Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:12:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013338.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_SRR6013338 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013338.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:12:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013338.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,044,662
Mapped reads	1,608,148 / 78.65%
Unmapped reads	436,514 / 21.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,731 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	208,085 / 10.18%
Duplication rate	9.86%
Clipped reads	848,958 / 41.52%

2.2. ACGT Content

Number/percentage of A's	28,197,611 / 27%
Number/percentage of C's	19,884,282 / 19.04%
Number/percentage of T's	32,451,725 / 31.07%
Number/percentage of G's	23,884,810 / 22.87%
Number/percentage of N's	12,147 / 0.01%
GC Percentage	41.91%

2.3. Coverage

Mean	0.0337

Standard Deviation	0.3625

2.4. Mapping Quality

Mean Mapping Quality	44

2.5. Mismatches and indels

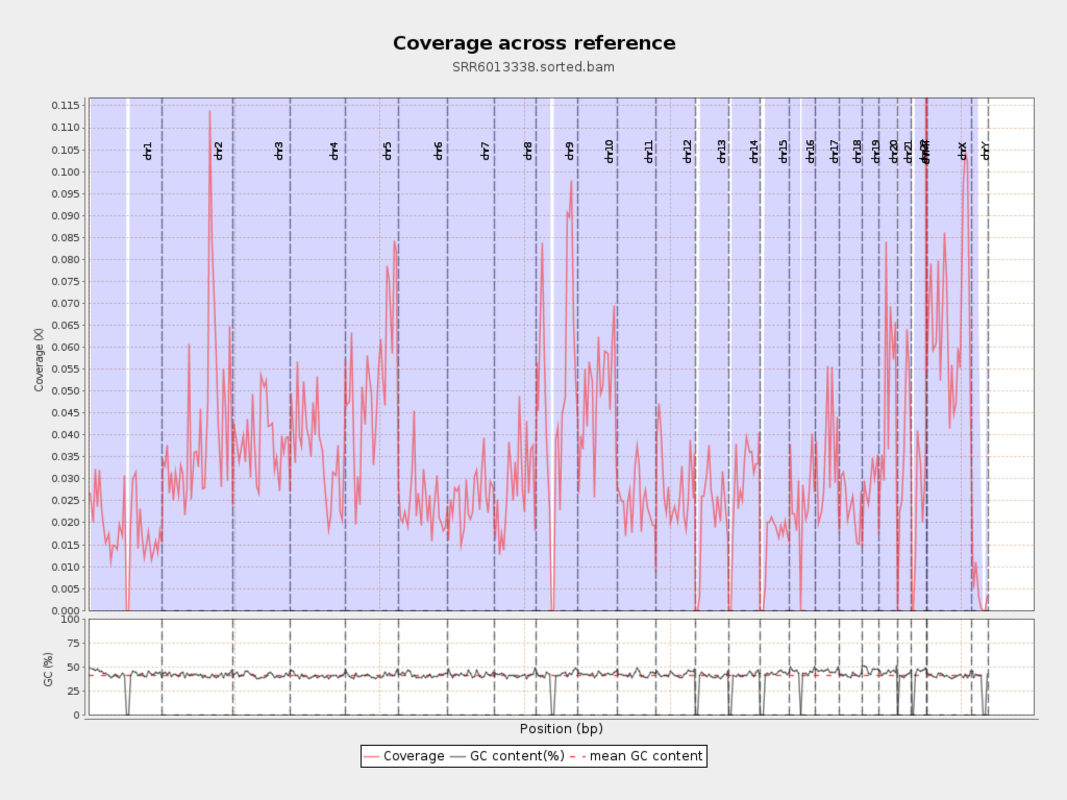
General error rate	0.76%
Mismatches	777,329
Insertions	6,798
Mapped reads with at least one insertion	0.42%
Deletions	22,637
Mapped reads with at least one deletion	1.39%
Homopolymer indels	46.58%

2.6. Chromosome stats

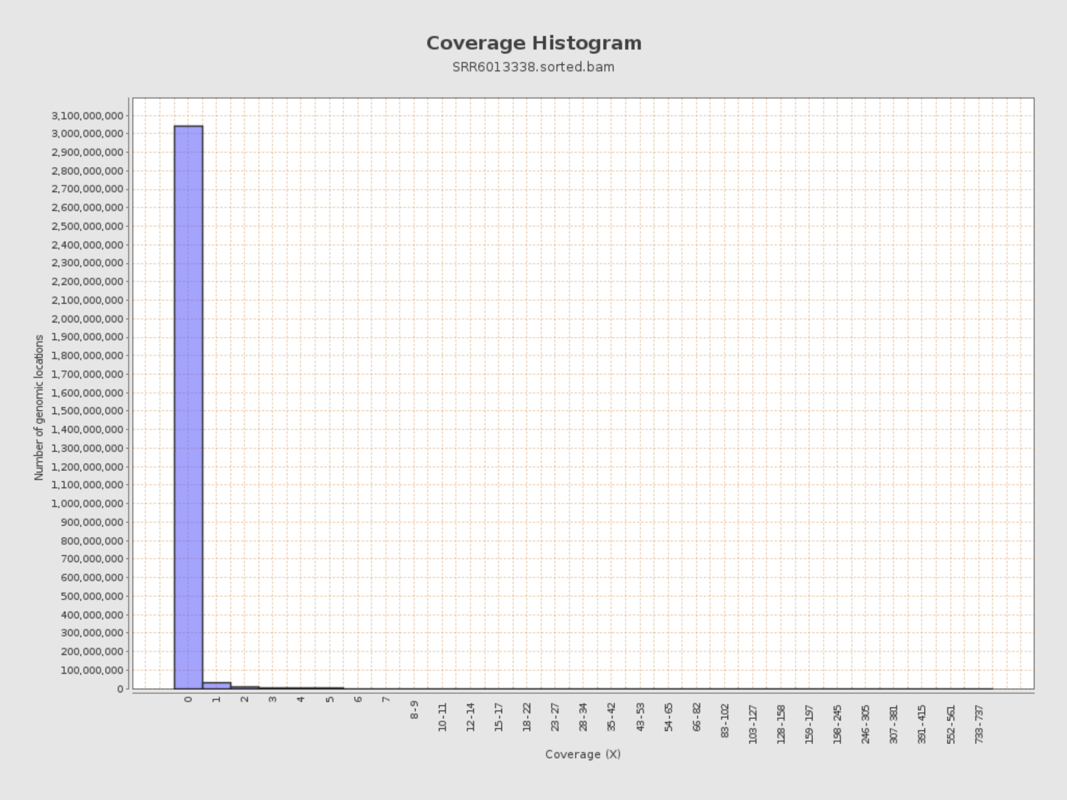
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4547256	0.0182	0.4083
chr2	243199373	10164692	0.0418	0.5406
chr3	198022430	7648891	0.0386	0.3316
chr4	191154276	6980256	0.0365	0.3223
chr5	180915260	9393974	0.0519	0.3836
chr6	171115067	4153702	0.0243	0.2874
chr7	159138663	4102781	0.0258	0.3005

chr8	146364022	4082478	0.0279	0.3836
chr9	141213431	7137633	0.0505	0.4237
chr10	135534747	6629525	0.0489	0.4106
chr11	135006516	3347866	0.0248	0.2797
chr12	133851895	3779939	0.0282	0.2817
chr13	115169878	2504030	0.0217	0.2464
chr14	107349540	2950141	0.0275	0.2871
chr15	102531392	1573631	0.0153	0.2003
chr16	90354753	2224965	0.0246	0.2696
chr17	81195210	2869398	0.0353	0.318
chr18	78077248	1832835	0.0235	0.4001
chr19	59128983	1698546	0.0287	0.3667
chr20	63025520	3170364	0.0503	0.3884
chr21	48129895	1734558	0.036	0.3264
chr22	51304566	1122197	0.0219	0.243
chrMT	16571	34919	2.1072	2.45
chrX	155270560	10540405	0.0679	0.4545
chrY	59373566	244985	0.0041	0.1098

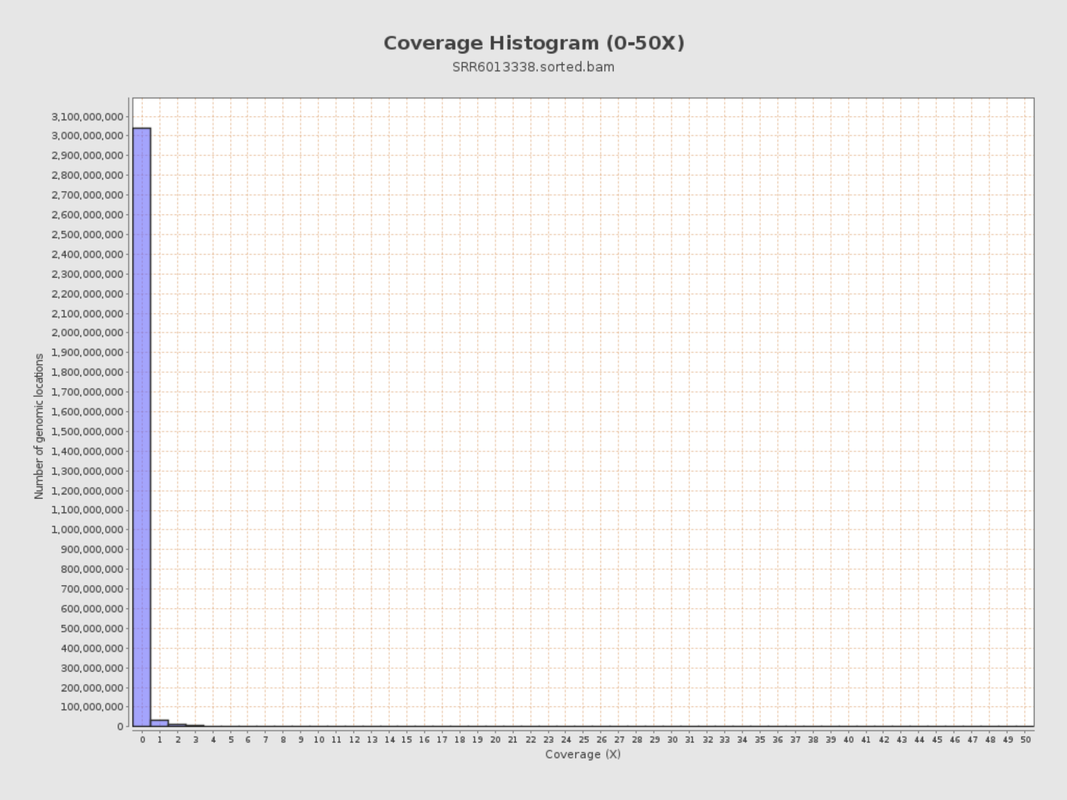
3. Results : Coverage across reference



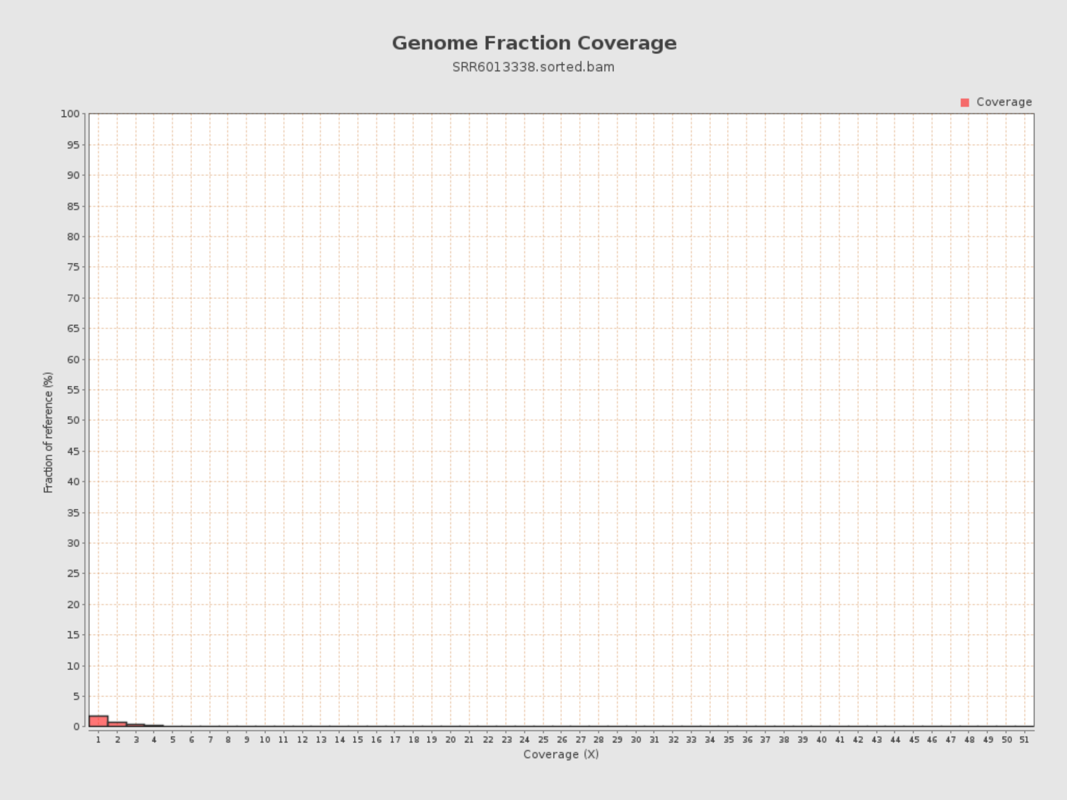
4. Results : Coverage Histogram



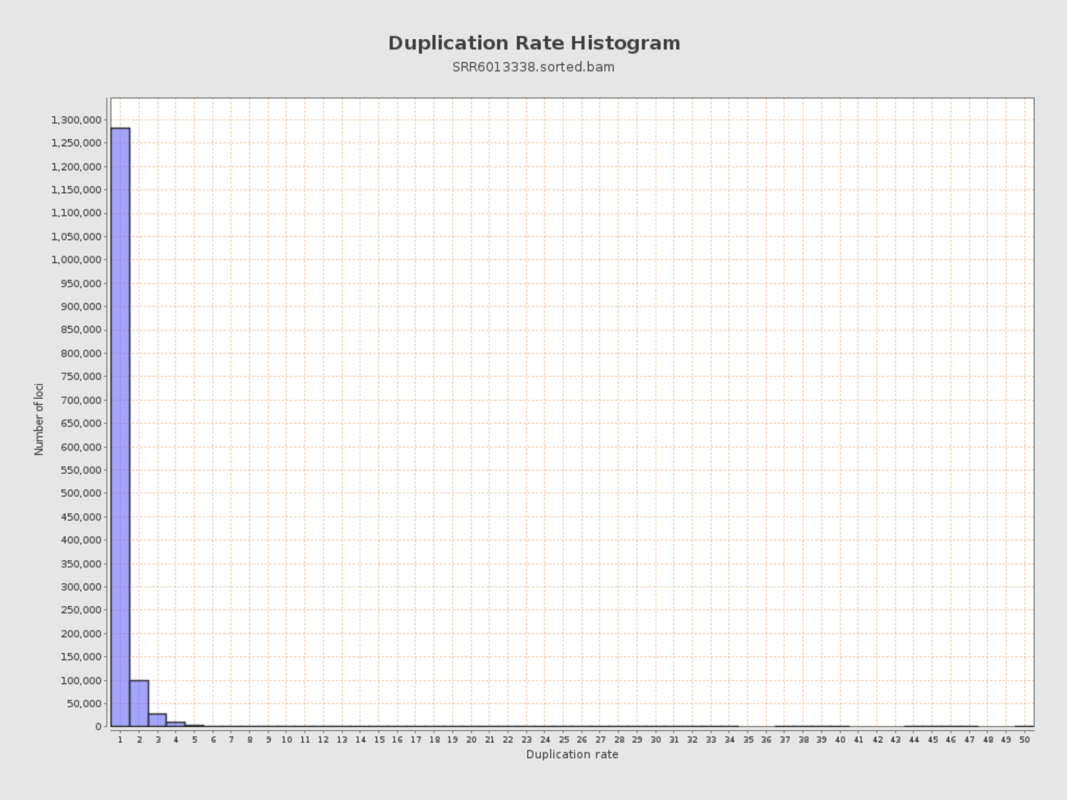
5. Results : Coverage Histogram (0-50X)



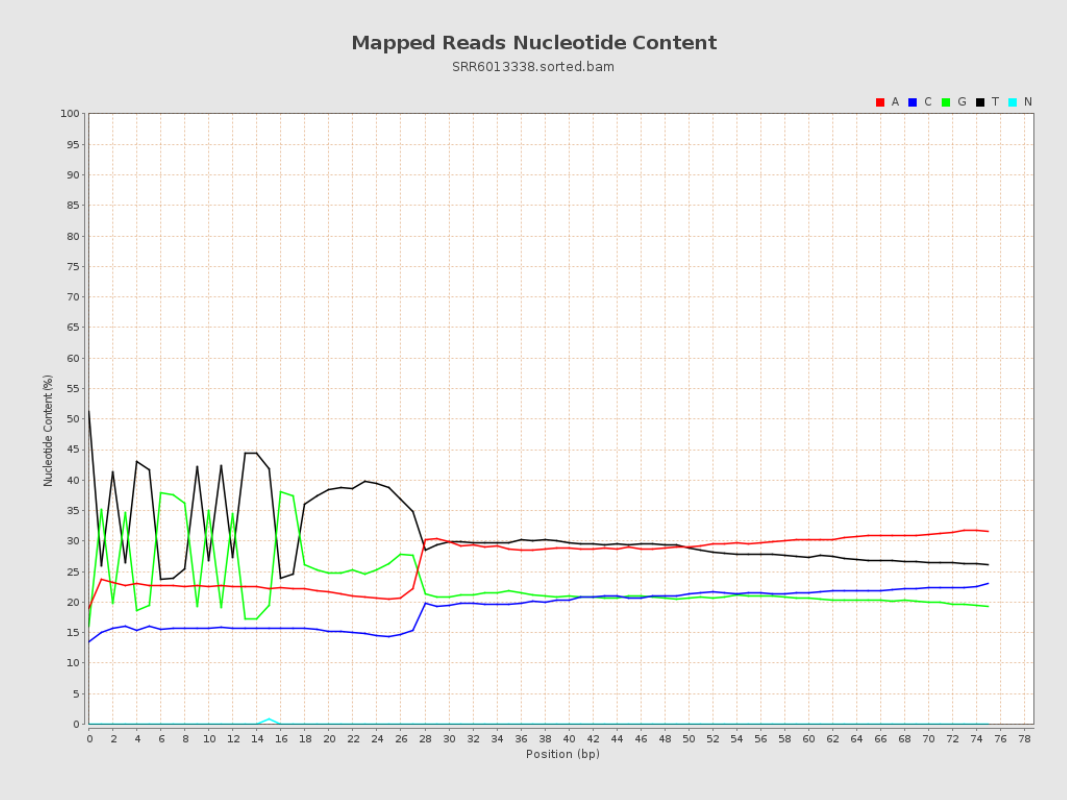
6. Results : Genome Fraction Coverage



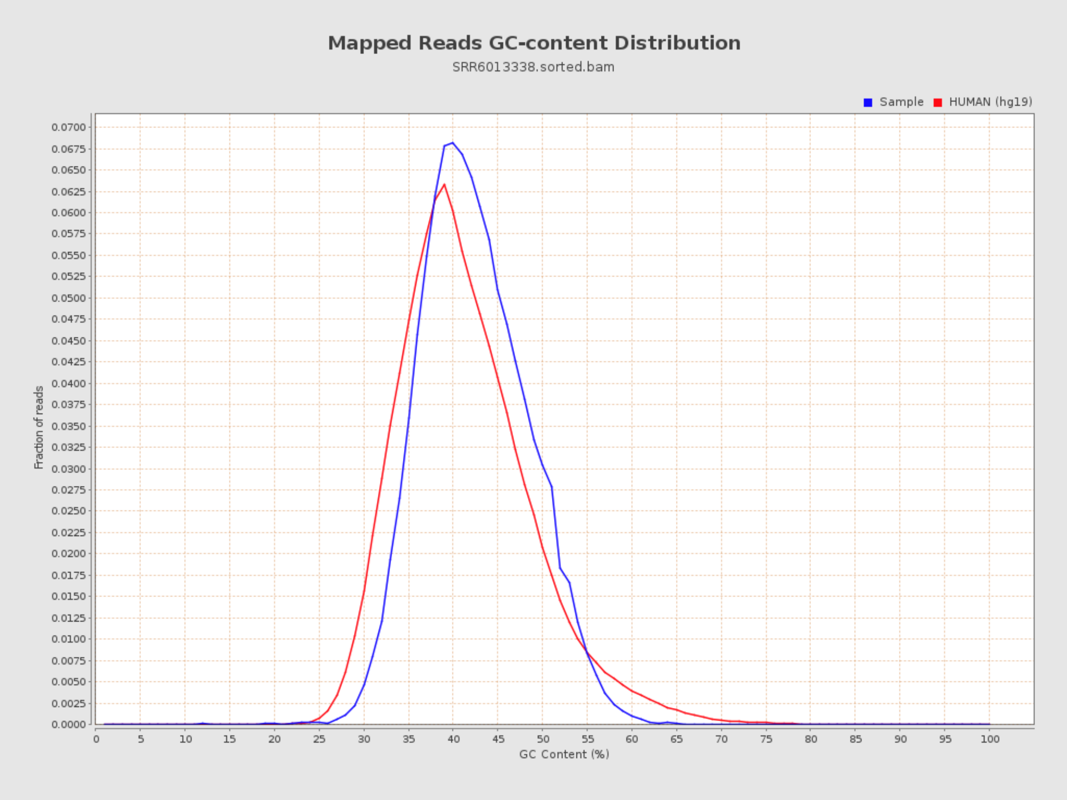
7. Results : Duplication Rate Histogram



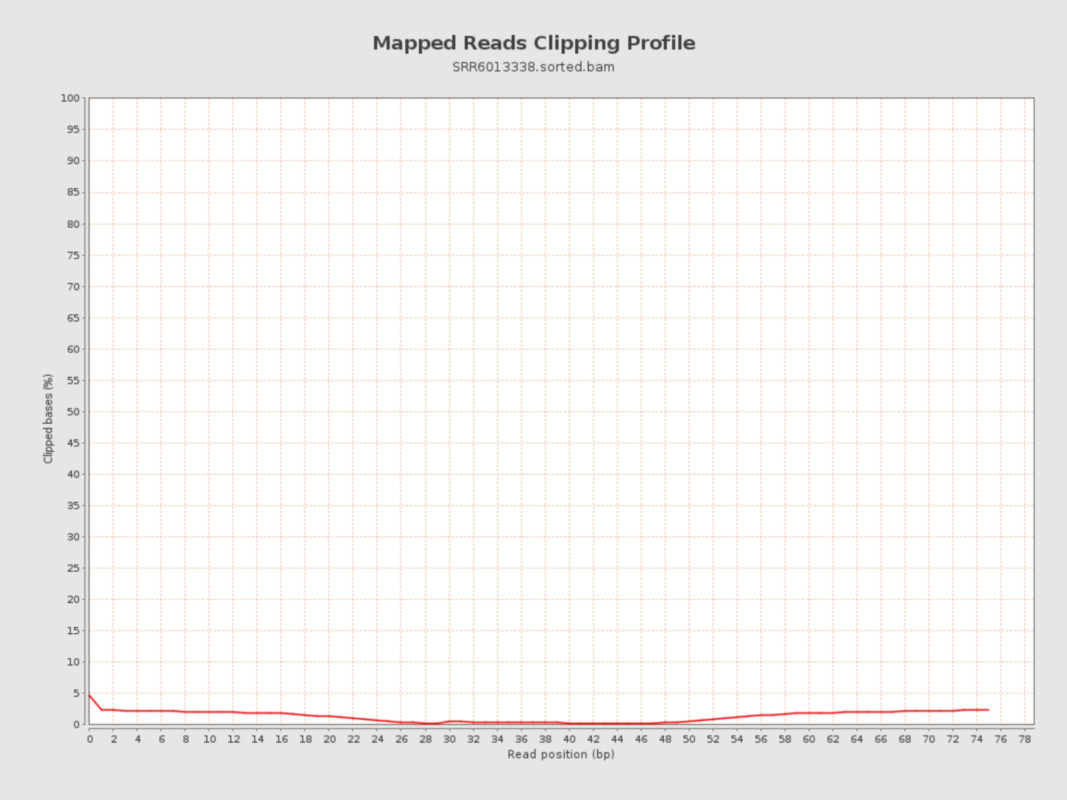
8. Results : Mapped Reads Nucleotide Content



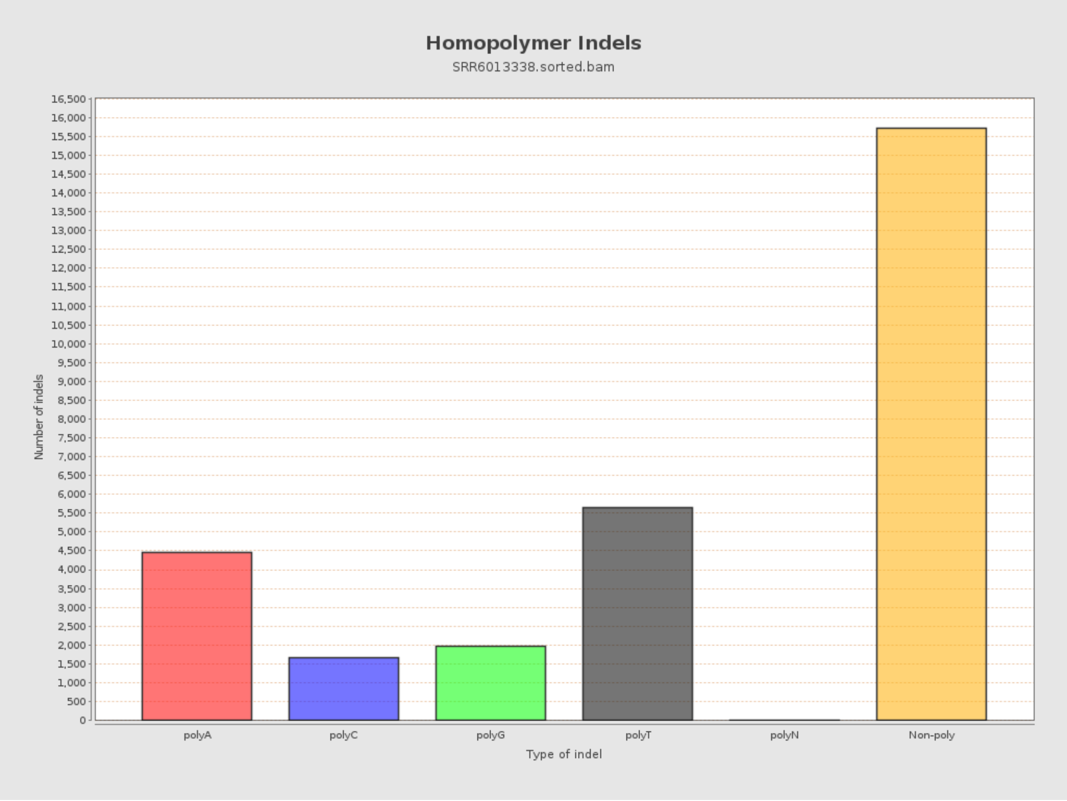
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



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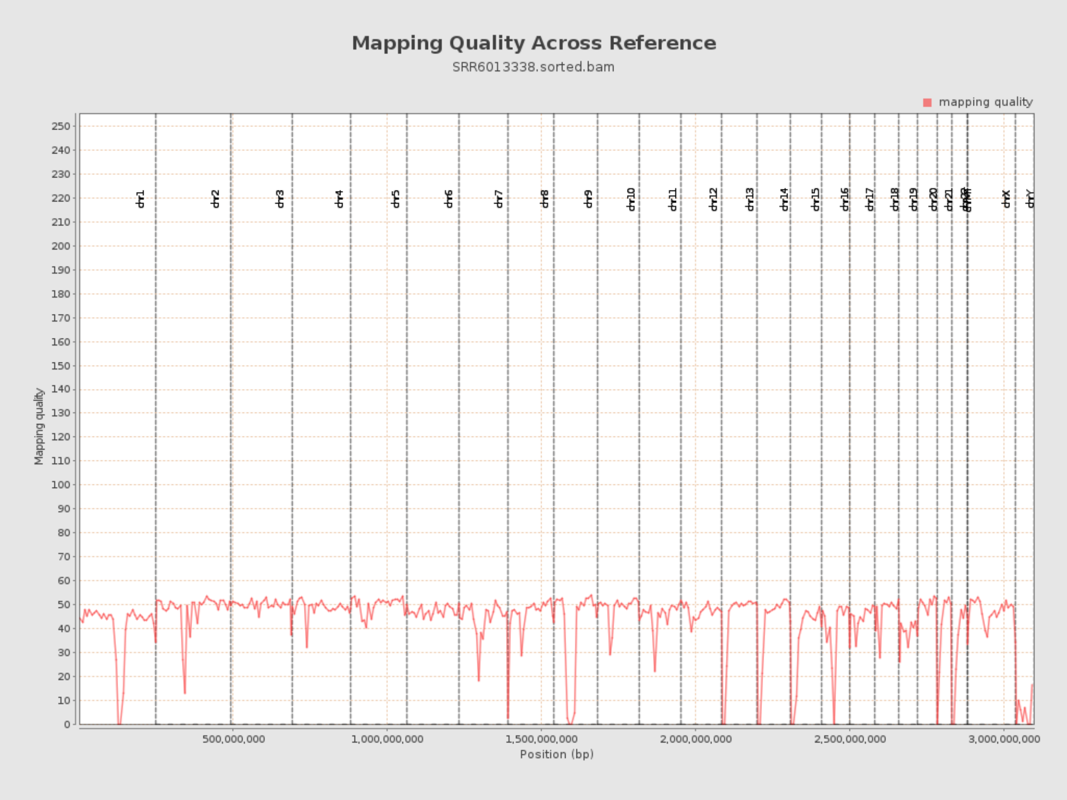
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram