Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:13:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548935.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_SRR1548935 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548935.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:13:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,778,149
Mapped reads	8,517,340 / 87.11%
Unmapped reads	1,260,809 / 12.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	344,205 / 3.52%
Duplication rate	2.58%
Clipped reads	691,604 / 7.07%

2.2. ACGT Content

Number/percentage of A's	98,377,880 / 29.2%
Number/percentage of C's	70,186,385 / 20.84%
Number/percentage of T's	98,689,142 / 29.3%
Number/percentage of G's	69,599,433 / 20.66%
Number/percentage of N's	2,996 / 0%
GC Percentage	41.5%

2.3. Coverage

Mean	0.1088
Standard Deviation	1.4926

2.4. Mapping Quality

Mean Mapping Quality	39.29

2.5. Mismatches and indels

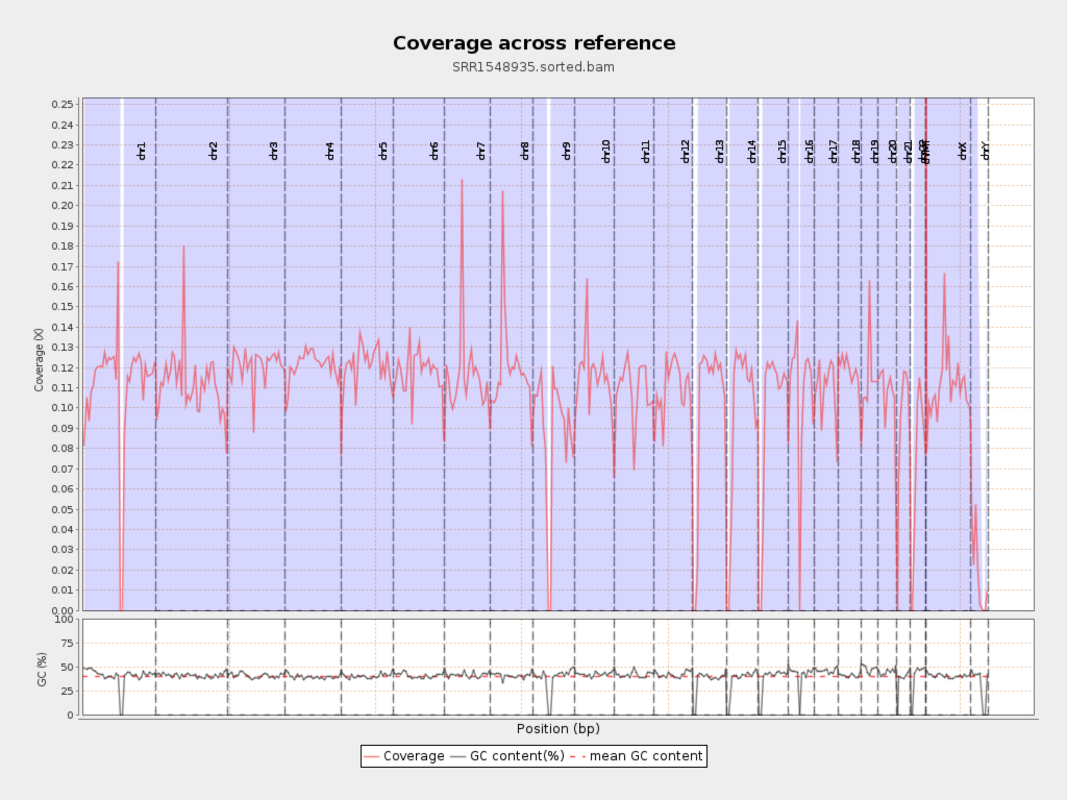
General error rate	0.31%
Mismatches	1,036,452
Insertions	11,836
Mapped reads with at least one insertion	0.14%
Deletions	27,823
Mapped reads with at least one deletion	0.33%
Homopolymer indels	39.56%

2.6. Chromosome stats

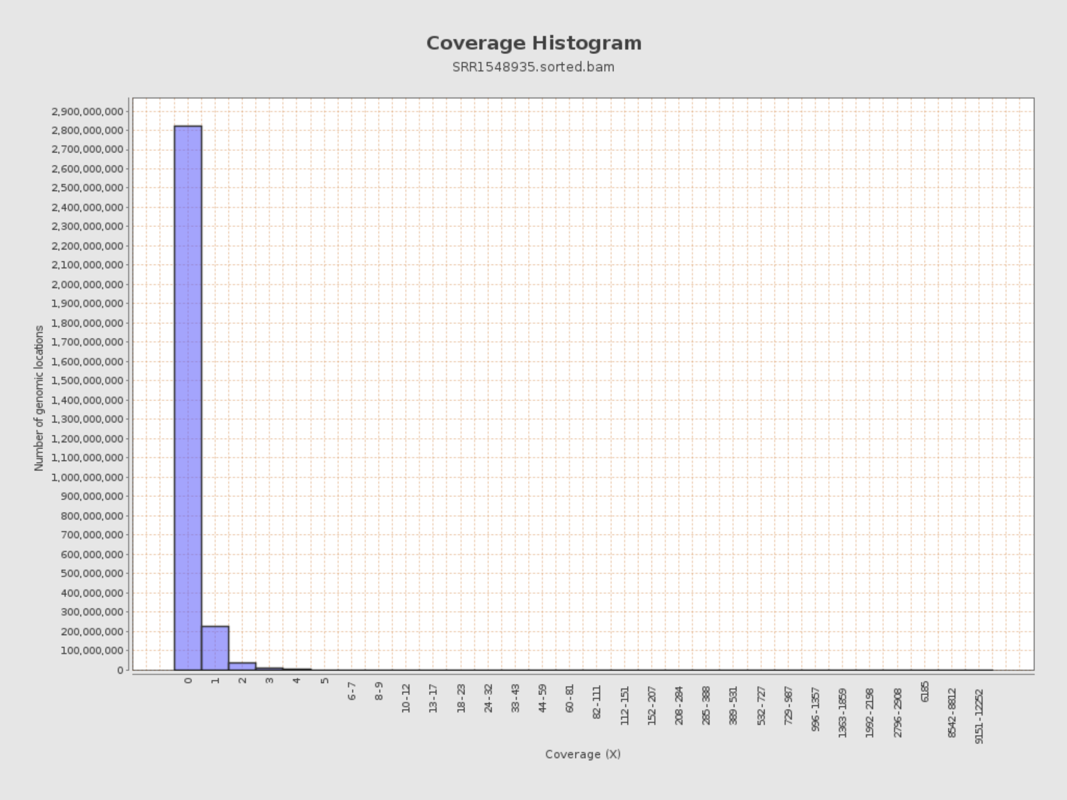
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27464819	0.1102	1.5507
chr2	243199373	27293960	0.1122	0.7374
chr3	198022430	24007557	0.1212	0.4167
chr4	191154276	23215630	0.1214	0.432
chr5	180915260	21810599	0.1206	0.4291
chr6	171115067	20249385	0.1183	0.4807
chr7	159138663	18534955	0.1165	1.1786
chr8	146364022	17553191	0.1199	5.9276

chr9	141213431	12451677	0.0882	0.6856
chr10	135534747	15717940	0.116	0.6717
chr11	135006516	14700719	0.1089	0.7066
chr12	133851895	14640443	0.1094	0.4257
chr13	115169878	11423737	0.0992	0.3666
chr14	107349540	10486895	0.0977	0.4515
chr15	102531392	9734470	0.0949	0.3645
chr16	90354753	9453526	0.1046	0.4543
chr17	81195210	8974010	0.1105	0.4447
chr18	78077248	9262416	0.1186	1.3837
chr19	59128983	6784818	0.1147	1.4743
chr20	63025520	6768453	0.1074	0.4182
chr21	48129895	4333470	0.09	0.4198
chr22	51304566	3631798	0.0708	0.3744
chrMT	16571	12077	0.7288	1.1571
chrX	155270560	17280696	0.1113	0.5396
chrY	59373566	1105096	0.0186	0.2323

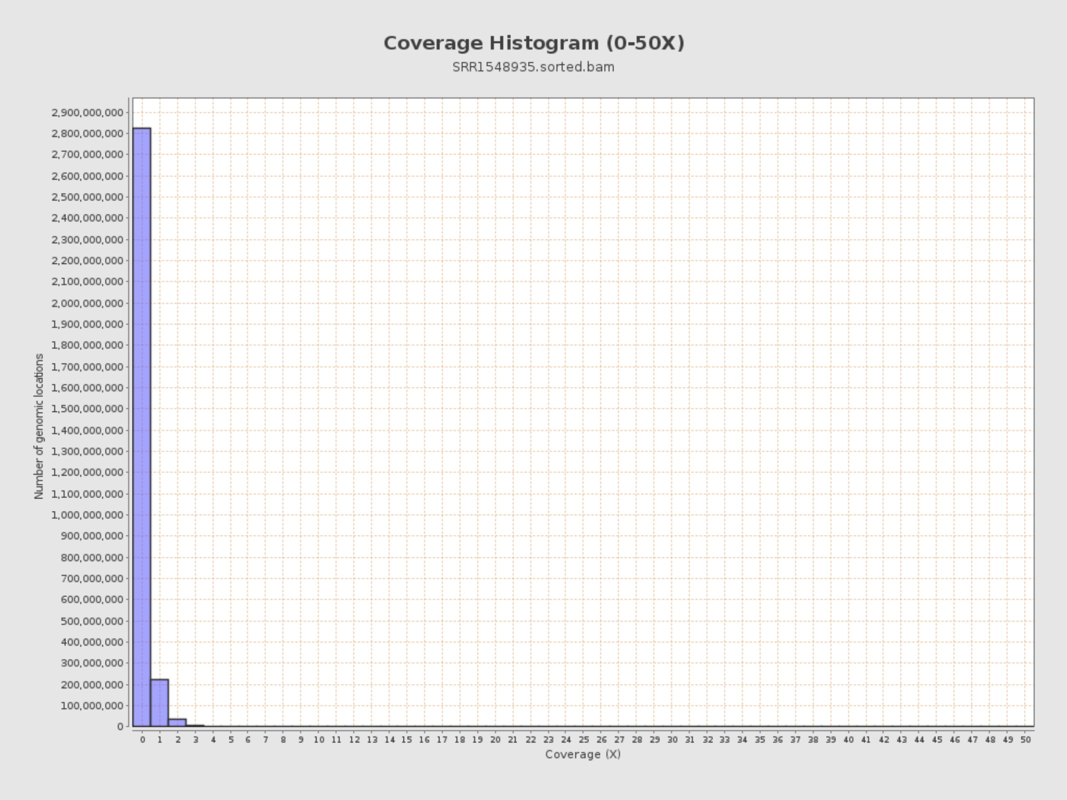
3. Results : Coverage across reference



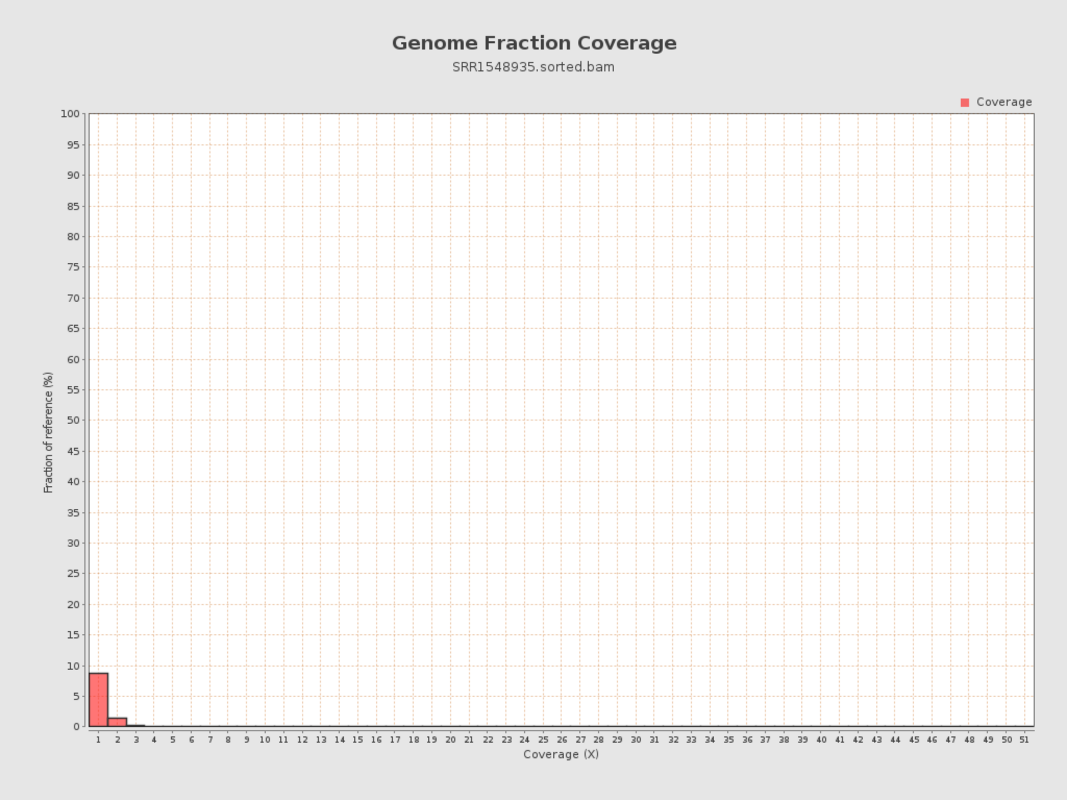
4. Results : Coverage Histogram



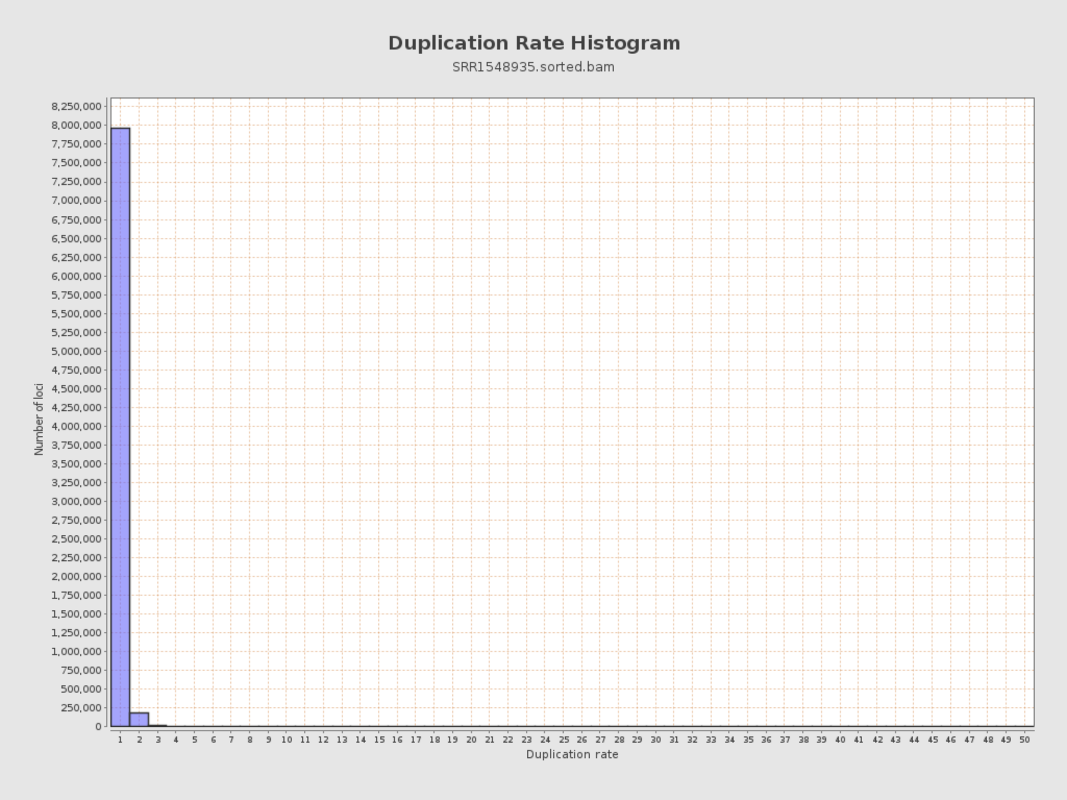
5. Results : Coverage Histogram (0-50X)



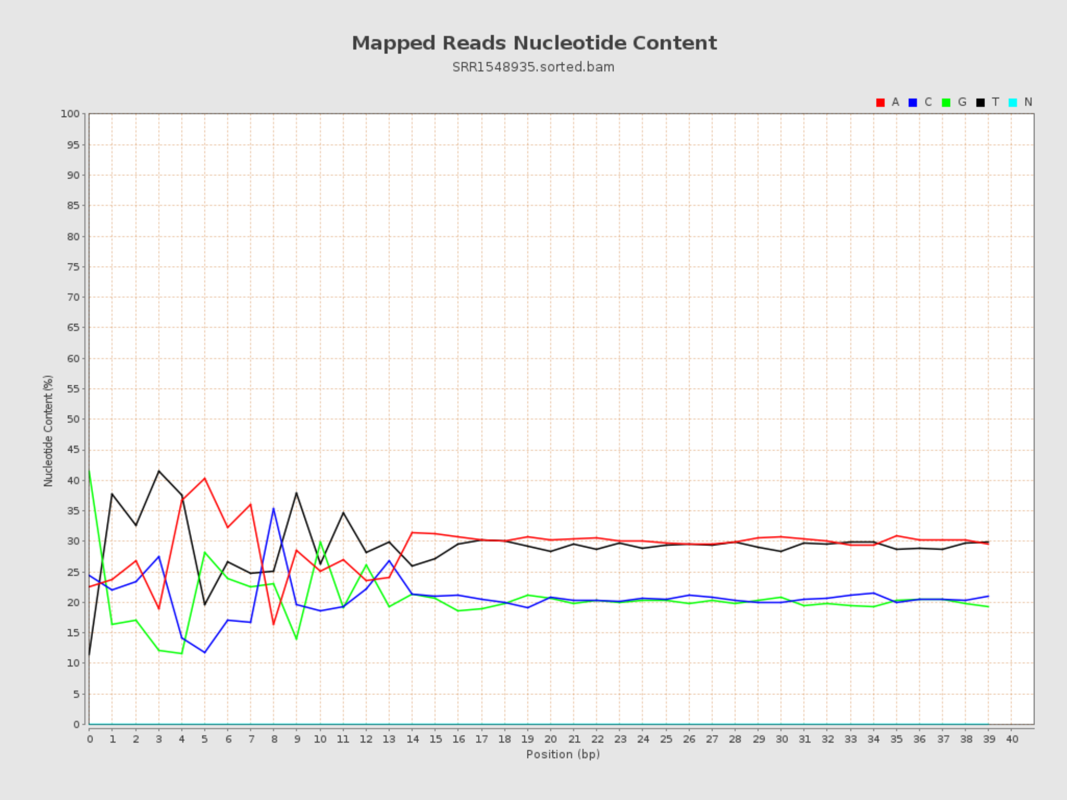
6. Results : Genome Fraction Coverage



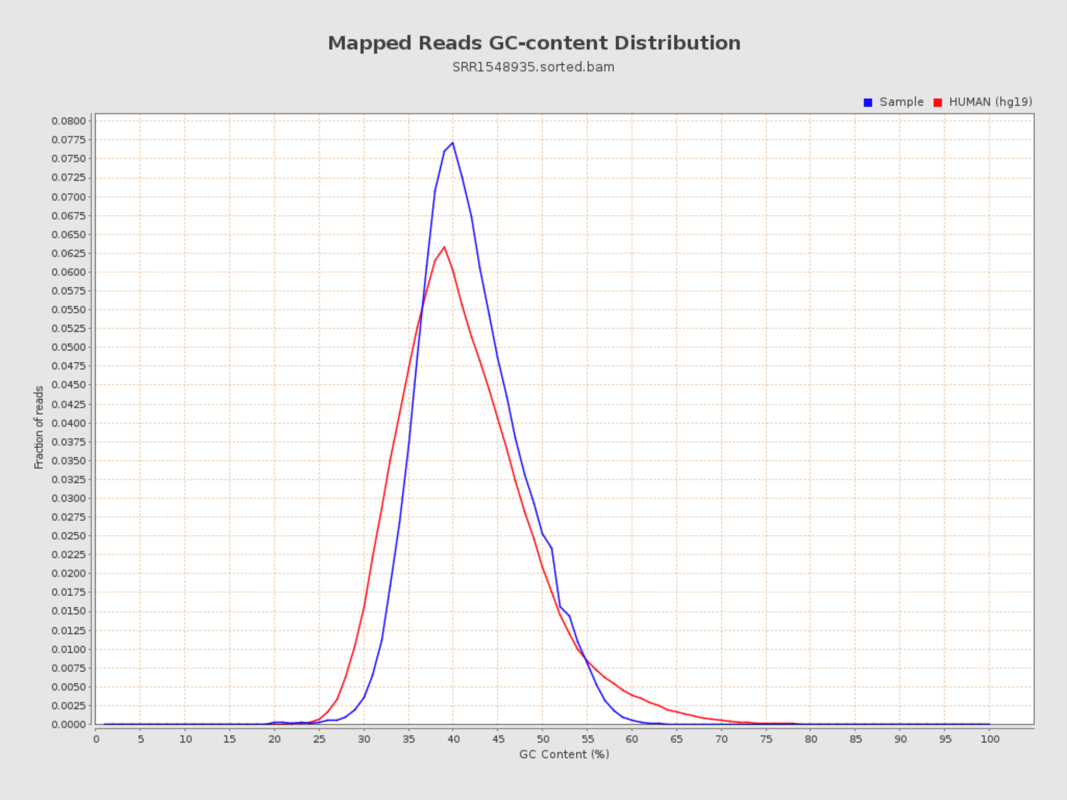
7. Results : Duplication Rate Histogram



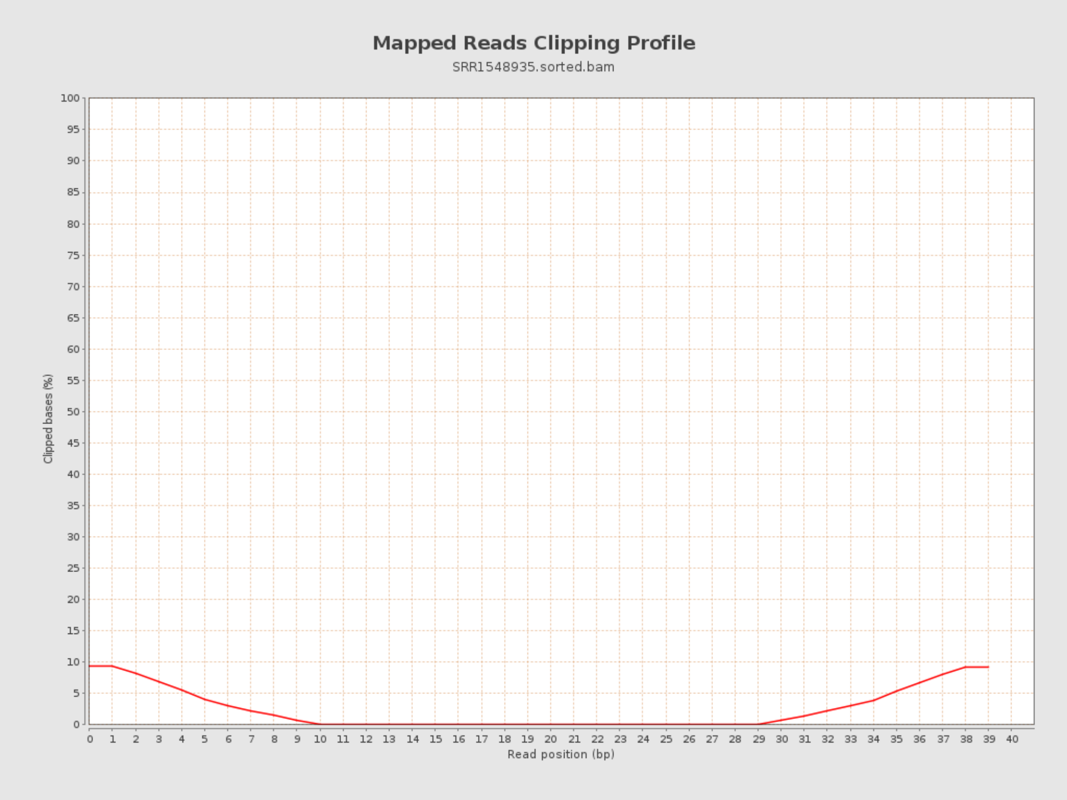
8. Results : Mapped Reads Nucleotide Content



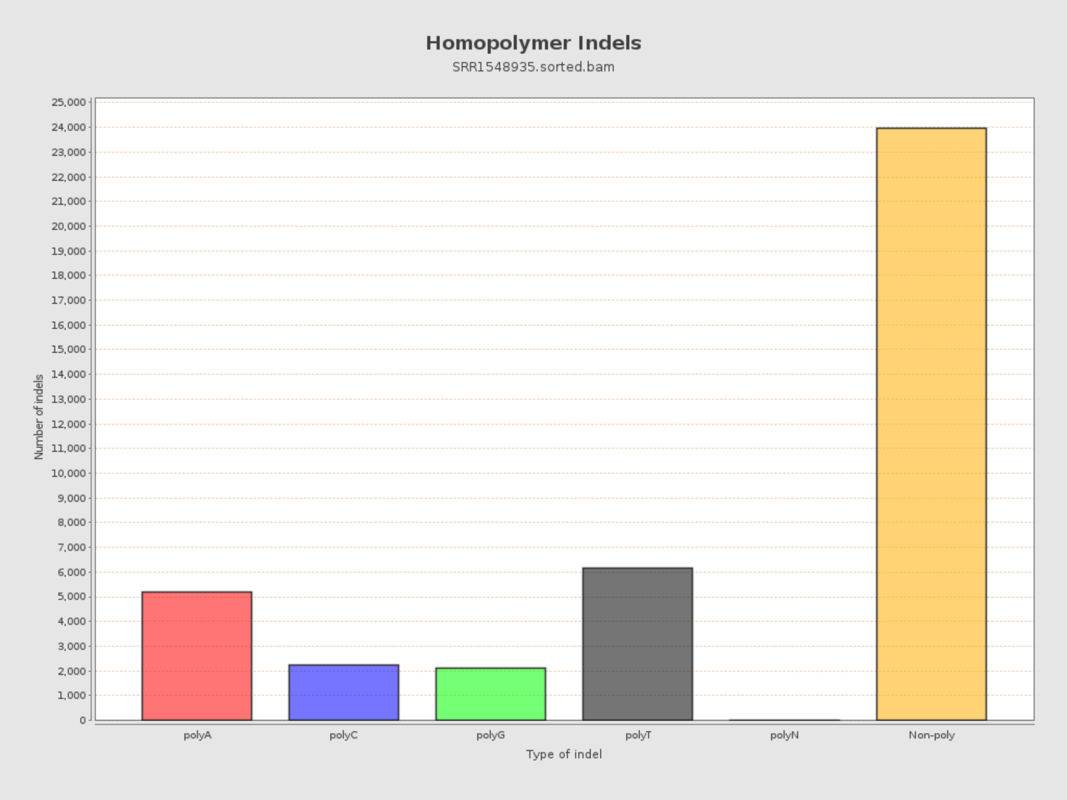
9. Results : Mapped Reads GC-content Distribution



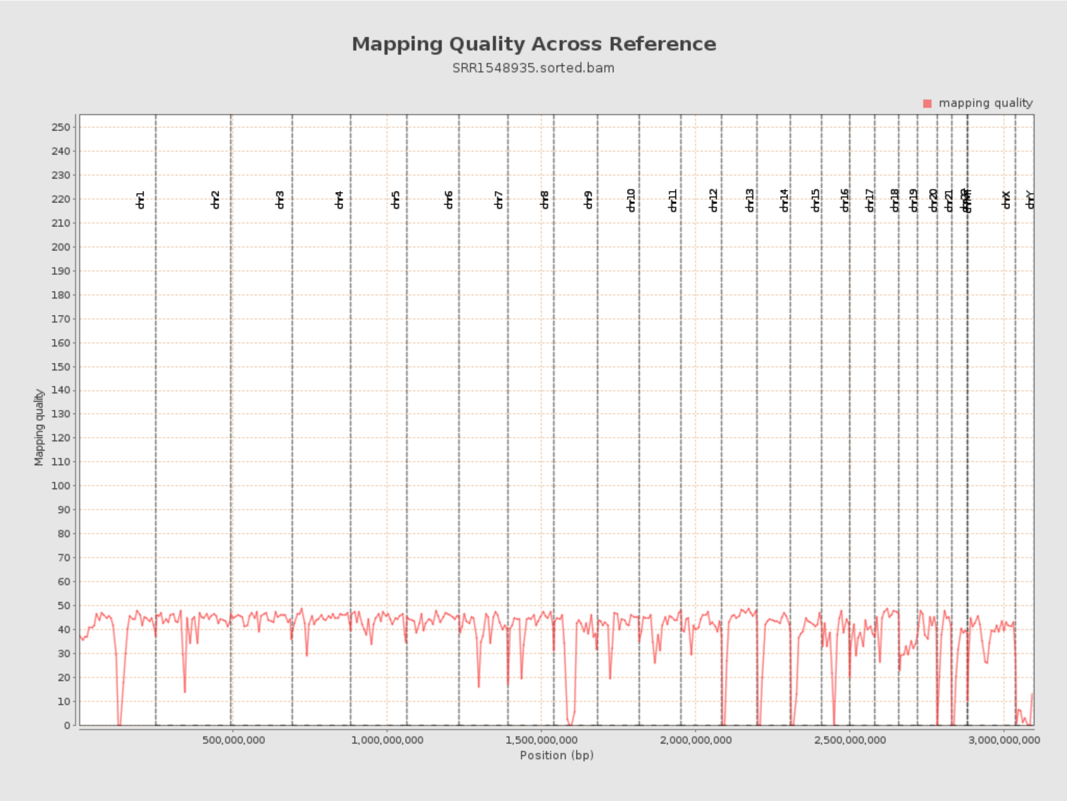
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram