Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:50:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548931.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_SRR1548931 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548931.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:50:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548931.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,478,495
Mapped reads	6,490,444 / 86.79%
Unmapped reads	988,051 / 13.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	227,701 / 3.04%
Duplication rate	2.54%
Clipped reads	531,486 / 7.11%

2.2. ACGT Content

Number/percentage of A's	75,060,029 / 29.24%
Number/percentage of C's	53,129,180 / 20.7%
Number/percentage of T's	75,487,746 / 29.41%
Number/percentage of G's	53,002,034 / 20.65%
Number/percentage of N's	2,219 / 0%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0829
Standard Deviation	0.9422

2.4. Mapping Quality

Mean Mapping Quality	40.99

2.5. Mismatches and indels

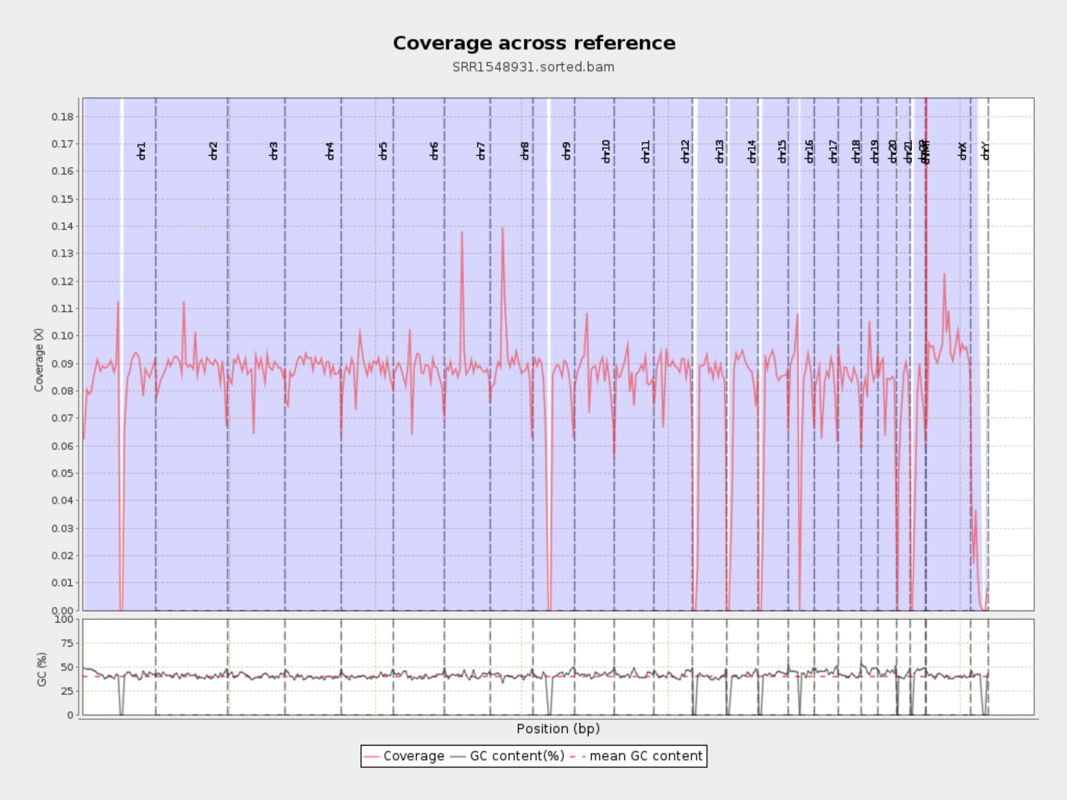
General error rate	0.29%
Mismatches	734,386
Insertions	8,890
Mapped reads with at least one insertion	0.14%
Deletions	21,239
Mapped reads with at least one deletion	0.33%
Homopolymer indels	40.68%

2.6. Chromosome stats

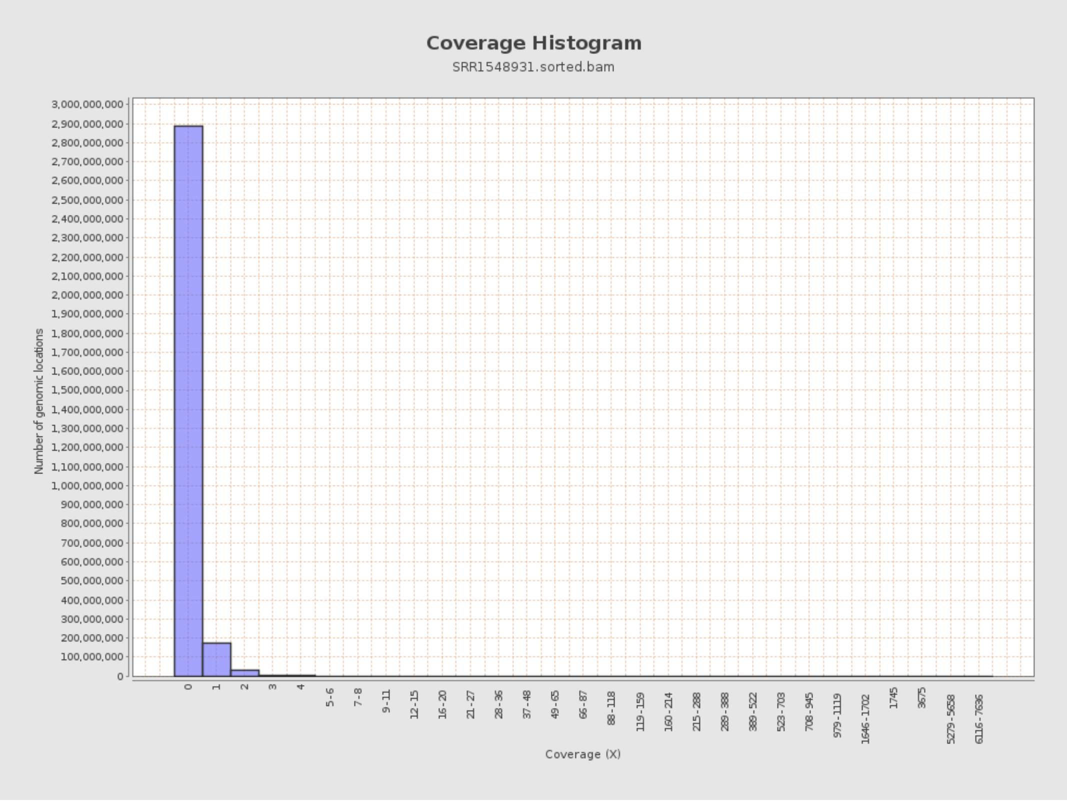
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20269959	0.0813	0.8724
chr2	243199373	21688330	0.0892	0.4938
chr3	198022430	17352144	0.0876	0.3512
chr4	191154276	16902822	0.0884	0.367
chr5	180915260	15867154	0.0877	0.3555
chr6	171115067	14906302	0.0871	0.3849
chr7	159138663	14331062	0.0901	0.7365
chr8	146364022	13357217	0.0913	3.6933

chr9	141213431	10739534	0.0761	0.4815
chr10	135534747	11808945	0.0871	0.4515
chr11	135006516	11572369	0.0857	0.5376
chr12	133851895	11707988	0.0875	0.3597
chr13	115169878	8412485	0.073	0.3187
chr14	107349540	7901197	0.0736	0.3744
chr15	102531392	7381713	0.072	0.3177
chr16	90354753	7056614	0.0781	0.359
chr17	81195210	6675514	0.0822	0.3627
chr18	78077248	6687653	0.0857	0.8382
chr19	59128983	5070916	0.0858	0.7815
chr20	63025520	5173888	0.0821	0.3495
chr21	48129895	3295075	0.0685	0.3468
chr22	51304566	2837466	0.0553	0.3334
chrMT	16571	8820	0.5323	0.9133
chrX	155270560	14904695	0.096	0.432
chrY	59373566	799290	0.0135	0.1895

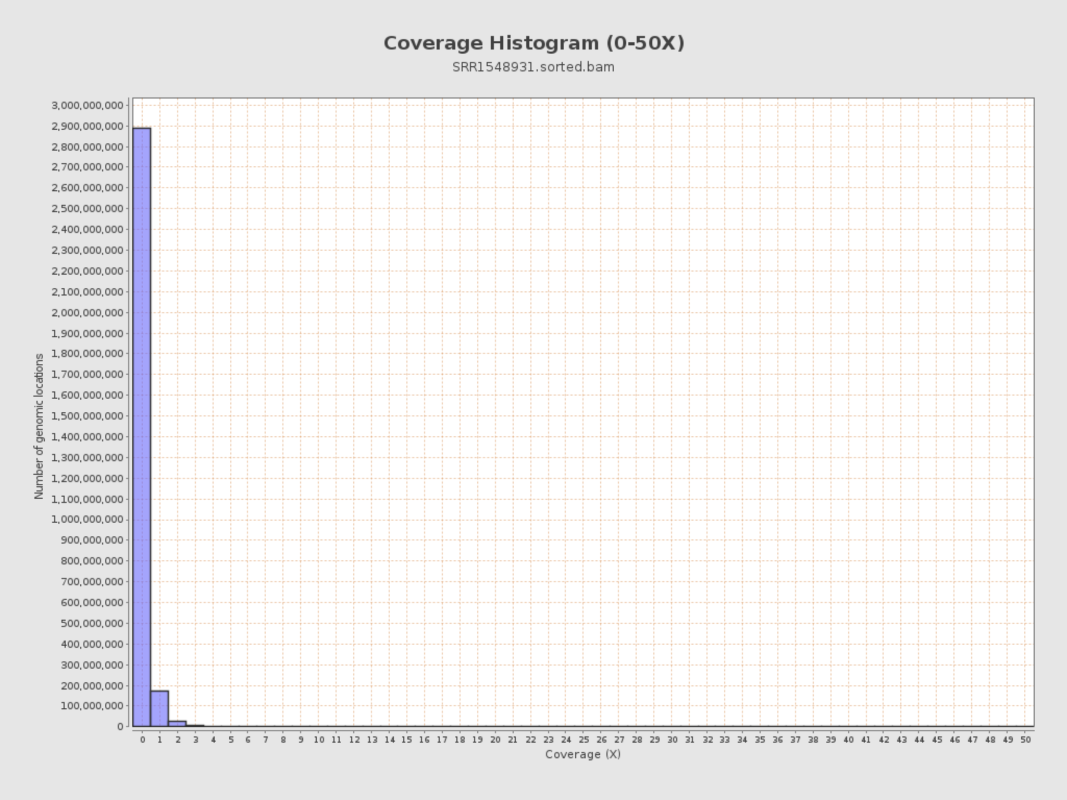
3. Results : Coverage across reference



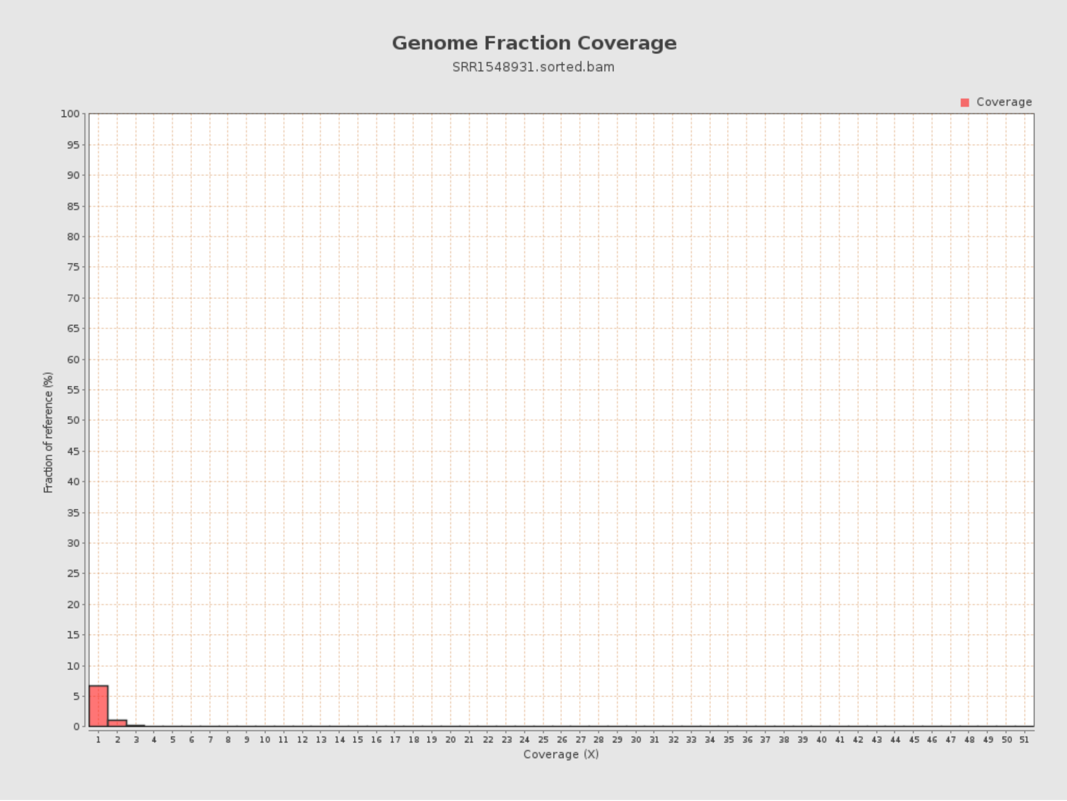
4. Results : Coverage Histogram



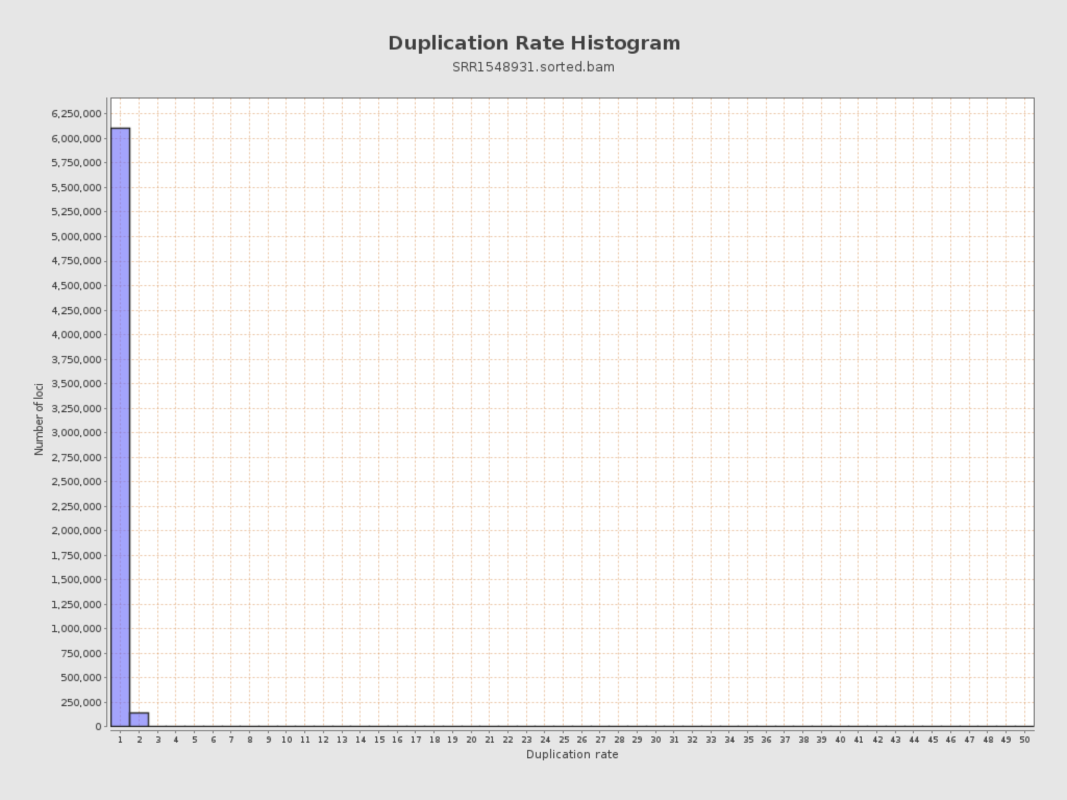
5. Results : Coverage Histogram (0-50X)



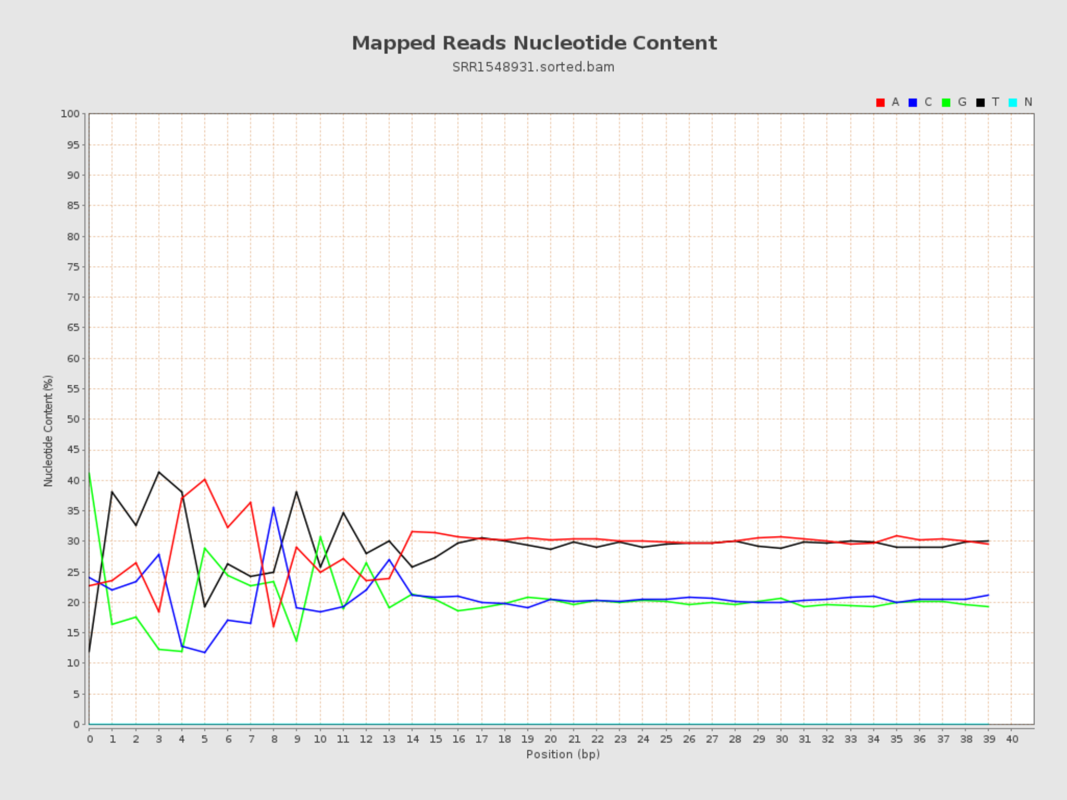
6. Results : Genome Fraction Coverage



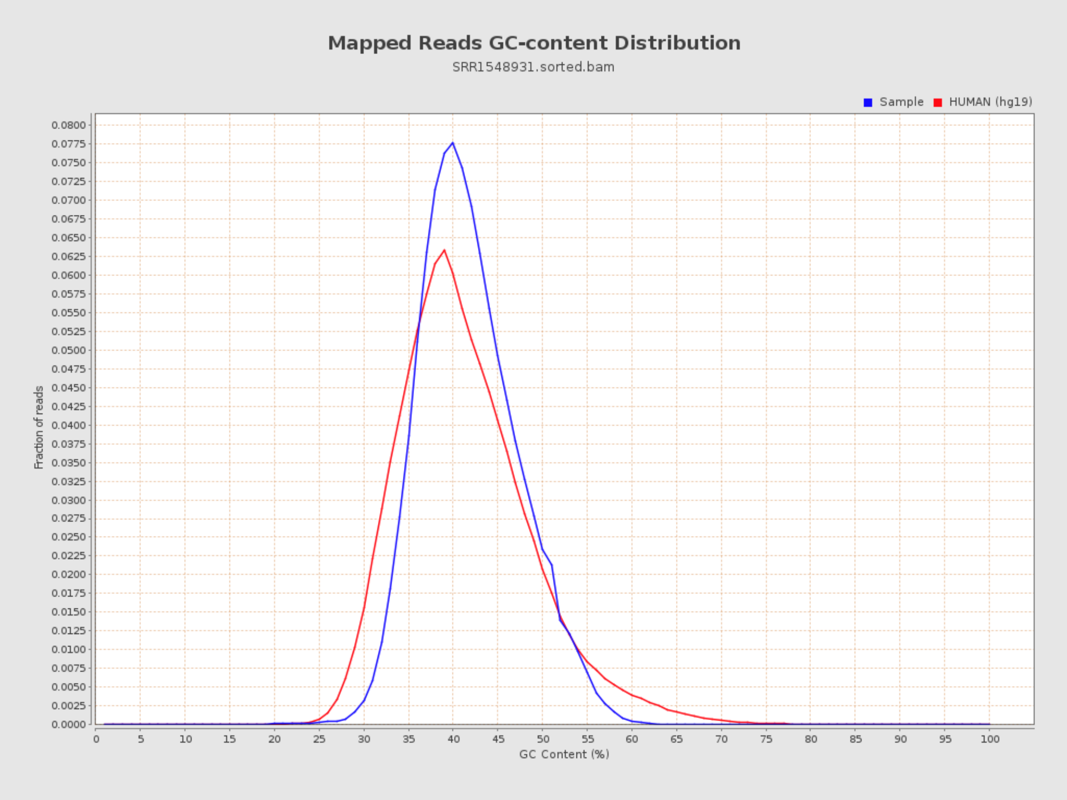
7. Results : Duplication Rate Histogram



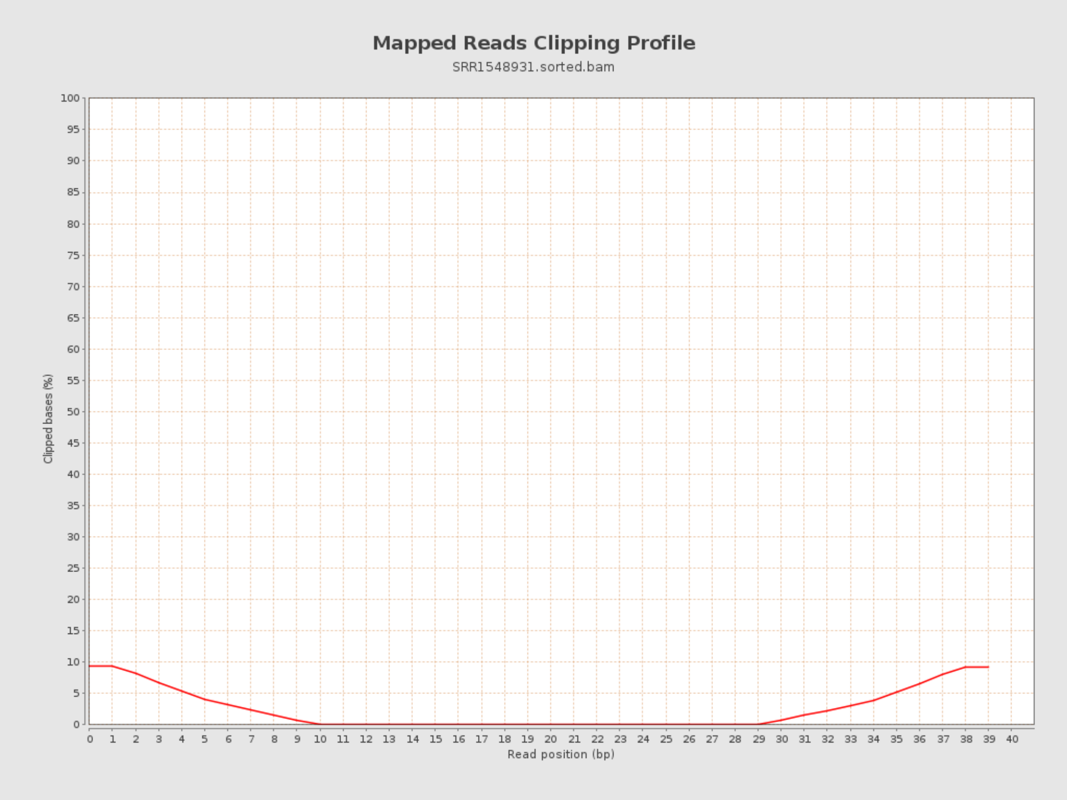
8. Results : Mapped Reads Nucleotide Content



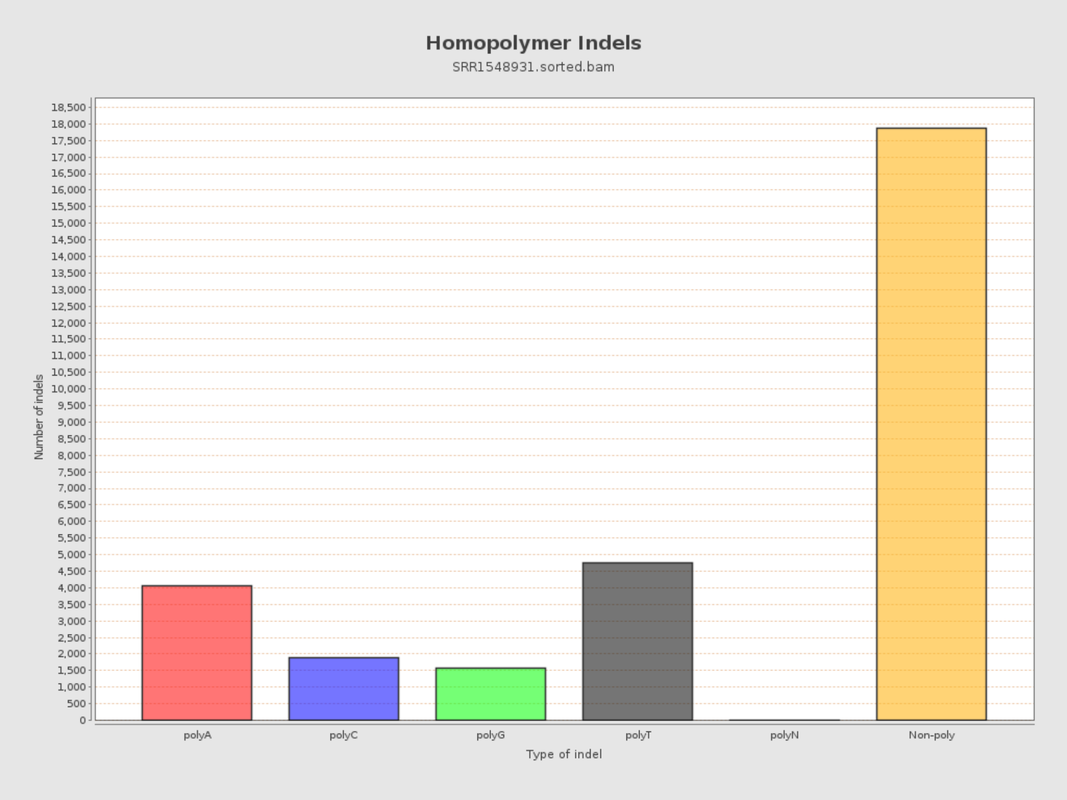
9. Results : Mapped Reads GC-content Distribution



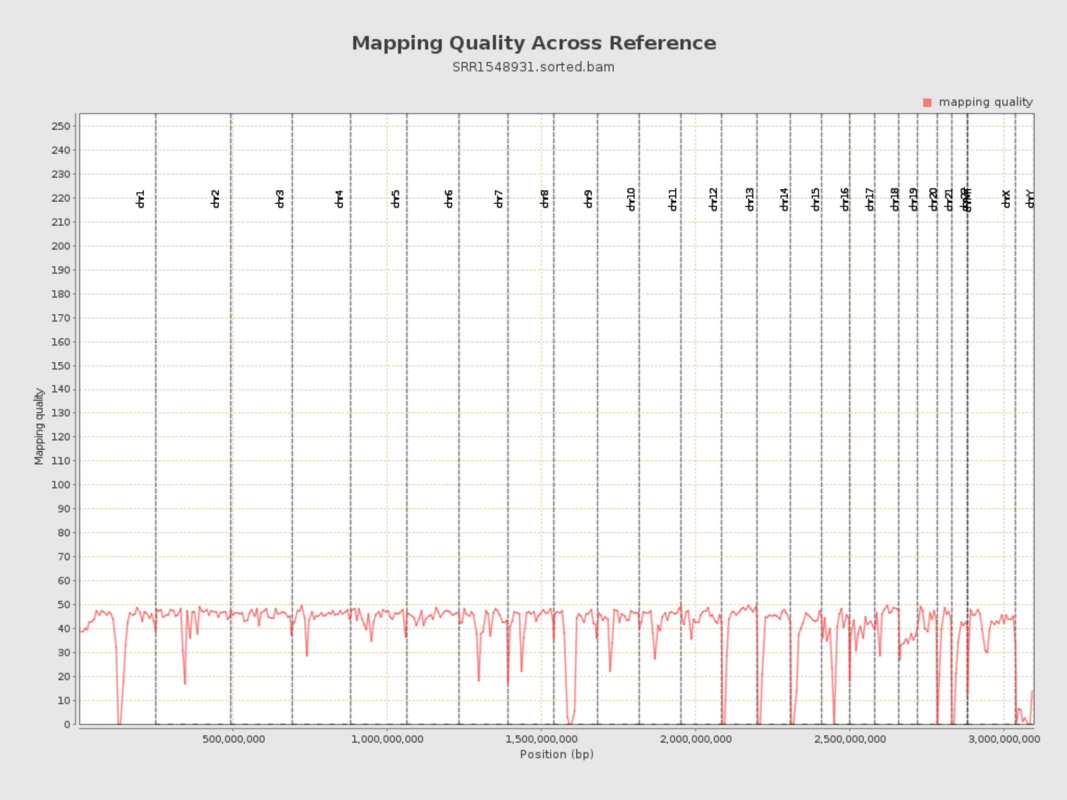
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram