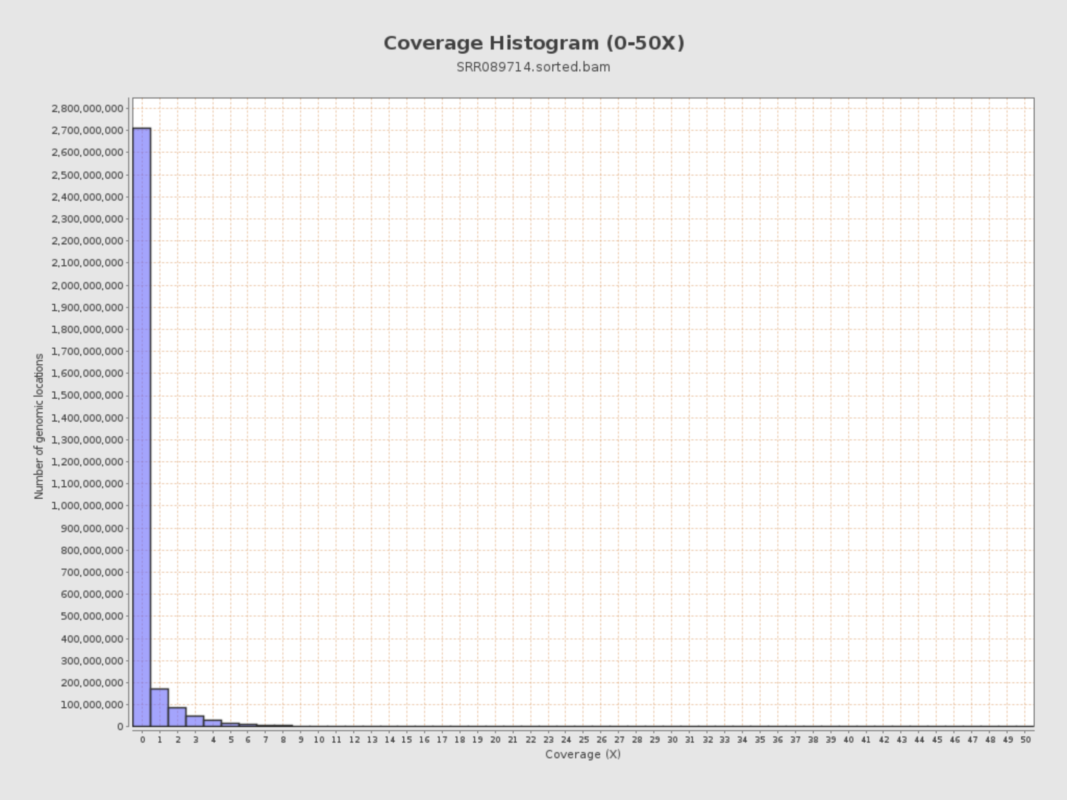
3. Results : Coverage across reference



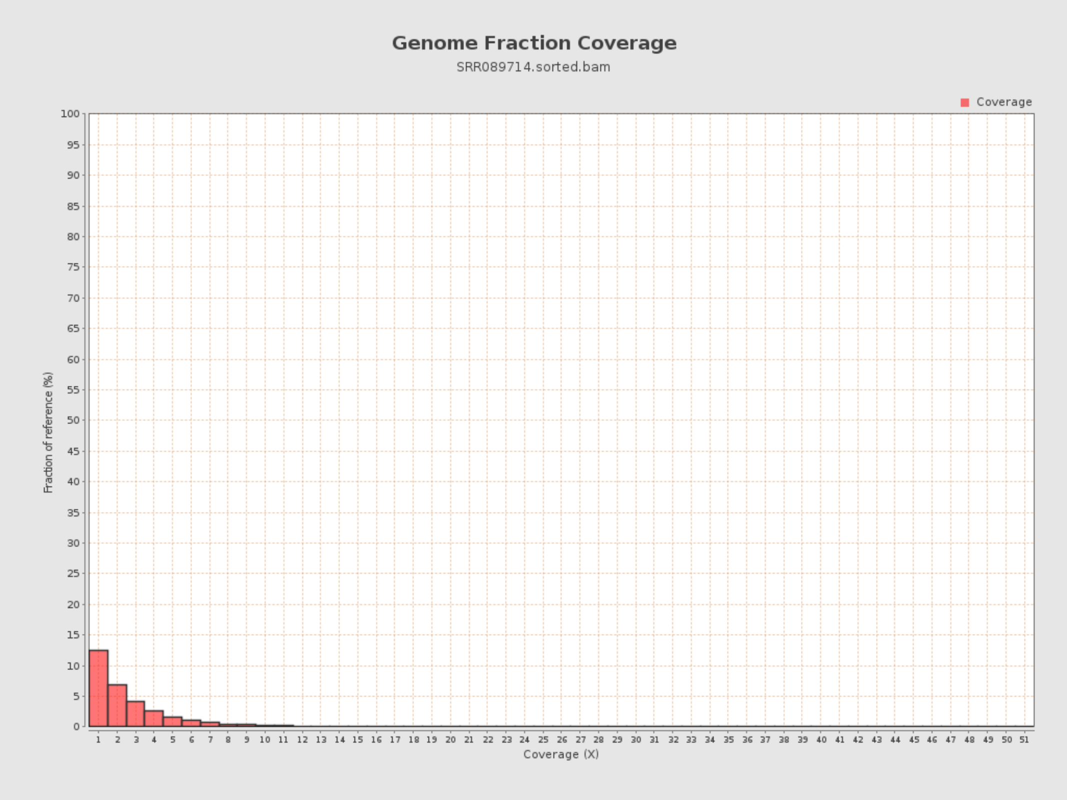
4. Results : Coverage Histogram



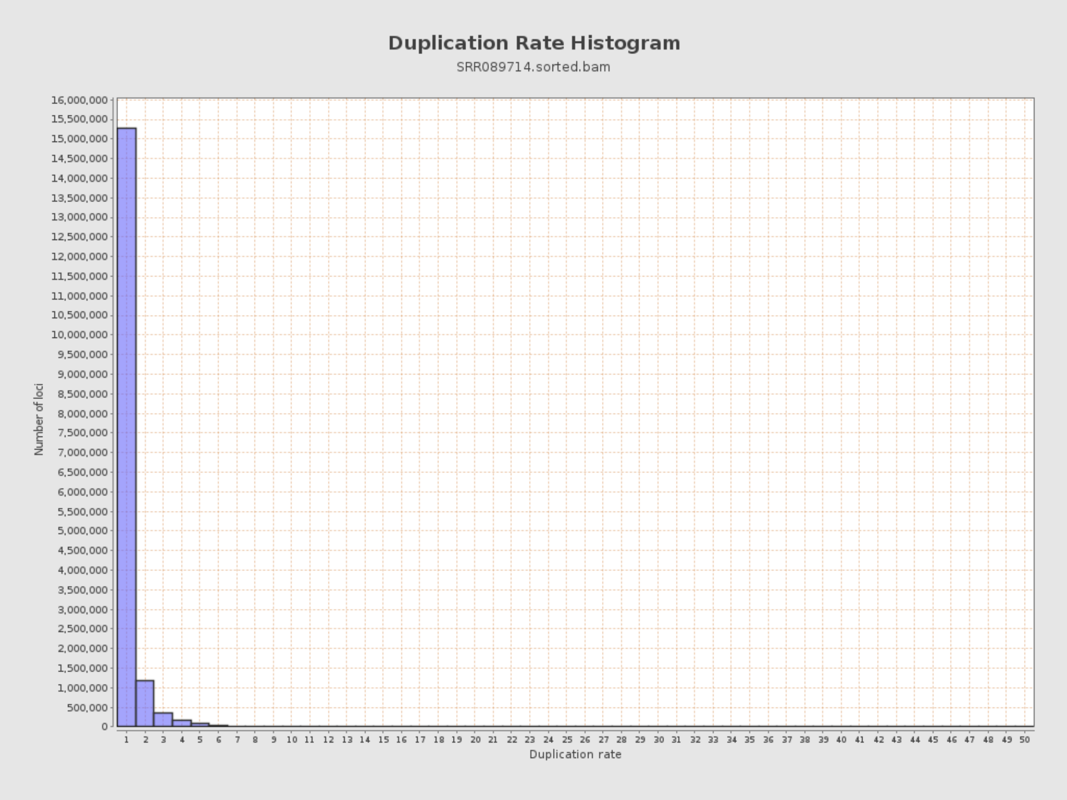
5. Results : Coverage Histogram (0-50X)



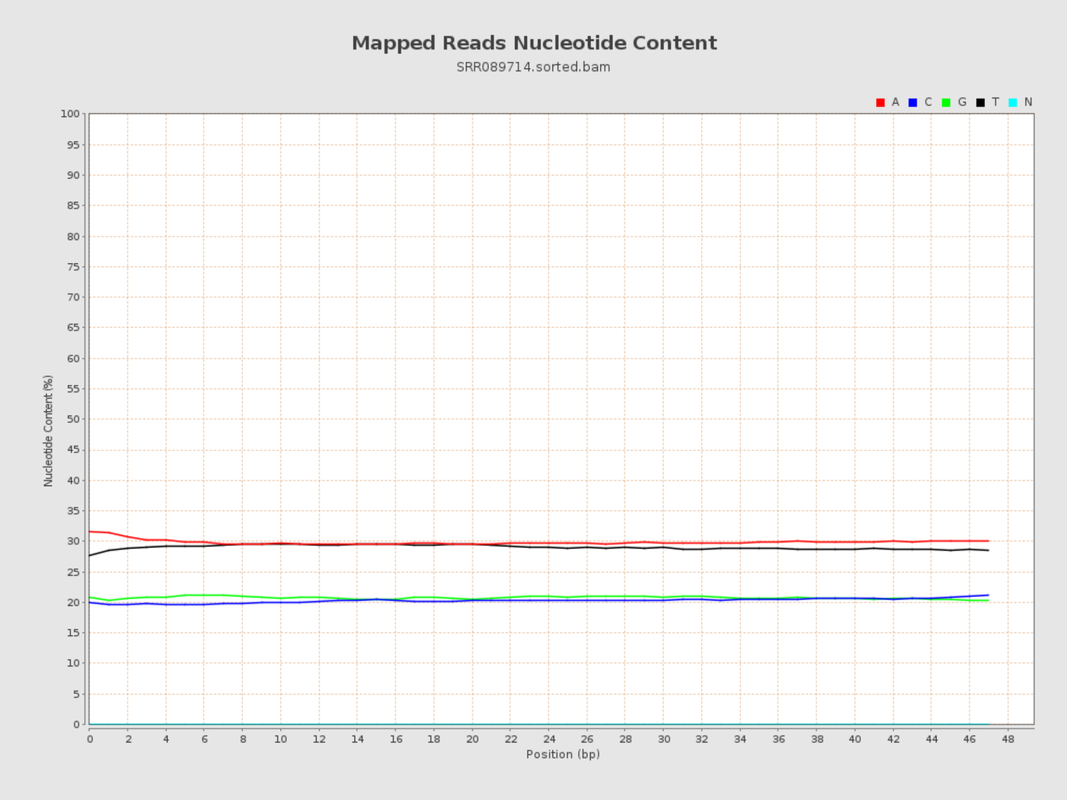
6. Results : Genome Fraction Coverage



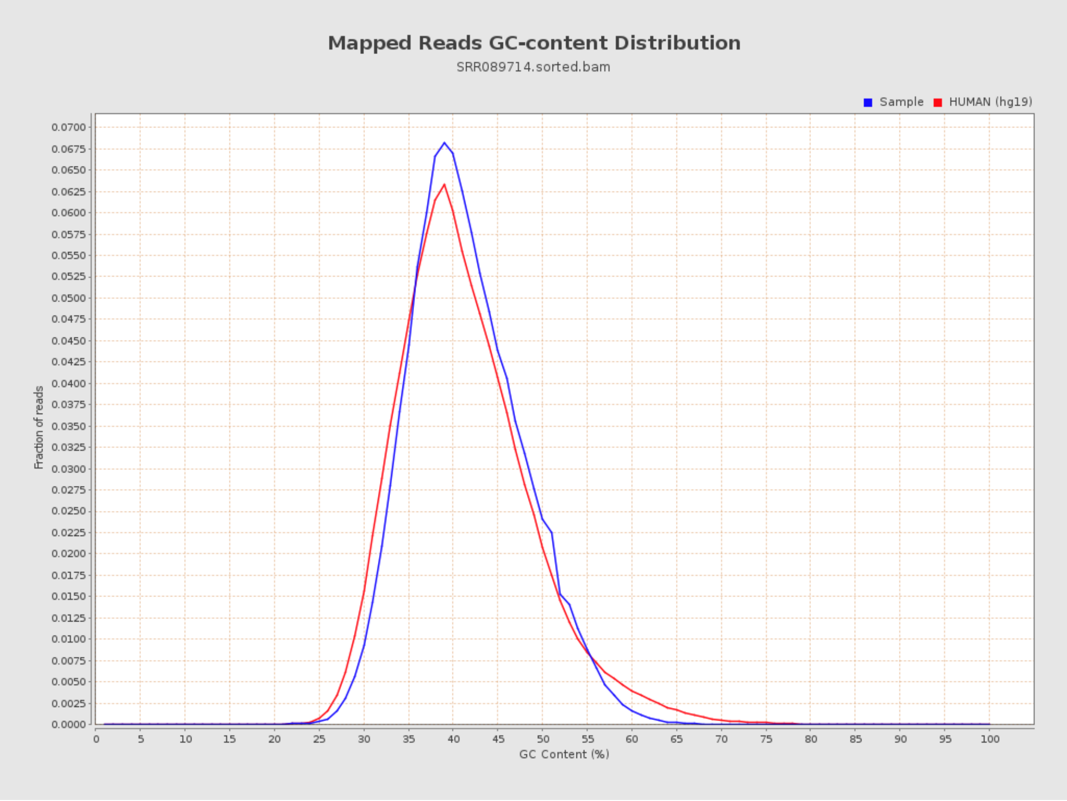
7. Results : Duplication Rate Histogram



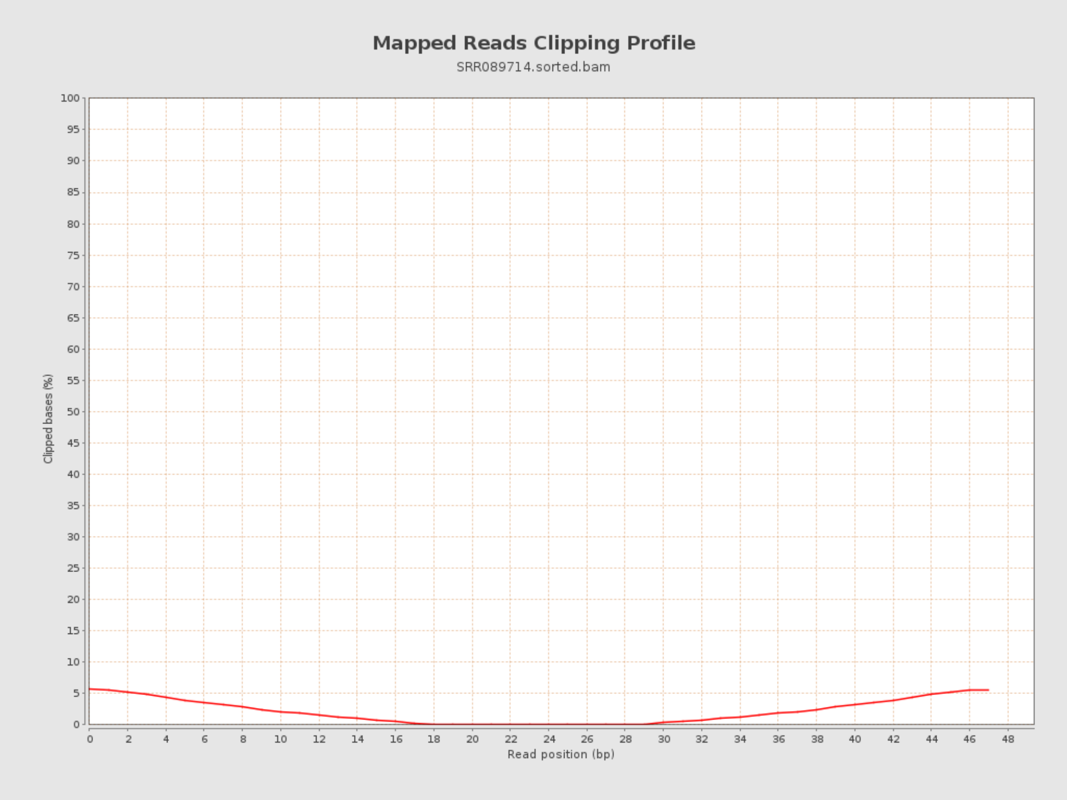
8. Results : Mapped Reads Nucleotide Content



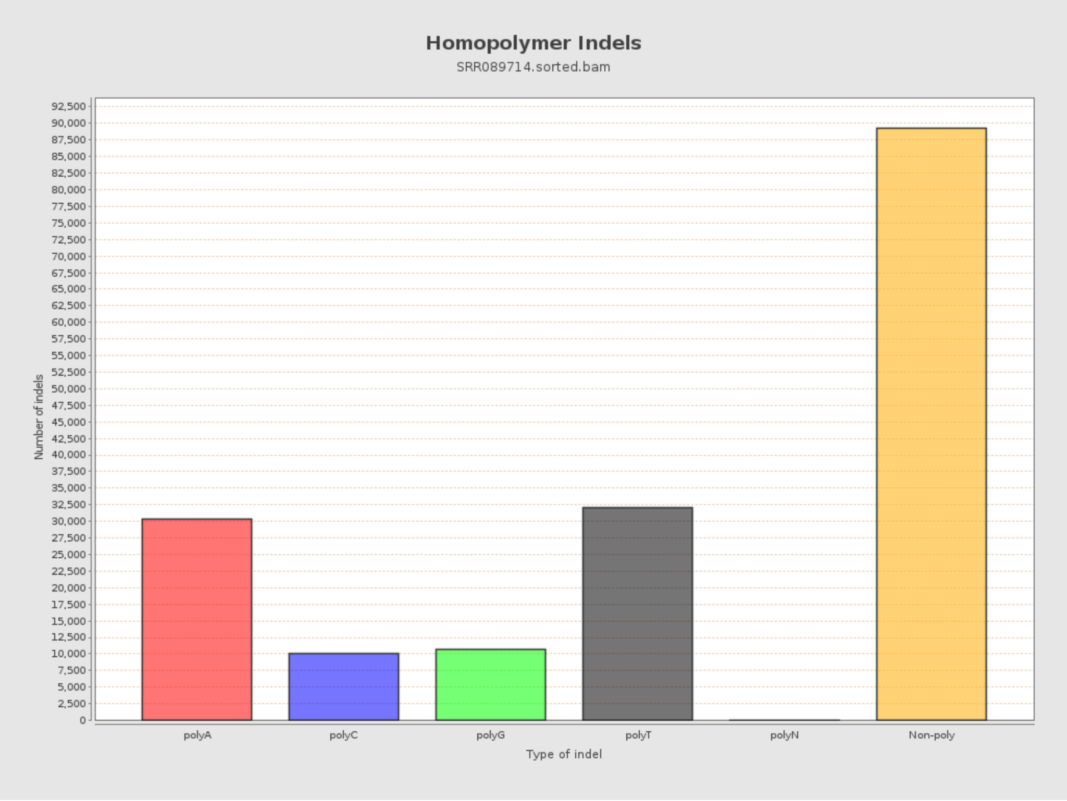
9. Results : Mapped Reads GC-content Distribution



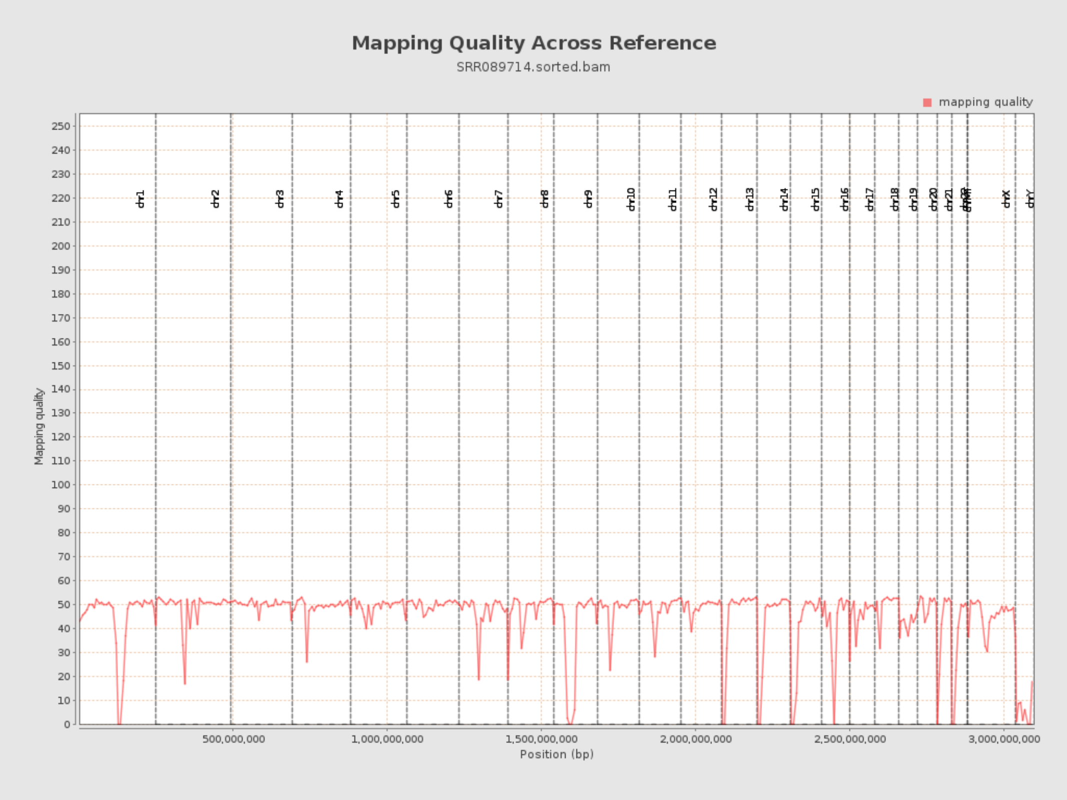
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram