Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:22:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068182.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_SRR6068182 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068182.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:22:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068182.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,544,993
Mapped reads	1,365,695 / 88.39%
Unmapped reads	179,298 / 11.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,443 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	149,532 / 9.68%
Duplication rate	8.68%
Clipped reads	628,180 / 40.66%

2.2. ACGT Content

Number/percentage of A's	25,902,400 / 28.38%
Number/percentage of C's	16,850,379 / 18.46%
Number/percentage of T's	28,997,318 / 31.78%
Number/percentage of G's	19,409,578 / 21.27%
Number/percentage of N's	96,863 / 0.11%
GC Percentage	39.73%

2.3. Coverage

Mean	0.0295

Standard Deviation	0.3326

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

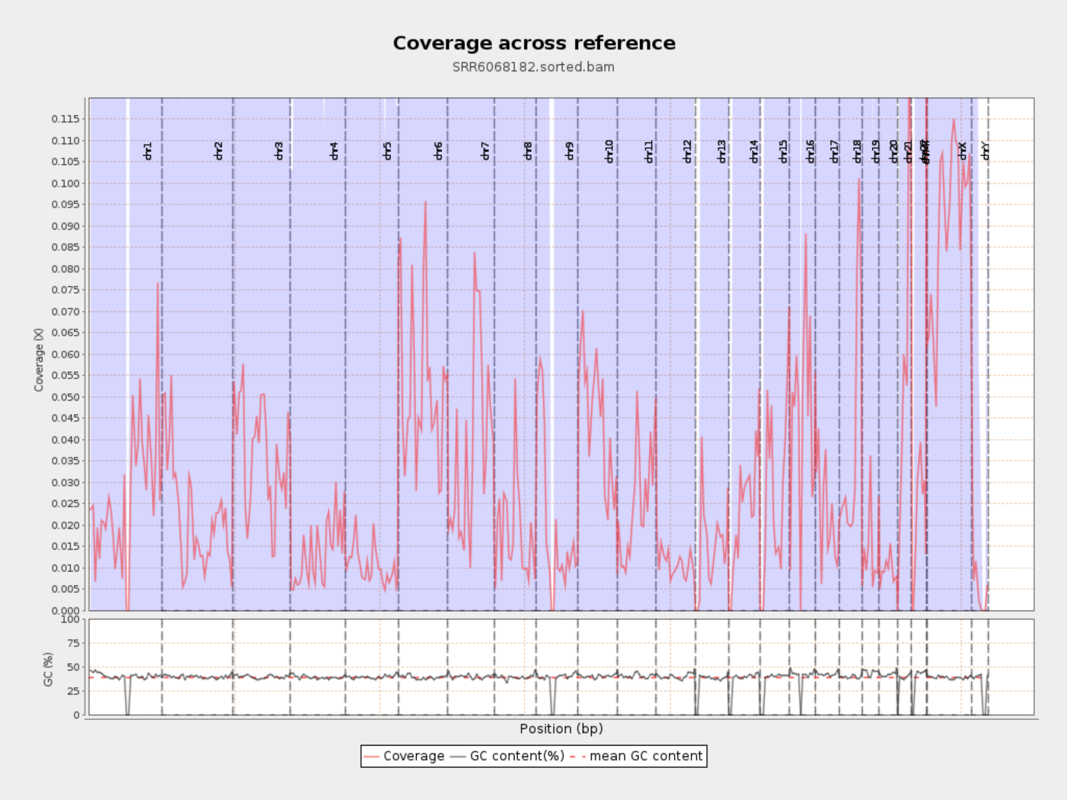
General error rate	0.85%
Mismatches	760,920
Insertions	6,275
Mapped reads with at least one insertion	0.46%
Deletions	24,080
Mapped reads with at least one deletion	1.74%
Homopolymer indels	47.2%

2.6. Chromosome stats

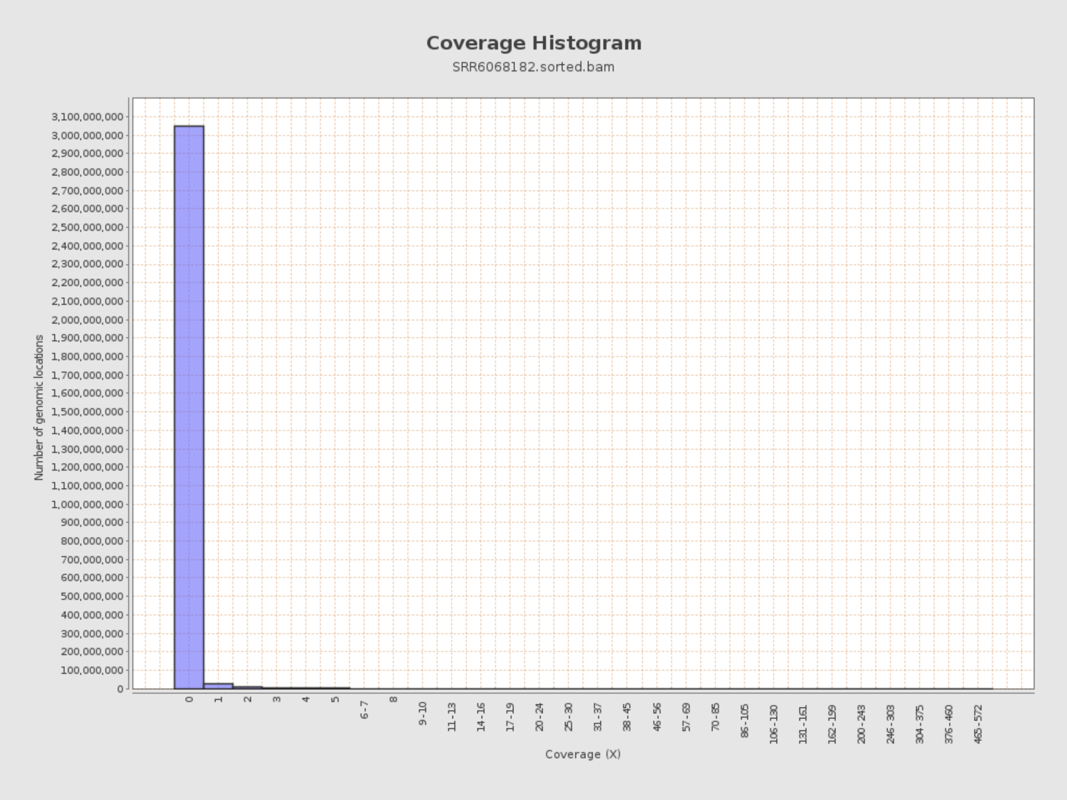
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6623051	0.0266	0.4853
chr2	243199373	5371409	0.0221	0.2879
chr3	198022430	7240691	0.0366	0.3157
chr4	191154276	2584597	0.0135	0.1936
chr5	180915260	1917621	0.0106	0.1626
chr6	171115067	9114679	0.0533	0.3979
chr7	159138663	6042259	0.038	0.4119

chr8	146364022	2663210	0.0182	0.404
chr9	141213431	2839737	0.0201	0.2557
chr10	135534747	6243504	0.0461	0.3788
chr11	135006516	3363663	0.0249	0.2754
chr12	133851895	1478168	0.011	0.1733
chr13	115169878	1647888	0.0143	0.1951
chr14	107349540	2460299	0.0229	0.2479
chr15	102531392	2776860	0.0271	0.2631
chr16	90354753	4099482	0.0454	0.3449
chr17	81195210	1806116	0.0222	0.2392
chr18	78077248	3106730	0.0398	0.4157
chr19	59128983	845072	0.0143	0.3123
chr20	63025520	597136	0.0095	0.1635
chr21	48129895	2814349	0.0585	0.4025
chr22	51304566	1112519	0.0217	0.2295
chrMT	16571	4621	0.2789	0.7676
chrX	155270560	14206594	0.0915	0.5317
chrY	59373566	336636	0.0057	0.1365

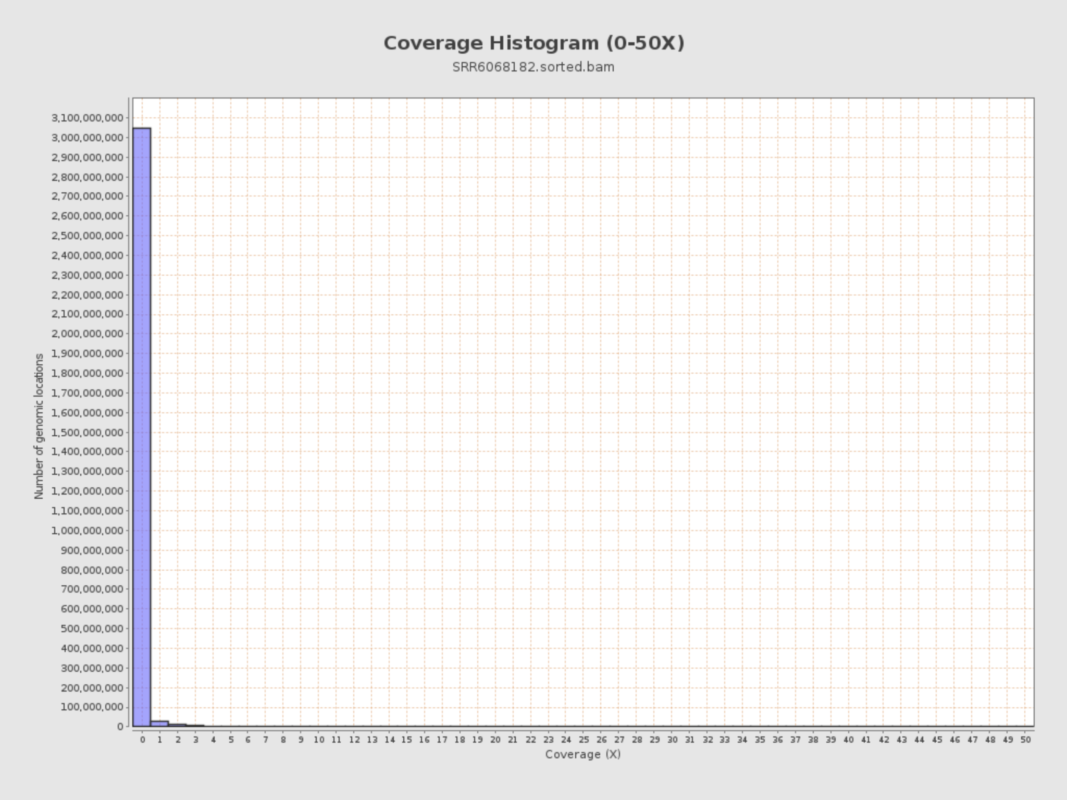
3. Results : Coverage across reference



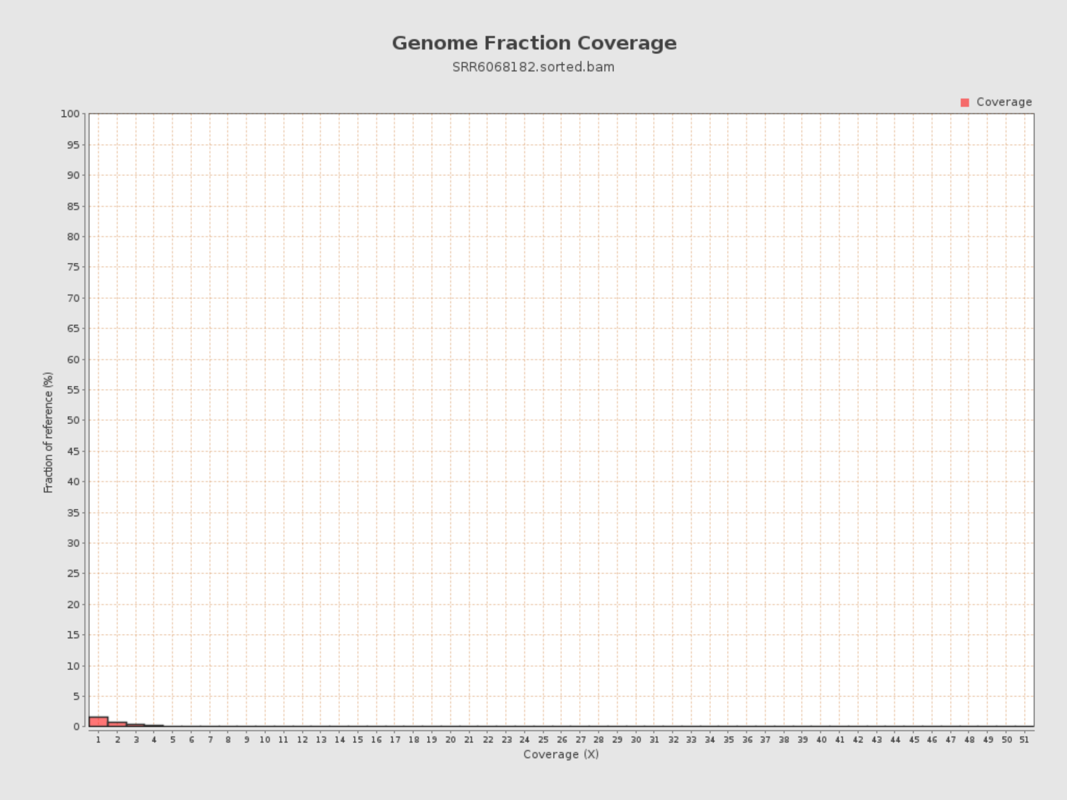
4. Results : Coverage Histogram



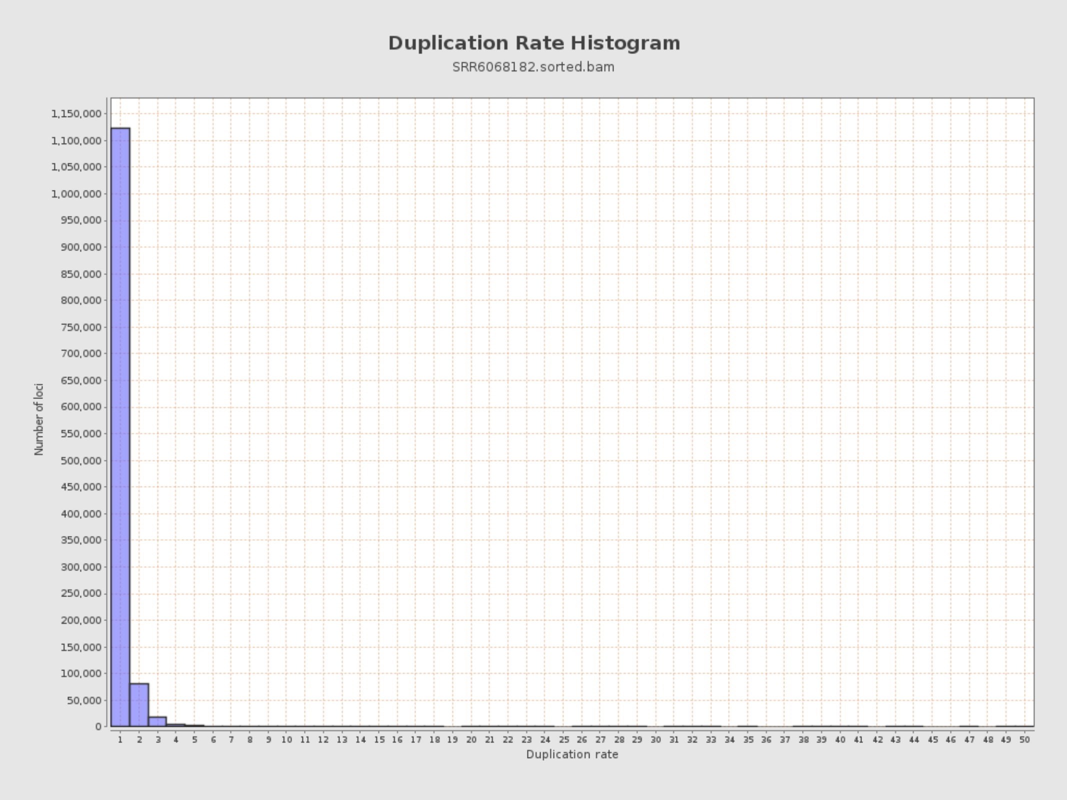
5. Results : Coverage Histogram (0-50X)



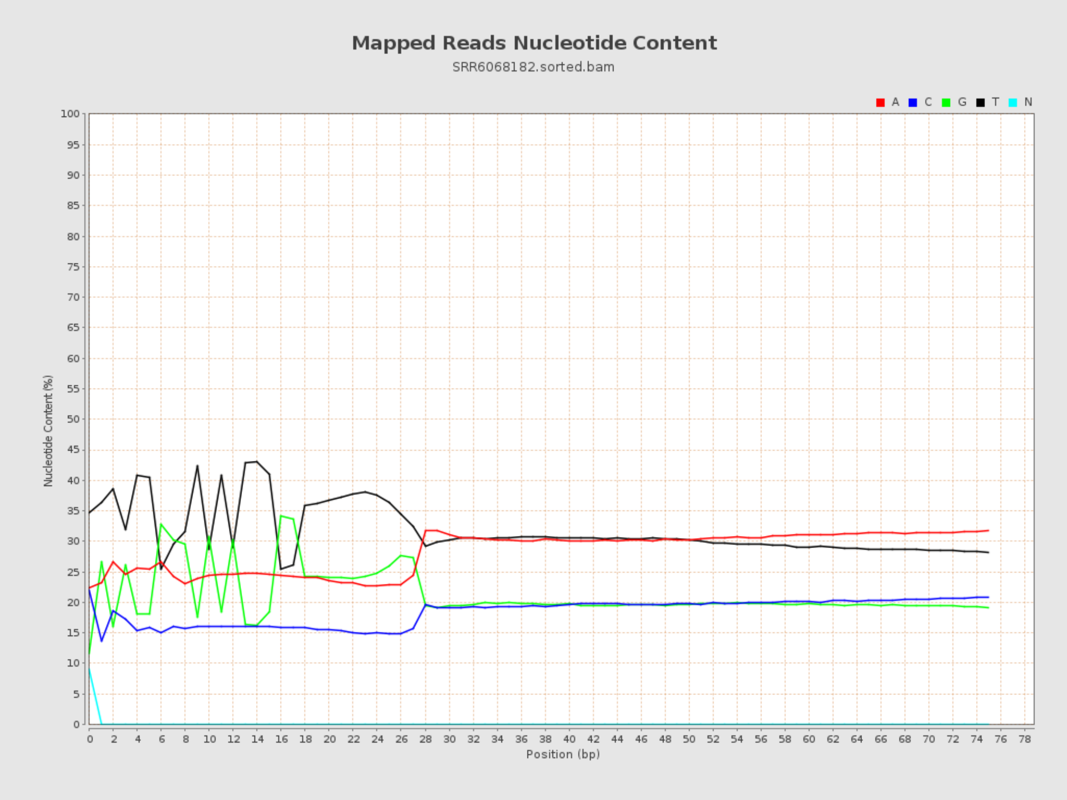
6. Results : Genome Fraction Coverage



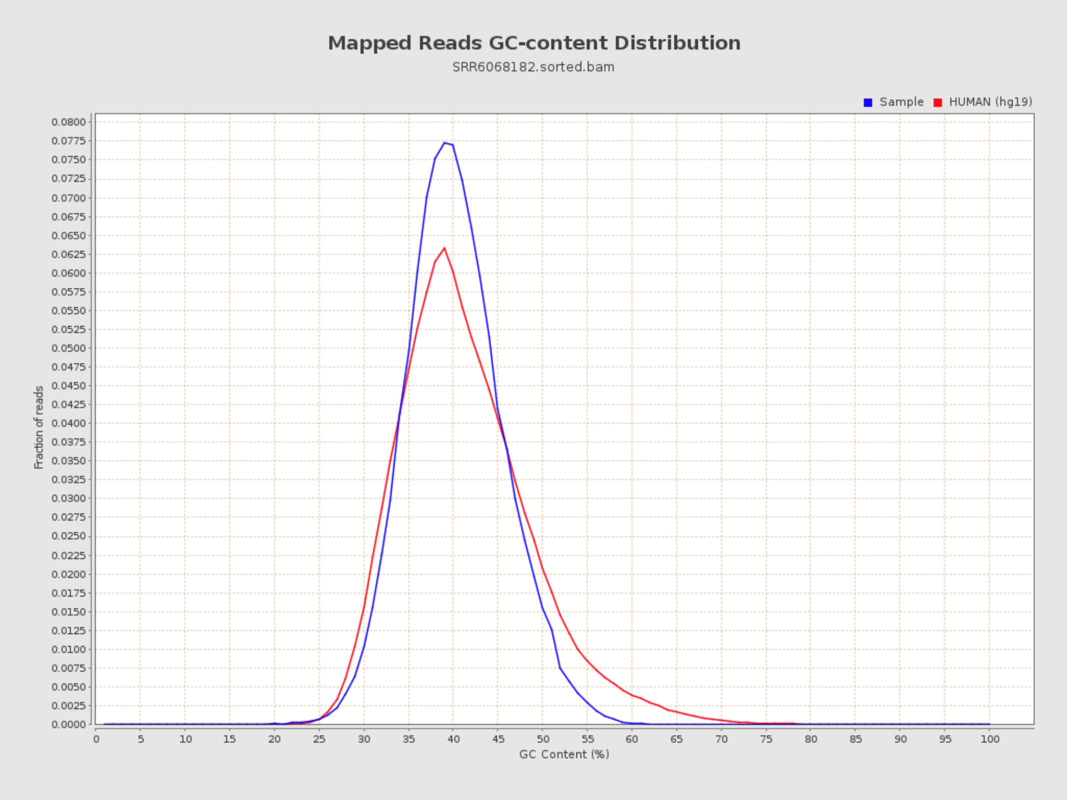
7. Results : Duplication Rate Histogram



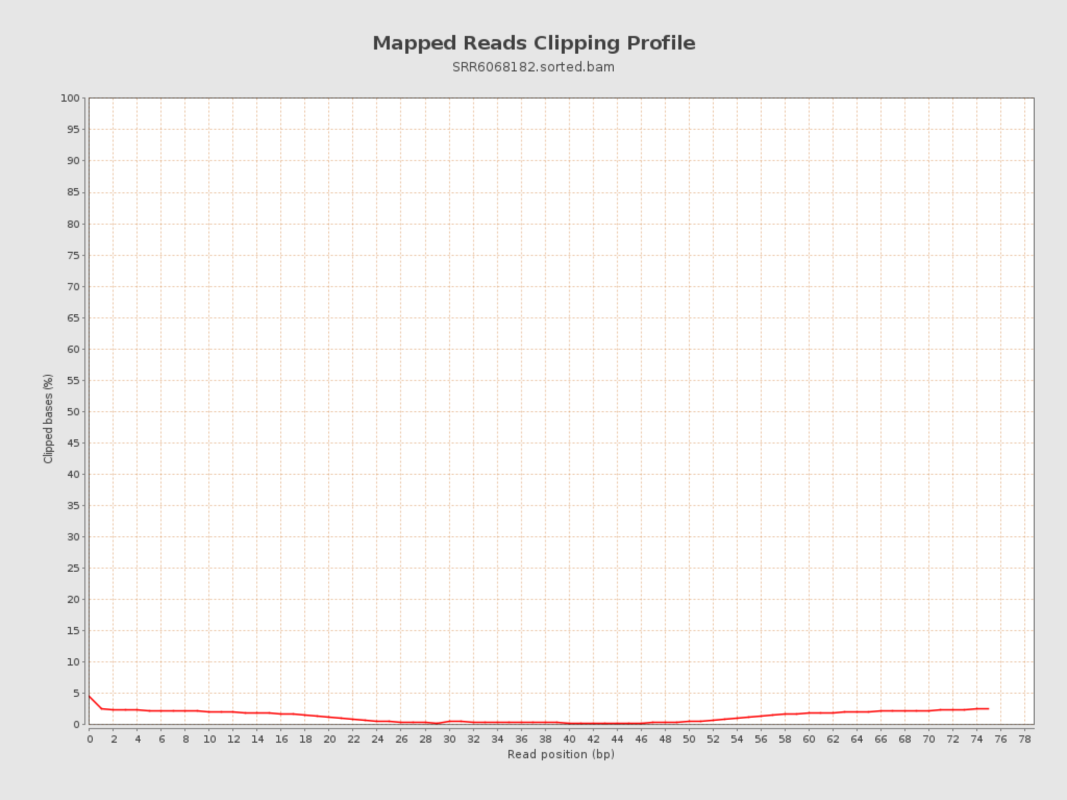
8. Results : Mapped Reads Nucleotide Content



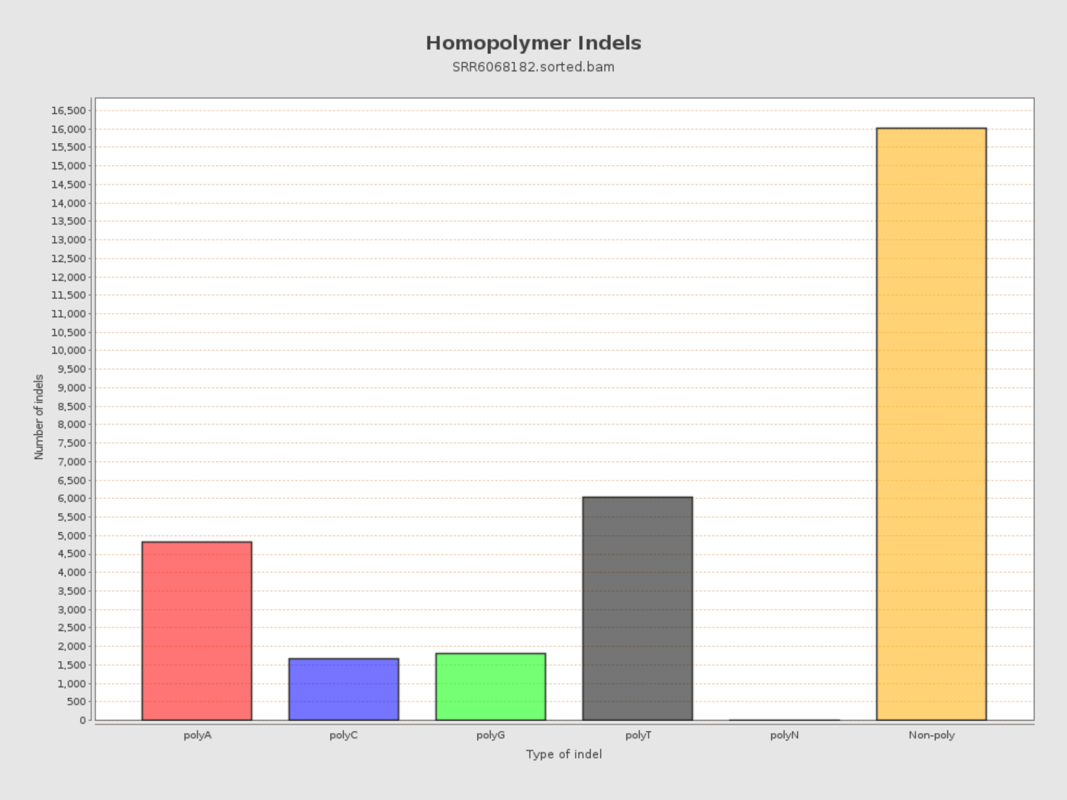
9. Results : Mapped Reads GC-content Distribution



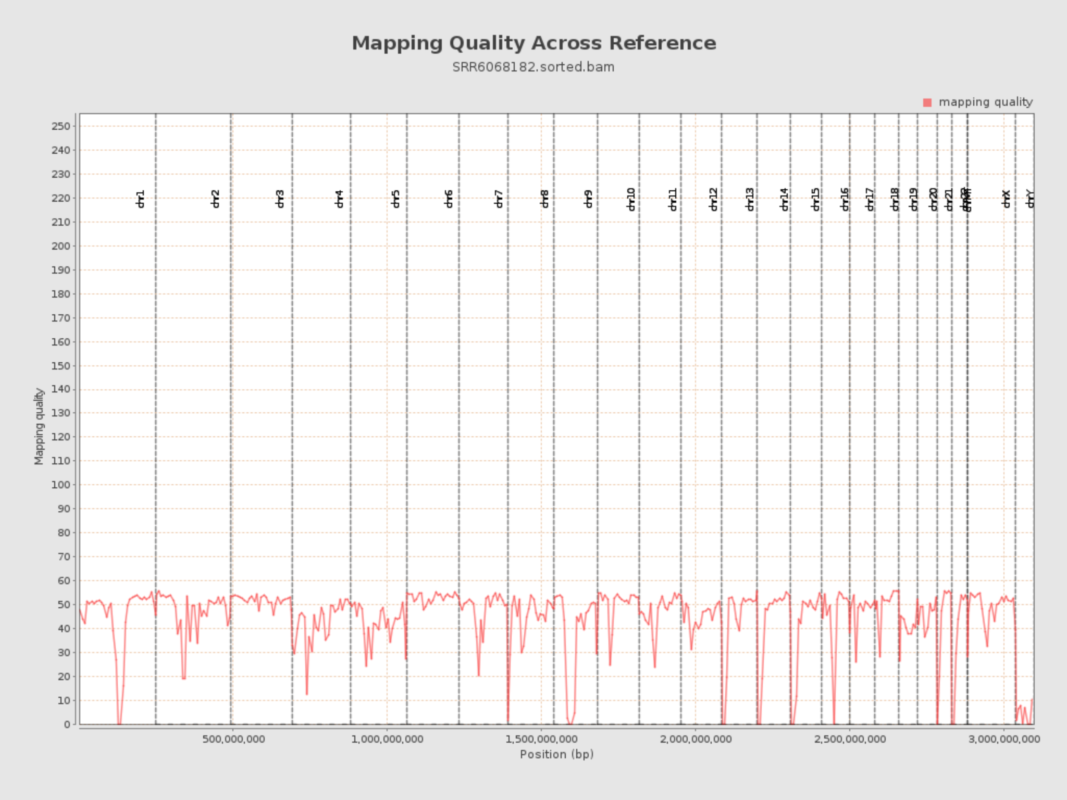
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram