Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:20:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068166.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_SRR6068166 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068166.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:20:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068166.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,678,054
Mapped reads	1,453,439 / 86.61%
Unmapped reads	224,615 / 13.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,653 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	140,410 / 8.37%
Duplication rate	7.84%
Clipped reads	575,479 / 34.29%

2.2. ACGT Content

Number/percentage of A's	28,590,851 / 28.83%
Number/percentage of C's	18,962,217 / 19.12%
Number/percentage of T's	30,839,709 / 31.09%
Number/percentage of G's	20,686,729 / 20.86%
Number/percentage of N's	103,505 / 0.1%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0321

Standard Deviation	0.3725

2.4. Mapping Quality

Mean Mapping Quality	47.45

2.5. Mismatches and indels

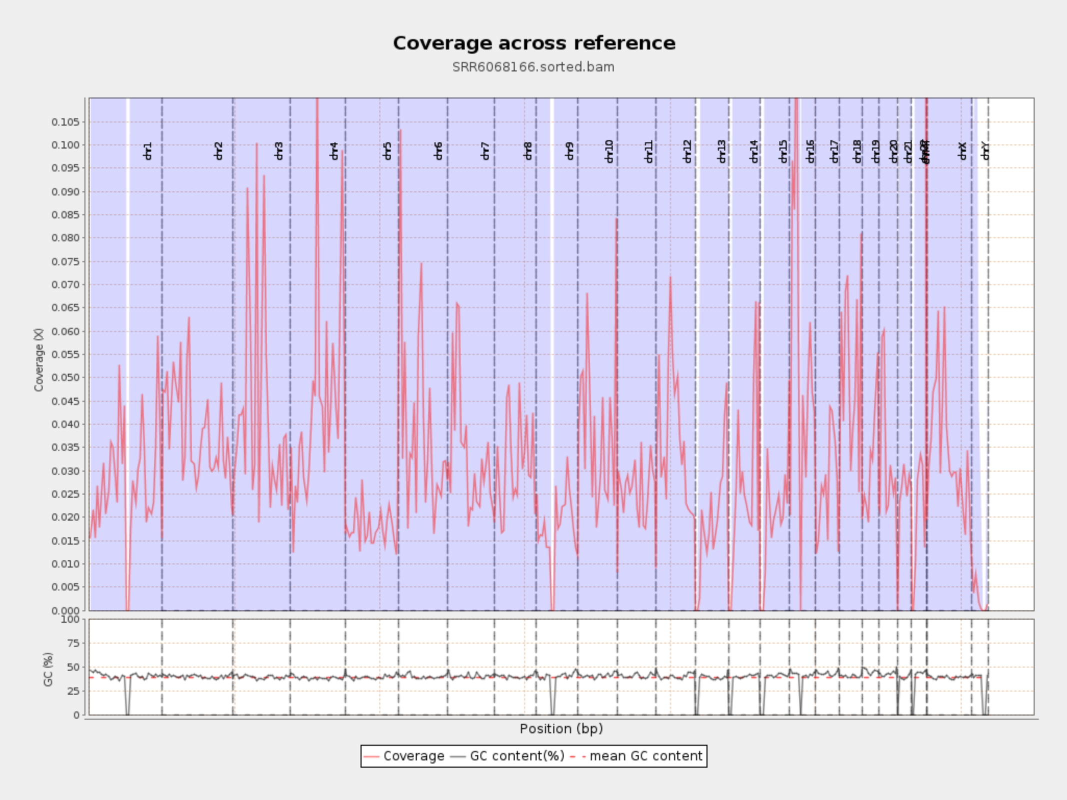
General error rate	0.83%
Mismatches	805,733
Insertions	6,830
Mapped reads with at least one insertion	0.47%
Deletions	23,551
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.53%

2.6. Chromosome stats

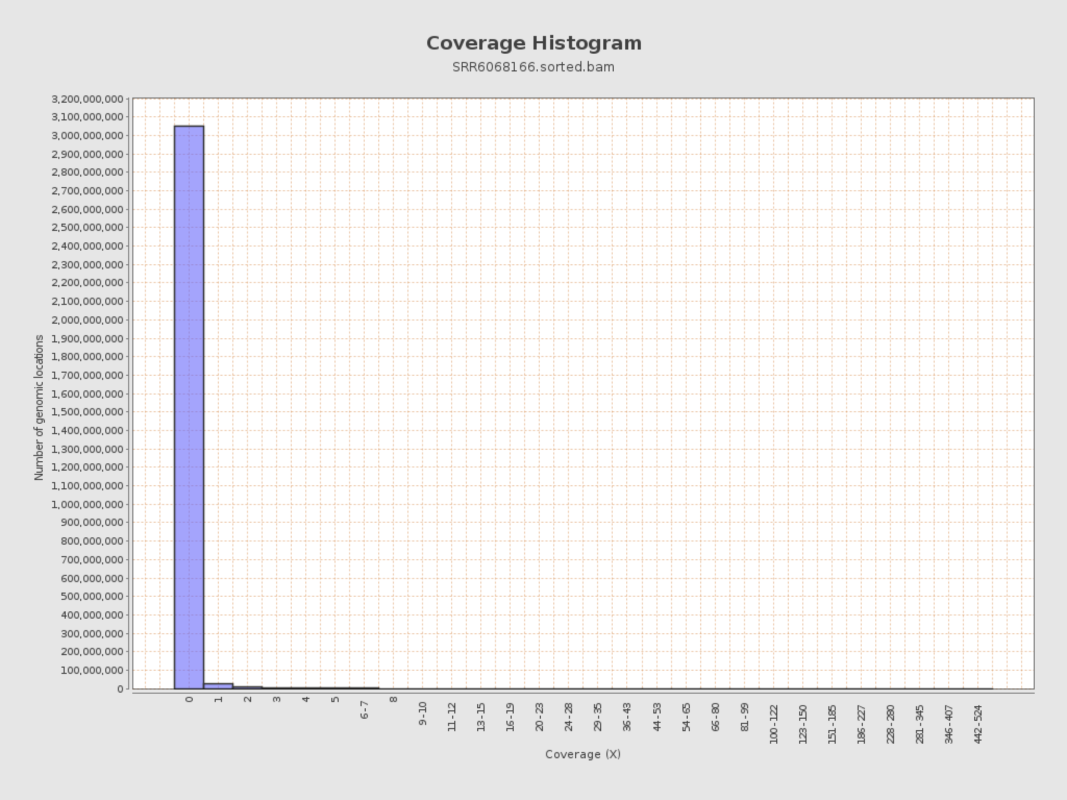
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6884536	0.0276	0.4188
chr2	243199373	9460953	0.0389	0.4289
chr3	198022430	8188042	0.0413	0.395
chr4	191154276	8621980	0.0451	0.4086
chr5	180915260	3219316	0.0178	0.2312
chr6	171115067	6663034	0.0389	0.4129
chr7	159138663	5383551	0.0338	0.3975

chr8	146364022	4608565	0.0315	0.4505
chr9	141213431	2464478	0.0175	0.2759
chr10	135534747	5251311	0.0387	0.4377
chr11	135006516	3477908	0.0258	0.3362
chr12	133851895	5021597	0.0375	0.3553
chr13	115169878	2286606	0.0199	0.2631
chr14	107349540	2799642	0.0261	0.2976
chr15	102531392	1991921	0.0194	0.25
chr16	90354753	5117953	0.0566	0.4629
chr17	81195210	2177484	0.0268	0.3004
chr18	78077248	3973018	0.0509	0.5175
chr19	59128983	1889611	0.032	0.3754
chr20	63025520	2087953	0.0331	0.3499
chr21	48129895	1175516	0.0244	0.2877
chr22	51304566	949084	0.0185	0.2536
chrMT	16571	16387	0.9889	1.5273
chrX	155270560	5359812	0.0345	0.3601
chrY	59373566	154548	0.0026	0.0822

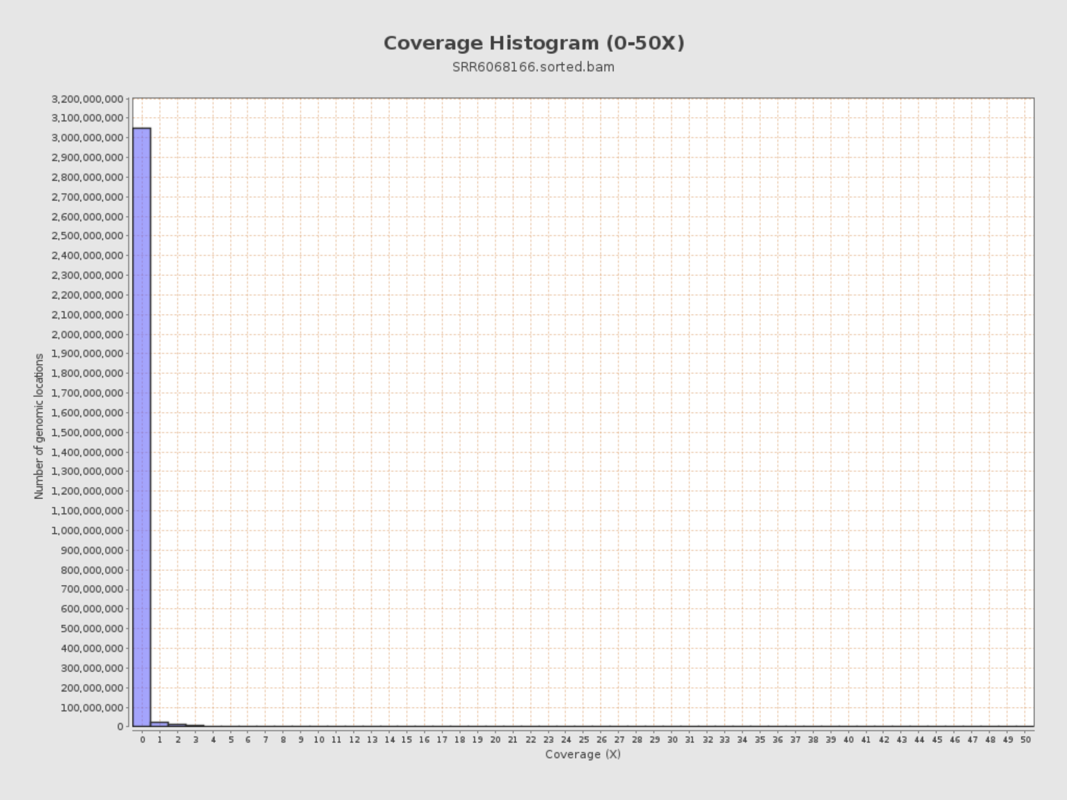
3. Results : Coverage across reference



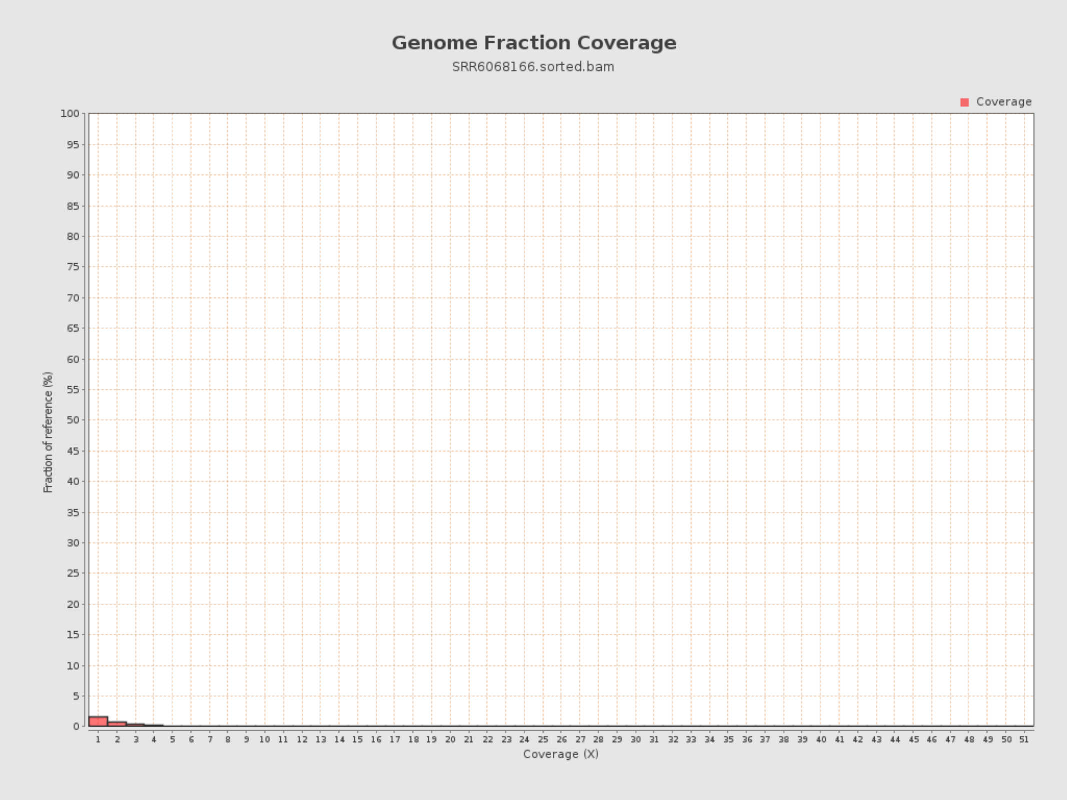
4. Results : Coverage Histogram



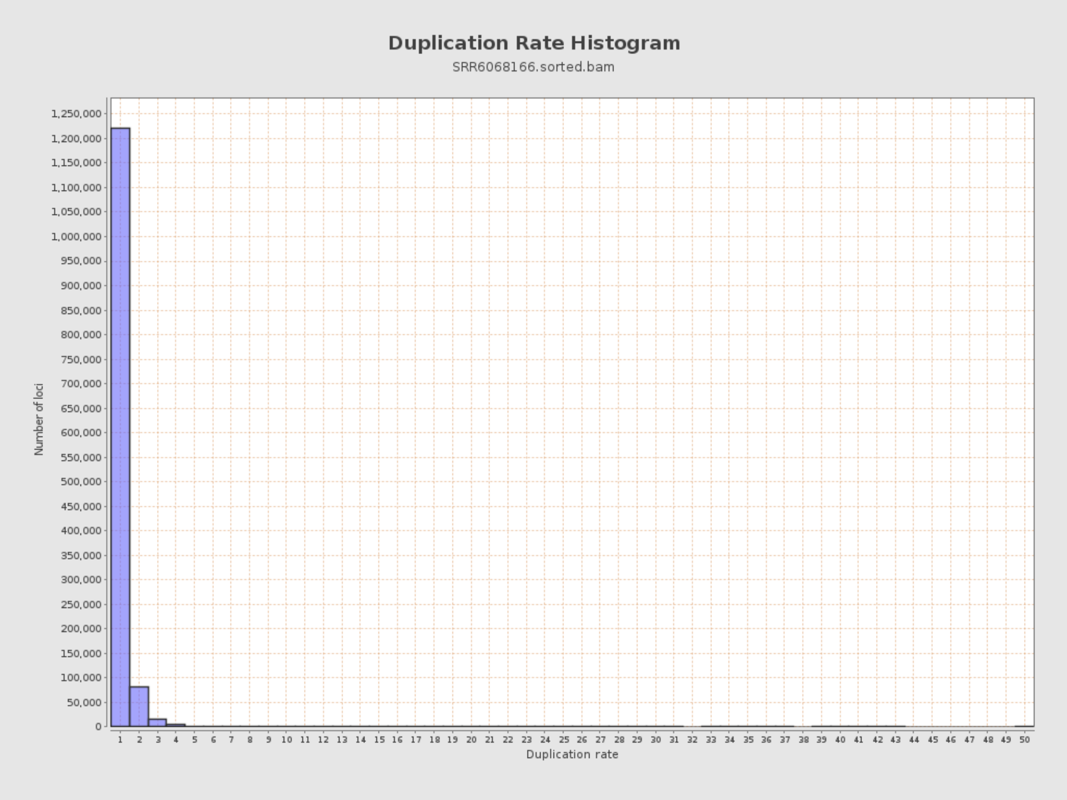
5. Results : Coverage Histogram (0-50X)



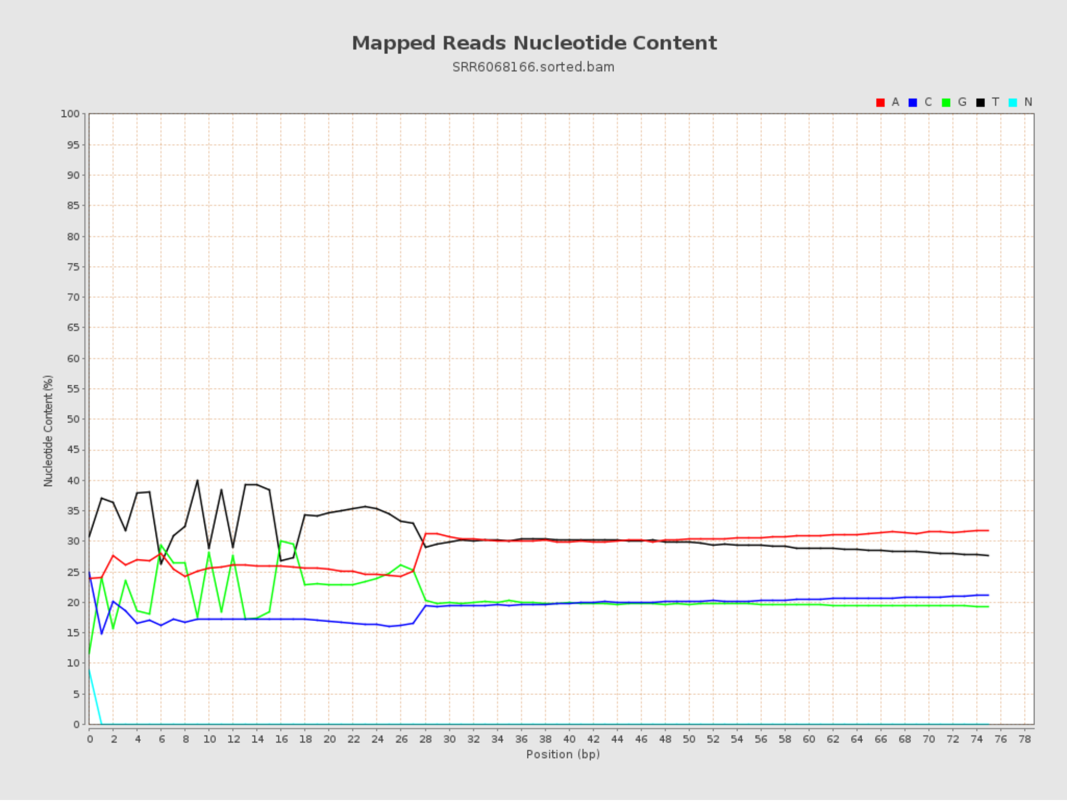
6. Results : Genome Fraction Coverage



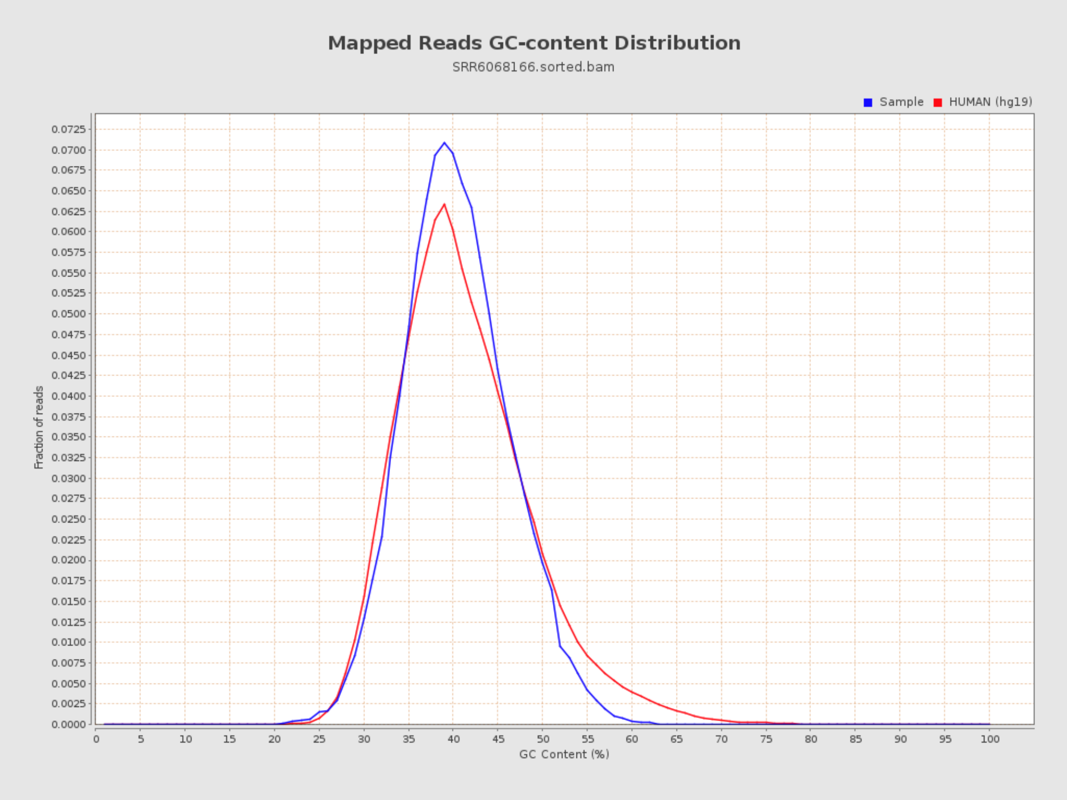
7. Results : Duplication Rate Histogram



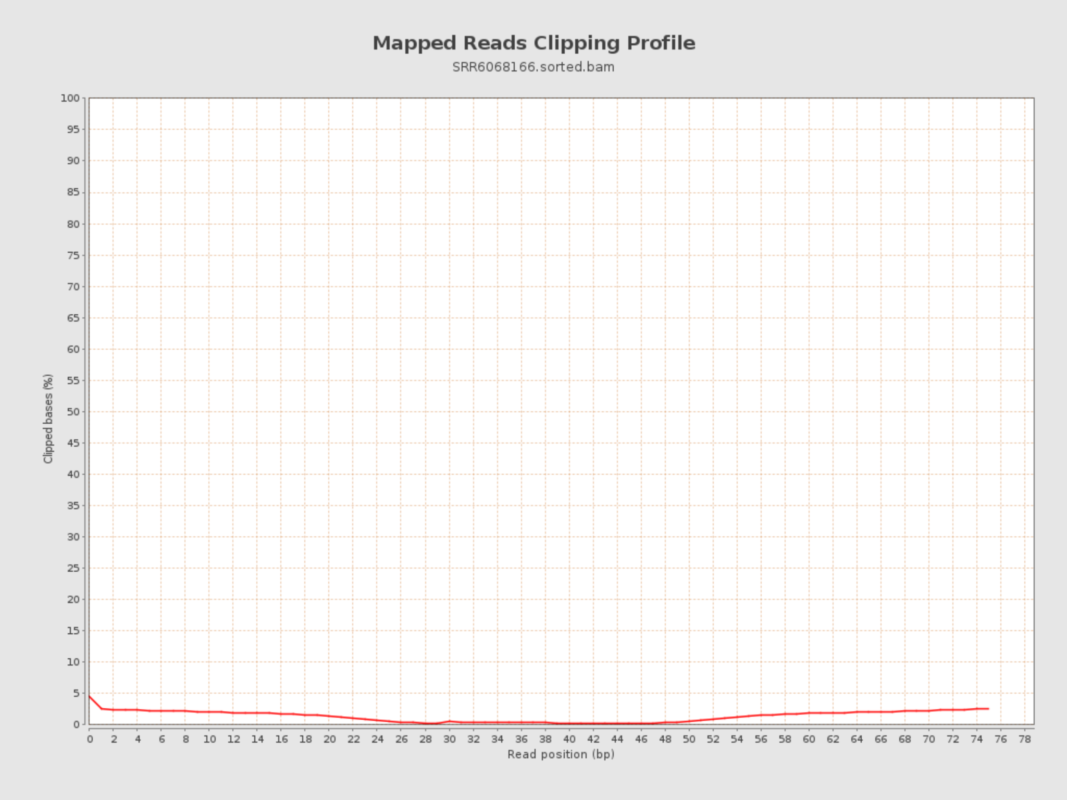
8. Results : Mapped Reads Nucleotide Content



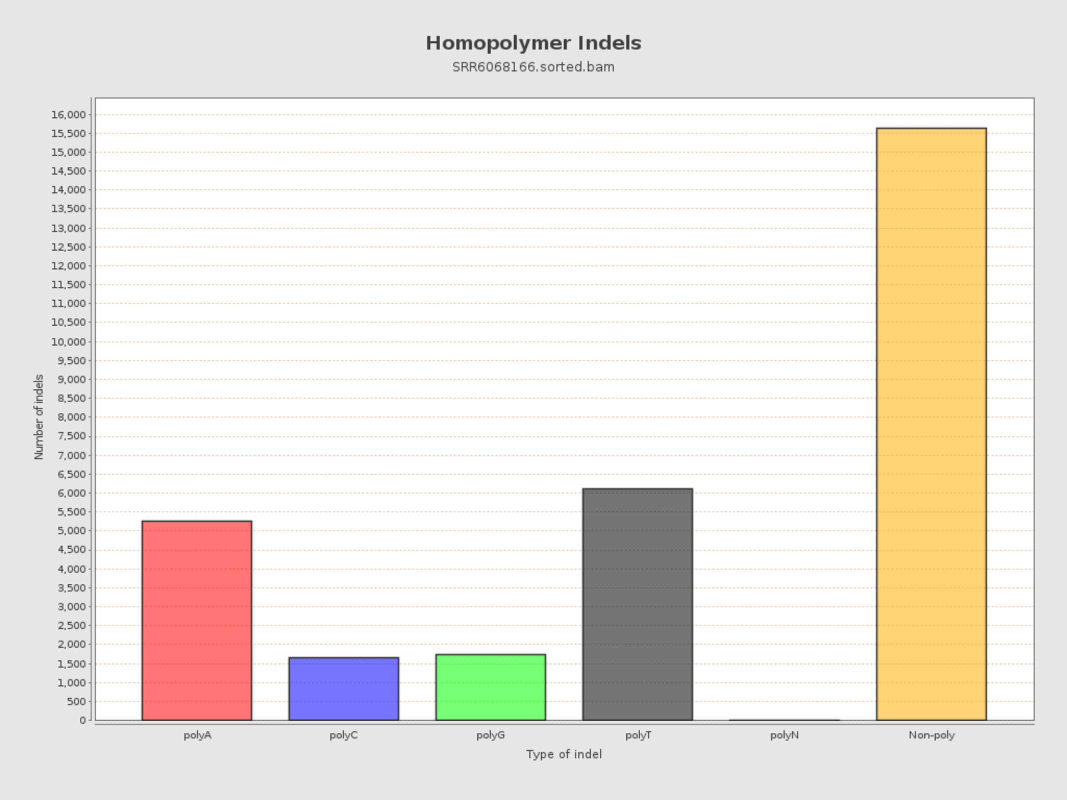
9. Results : Mapped Reads GC-content Distribution



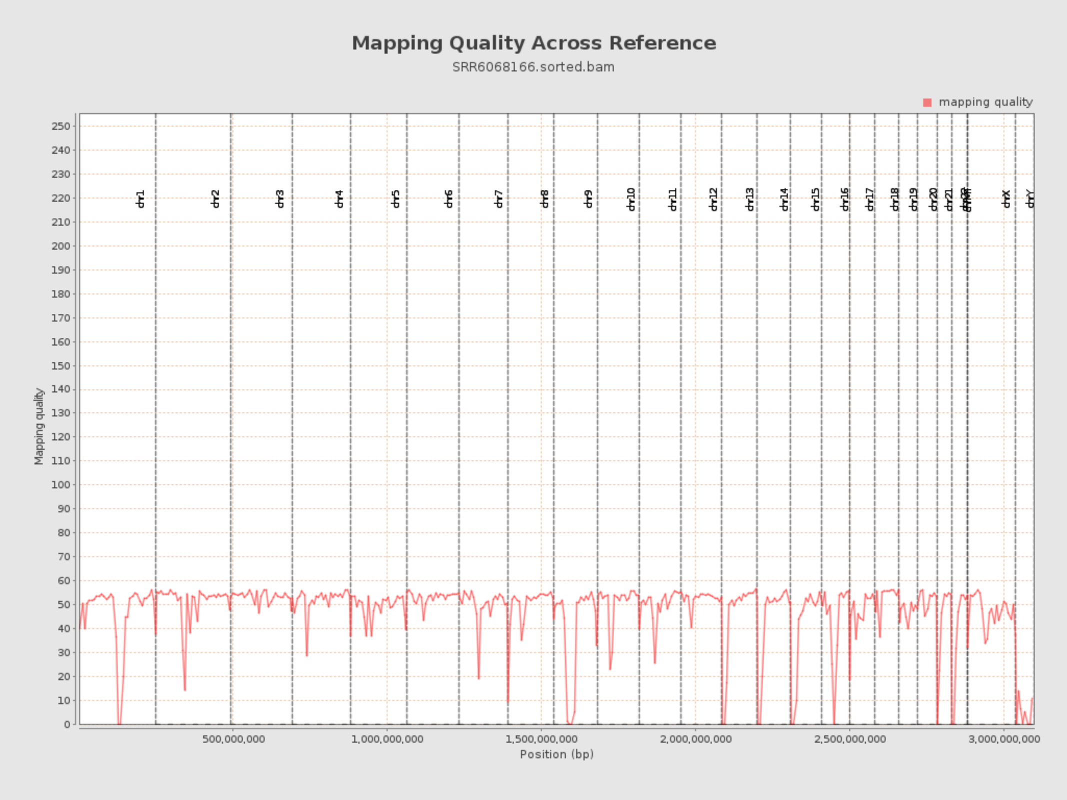
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram