Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:42:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080820.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_SRR3080820 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080820.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:42:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080820.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,024,619
Mapped reads	2,773,771 / 91.71%
Unmapped reads	250,848 / 8.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,754 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	168,912 / 5.58%
Duplication rate	4.96%
Clipped reads	1,011,082 / 33.43%

2.2. ACGT Content

Number/percentage of A's	54,375,416 / 28.57%
Number/percentage of C's	35,525,654 / 18.67%
Number/percentage of T's	60,101,775 / 31.58%
Number/percentage of G's	40,299,363 / 21.17%
Number/percentage of N's	26,966 / 0.01%
GC Percentage	39.84%

2.3. Coverage

Mean	0.0615

Standard Deviation	0.5504

2.4. Mapping Quality

Mean Mapping Quality	46.87

2.5. Mismatches and indels

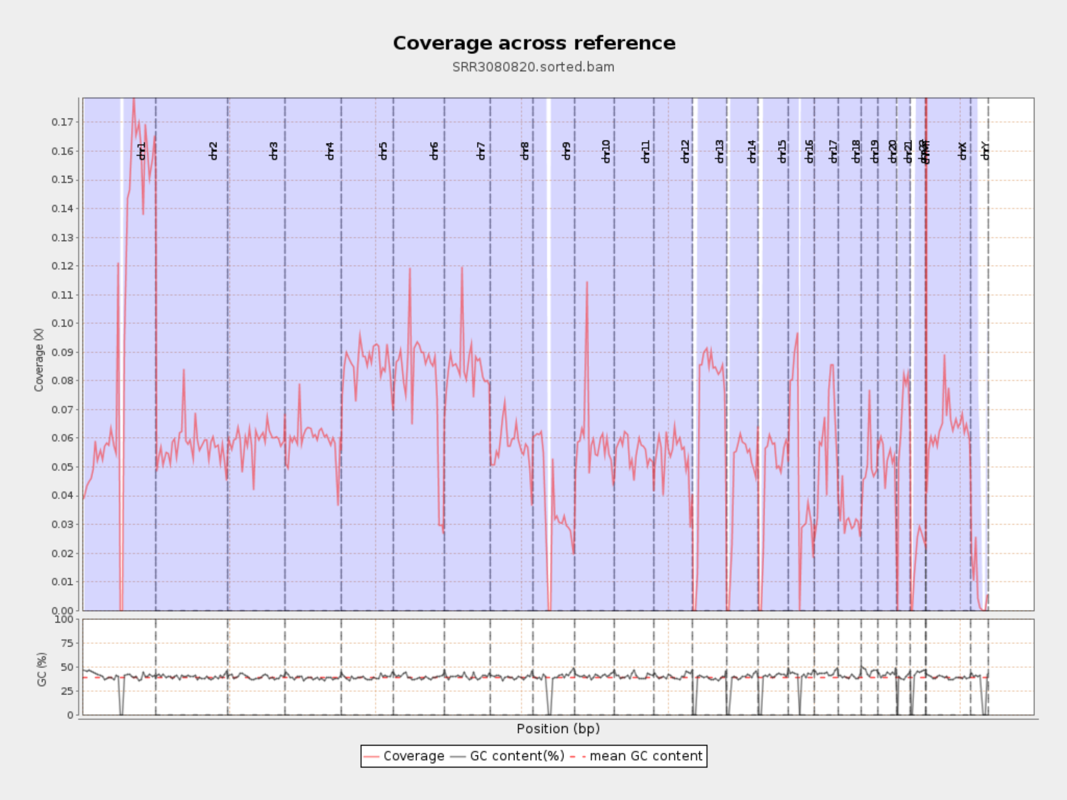
General error rate	0.85%
Mismatches	1,598,170
Insertions	14,362
Mapped reads with at least one insertion	0.51%
Deletions	44,937
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47.37%

2.6. Chromosome stats

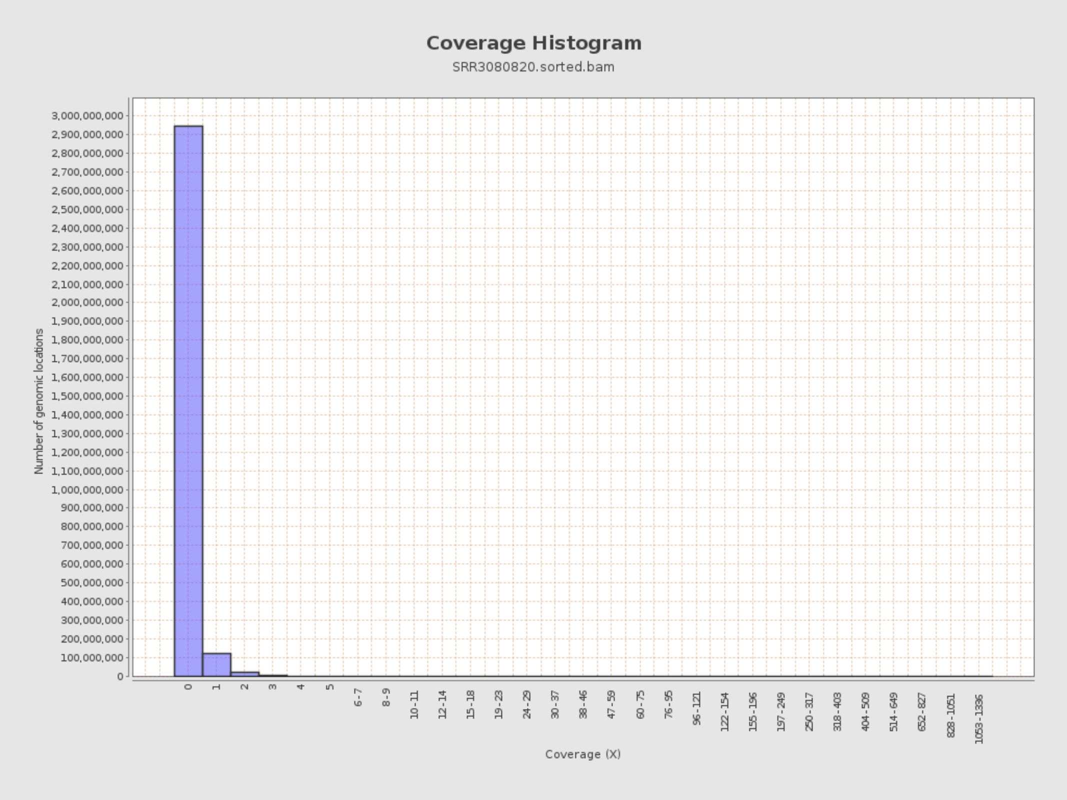
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24065560	0.0966	1.2533
chr2	243199373	13983214	0.0575	0.4399
chr3	198022430	11720025	0.0592	0.3078
chr4	191154276	11401034	0.0596	0.3154
chr5	180915260	15478754	0.0856	0.3543
chr6	171115067	13805496	0.0807	0.4953
chr7	159138663	13522812	0.085	0.7272

chr8	146364022	8341014	0.057	0.6866
chr9	141213431	5137242	0.0364	0.327
chr10	135534747	8083681	0.0596	0.5911
chr11	135006516	7461404	0.0553	0.3413
chr12	133851895	7195935	0.0538	0.2849
chr13	115169878	8130989	0.0706	0.3234
chr14	107349540	4929299	0.0459	0.2752
chr15	102531392	4627063	0.0451	0.2563
chr16	90354753	4312274	0.0477	0.3127
chr17	81195210	4828811	0.0595	0.3162
chr18	78077248	2501956	0.032	0.6529
chr19	59128983	3032460	0.0513	0.8663
chr20	63025520	3337788	0.053	0.2875
chr21	48129895	3071935	0.0638	0.3288
chr22	51304566	965724	0.0188	0.1613
chrMT	16571	106482	6.4258	4.5704
chrX	155270560	9901922	0.0638	0.3329
chrY	59373566	465351	0.0078	0.1901

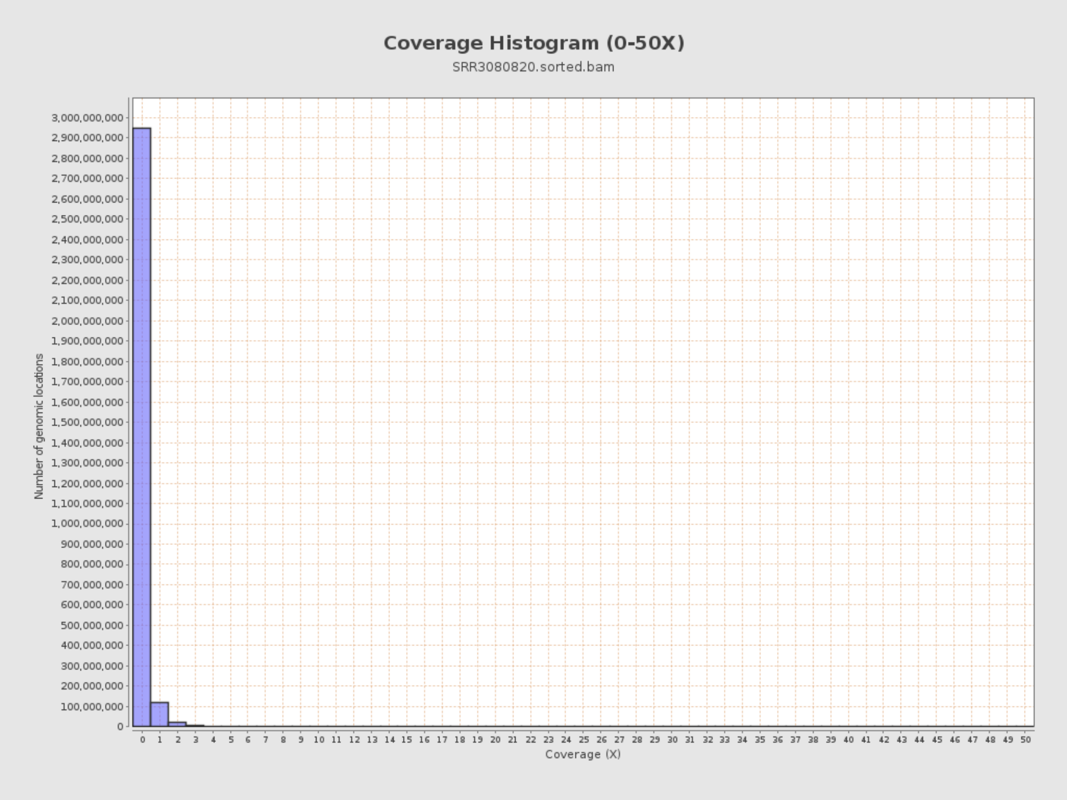
3. Results : Coverage across reference



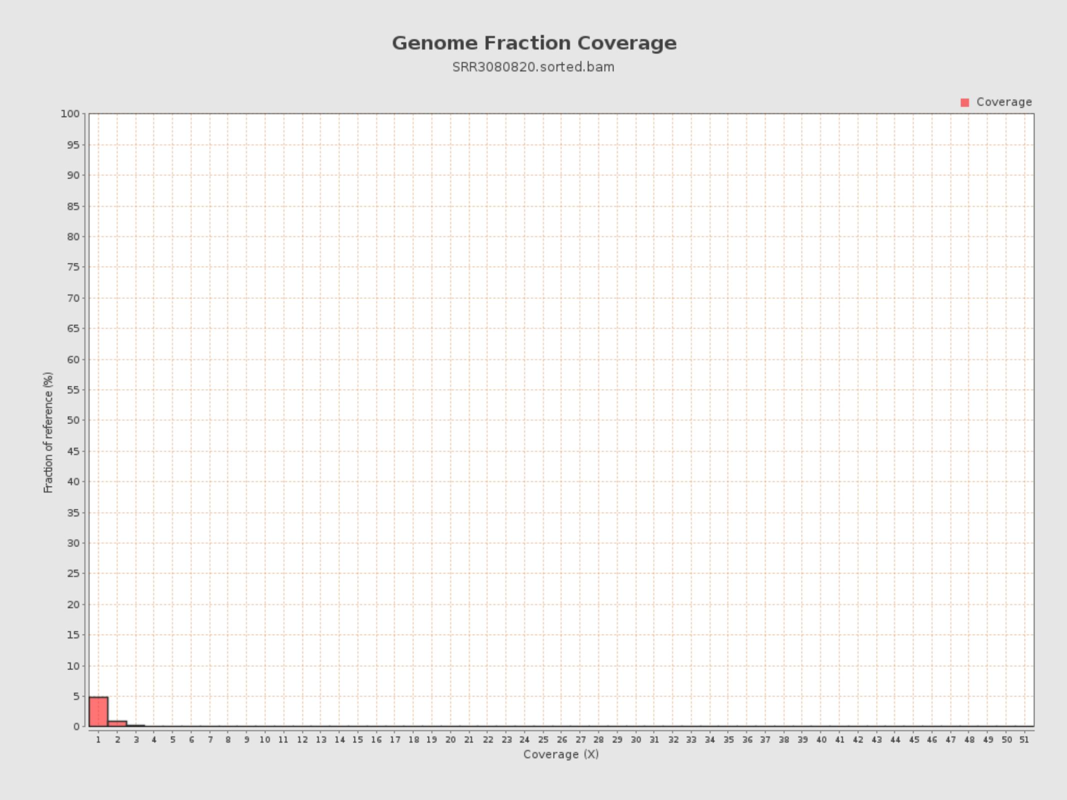
4. Results : Coverage Histogram



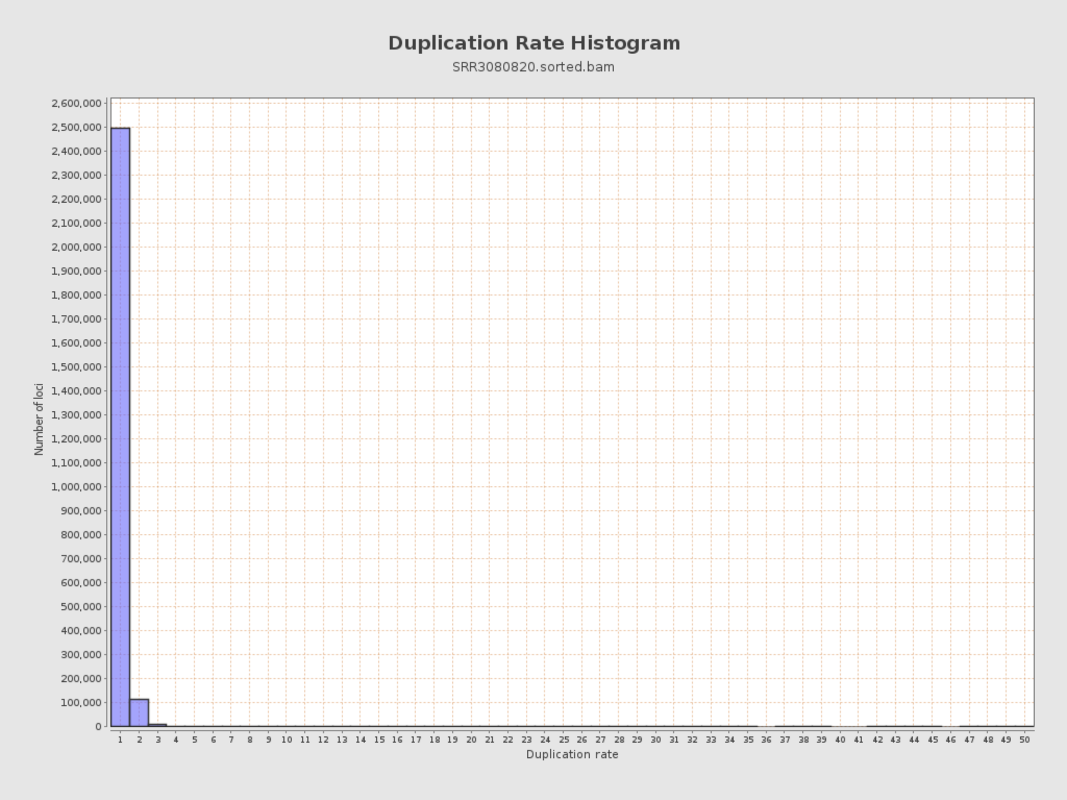
5. Results : Coverage Histogram (0-50X)



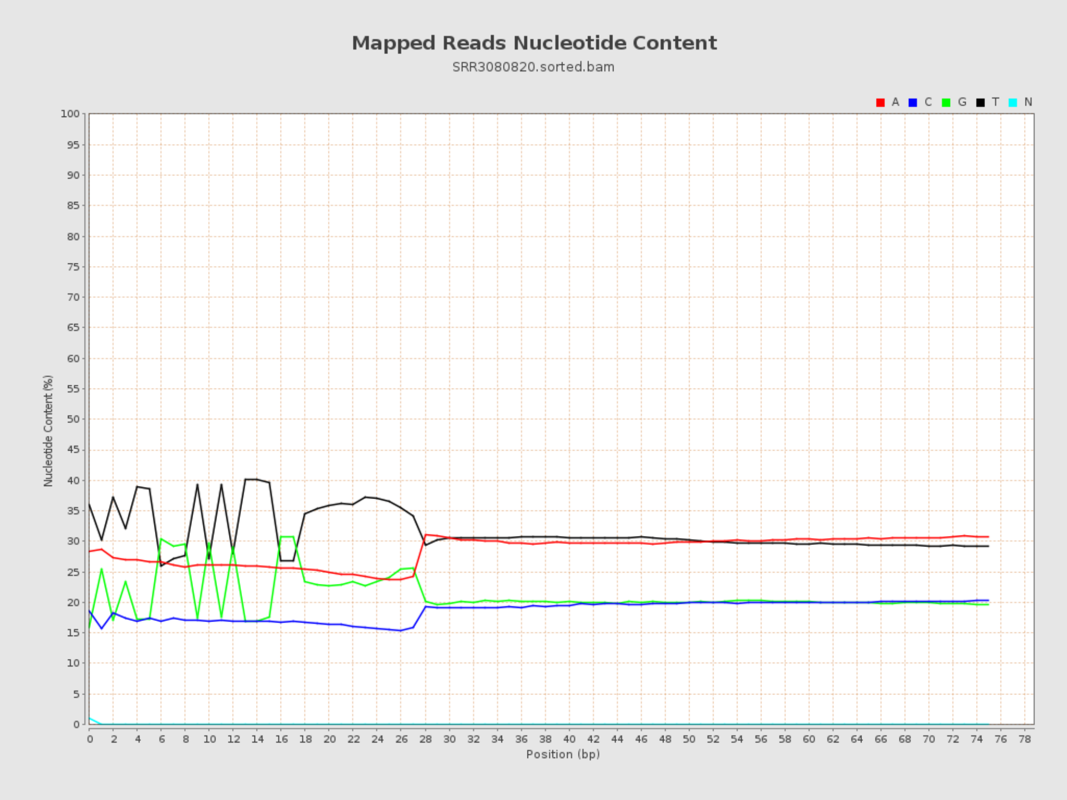
6. Results : Genome Fraction Coverage



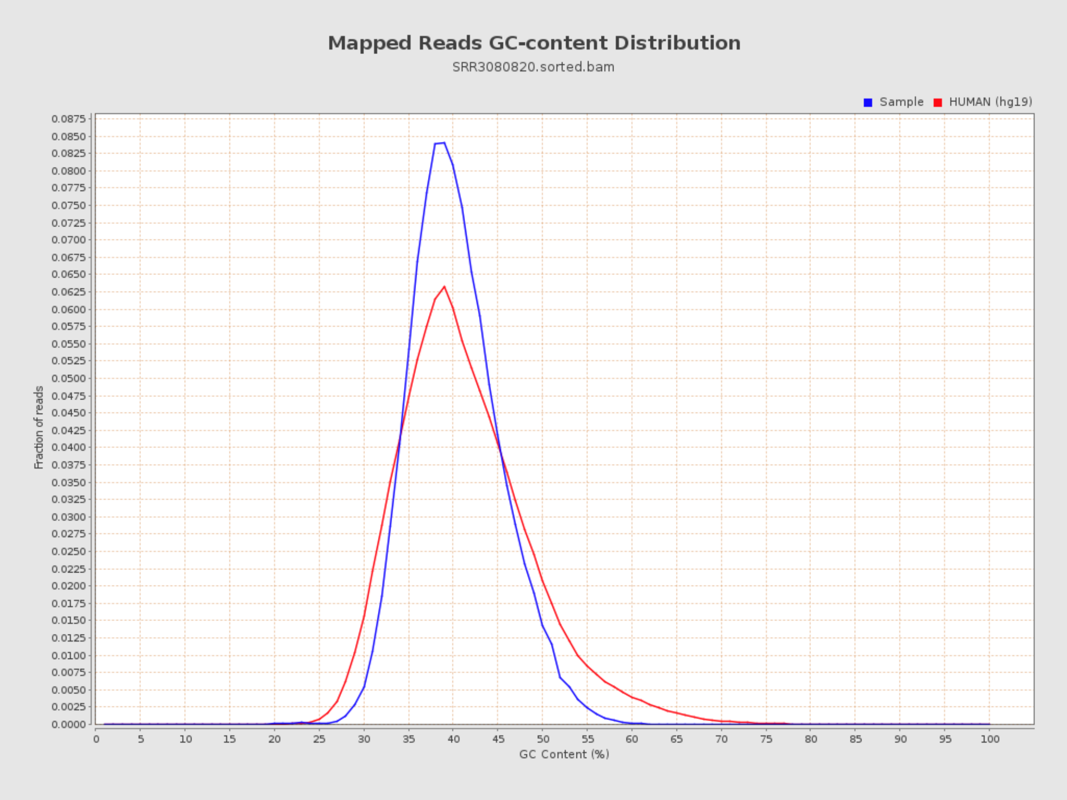
7. Results : Duplication Rate Histogram



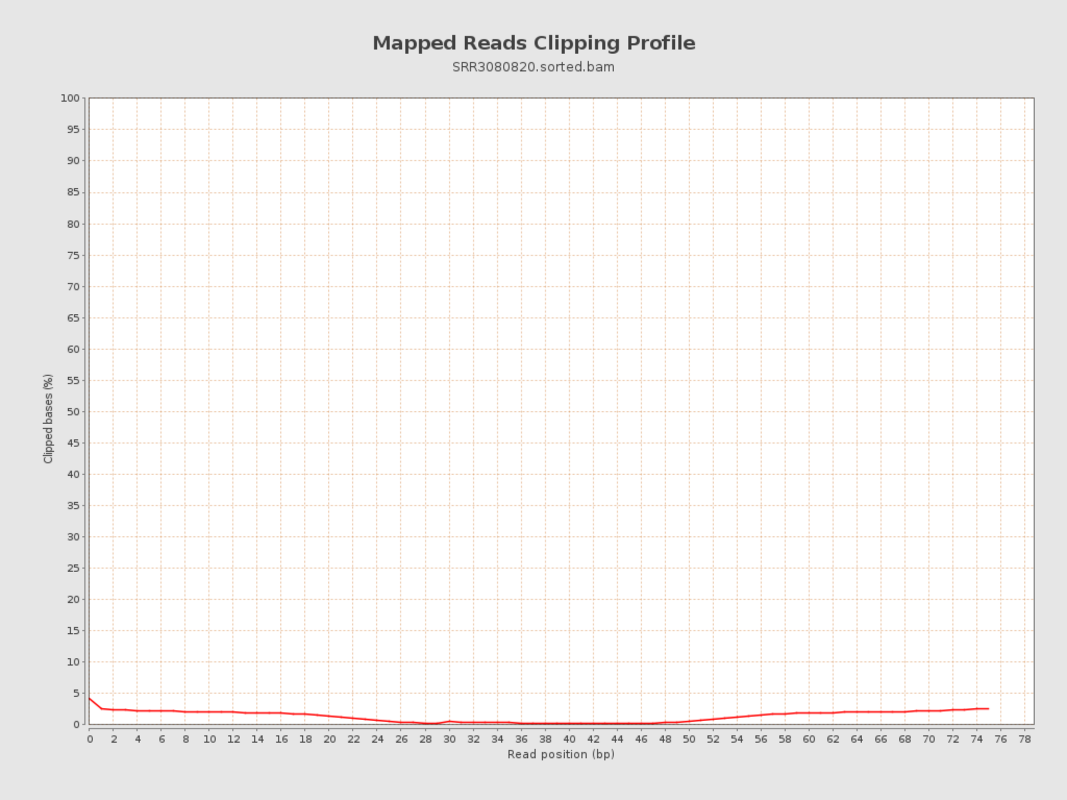
8. Results : Mapped Reads Nucleotide Content



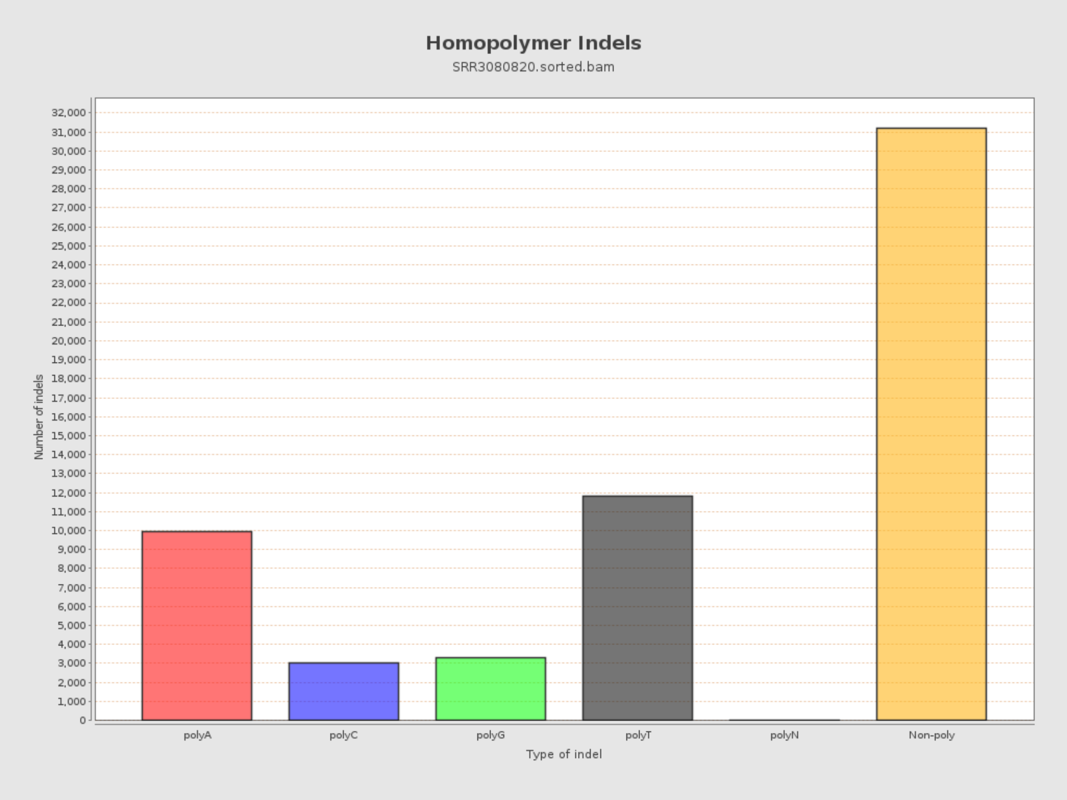
9. Results : Mapped Reads GC-content Distribution



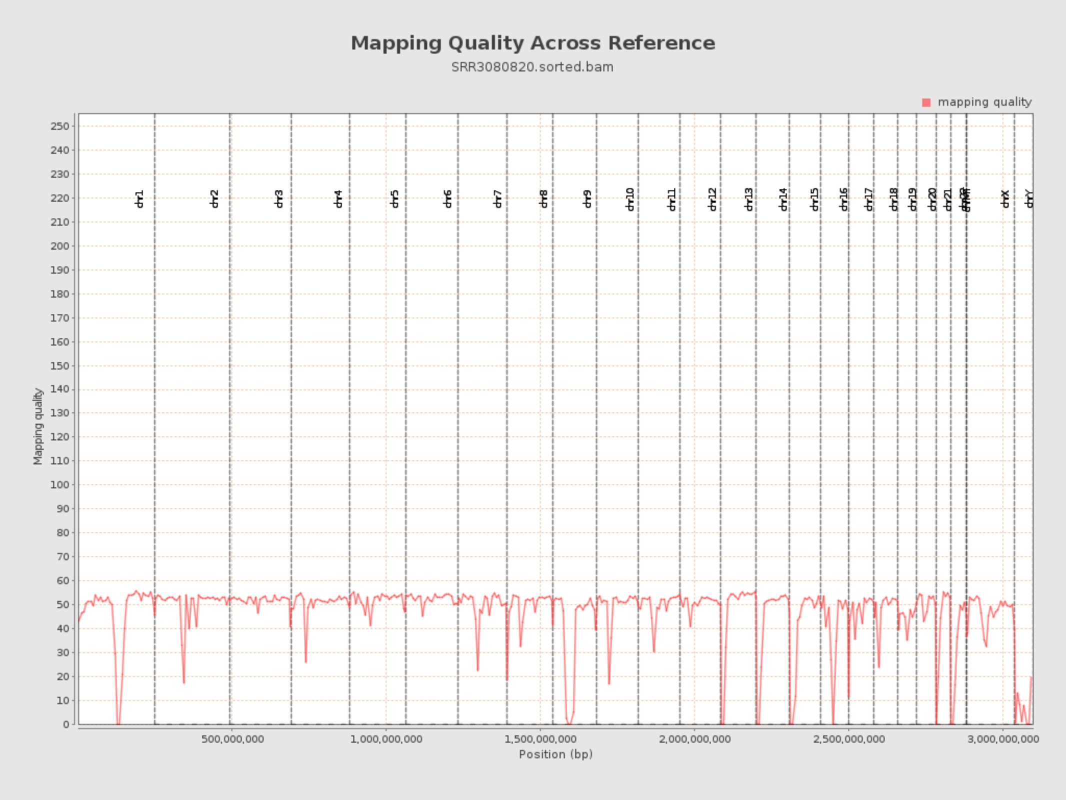
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram