Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:00:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068114.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_SRR6068114 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:00:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,418,555
Mapped reads	650,242 / 45.84%
Unmapped reads	768,313 / 54.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,770 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	134,961 / 9.51%
Duplication rate	12.83%
Clipped reads	384,490 / 27.1%

2.2. ACGT Content

Number/percentage of A's	10,647,107 / 26.24%
Number/percentage of C's	7,163,652 / 17.66%
Number/percentage of T's	13,148,380 / 32.41%
Number/percentage of G's	9,573,411 / 23.6%
Number/percentage of N's	36,319 / 0.09%
GC Percentage	41.26%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.2976

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

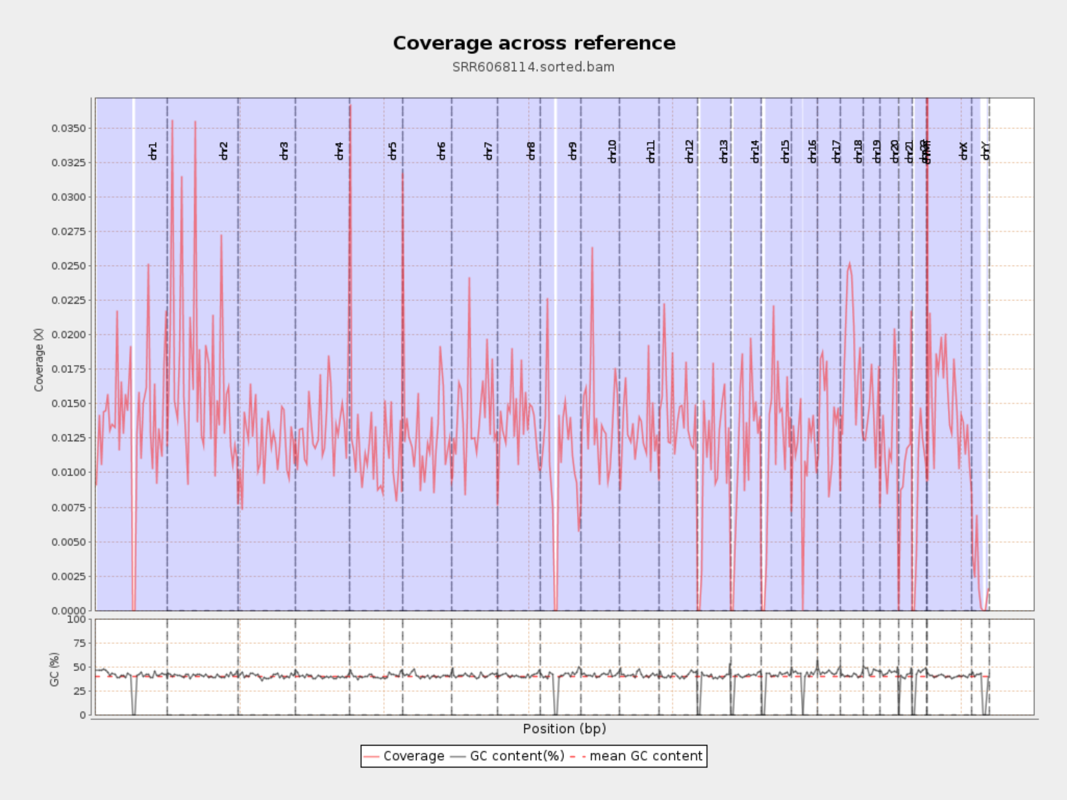
General error rate	0.97%
Mismatches	387,413
Insertions	3,036
Mapped reads with at least one insertion	0.46%
Deletions	9,587
Mapped reads with at least one deletion	1.46%
Homopolymer indels	46.16%

2.6. Chromosome stats

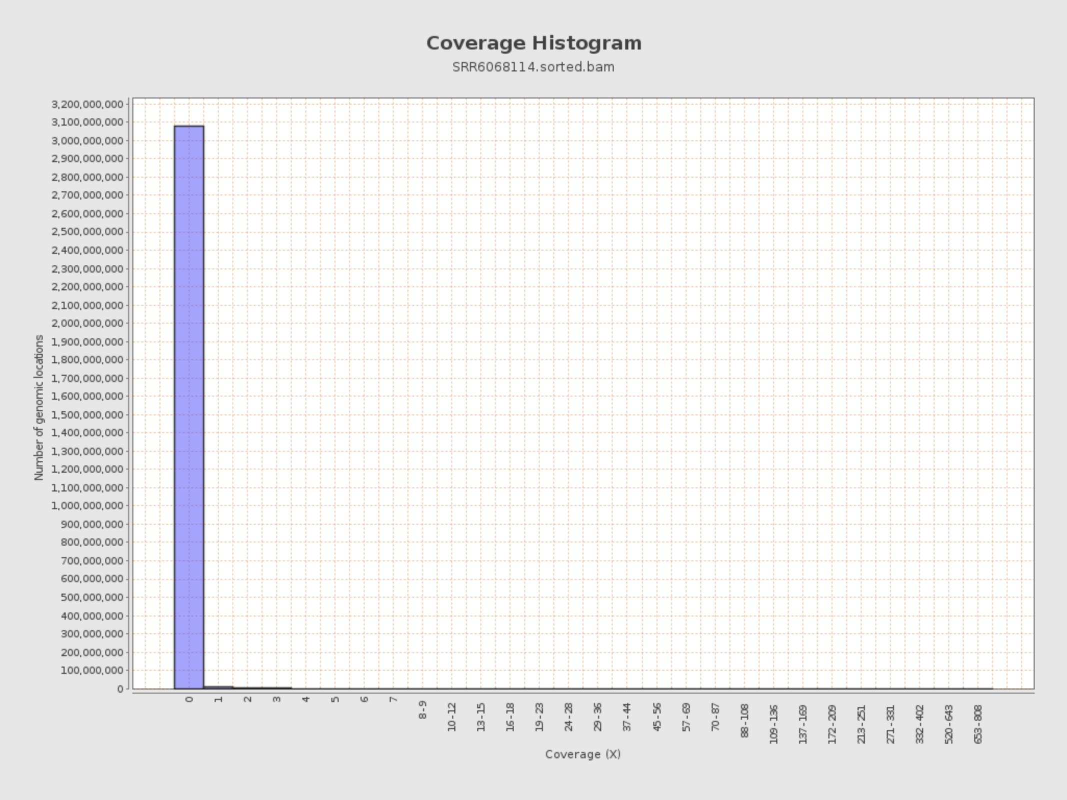
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3420456	0.0137	0.3016
chr2	243199373	4157150	0.0171	0.362
chr3	198022430	2417132	0.0122	0.2365
chr4	191154276	2565939	0.0134	0.4154
chr5	180915260	2070496	0.0114	0.2247
chr6	171115067	2215182	0.0129	0.2818
chr7	159138663	2270884	0.0143	0.2814

chr8	146364022	2019154	0.0138	0.2773
chr9	141213431	1518461	0.0108	0.2376
chr10	135534747	1896694	0.014	0.2781
chr11	135006516	1766517	0.0131	0.2446
chr12	133851895	1950980	0.0146	0.2588
chr13	115169878	1230101	0.0107	0.243
chr14	107349540	1227816	0.0114	0.2897
chr15	102531392	1216358	0.0119	0.5537
chr16	90354753	995952	0.011	0.2312
chr17	81195210	1148848	0.0141	0.2446
chr18	78077248	1468994	0.0188	0.3396
chr19	59128983	837043	0.0142	0.305
chr20	63025520	803541	0.0127	0.2515
chr21	48129895	512655	0.0107	0.211
chr22	51304566	431983	0.0084	0.2079
chrMT	16571	17304	1.0442	2.2289
chrX	155270560	2306556	0.0149	0.2835
chrY	59373566	118441	0.002	0.1349

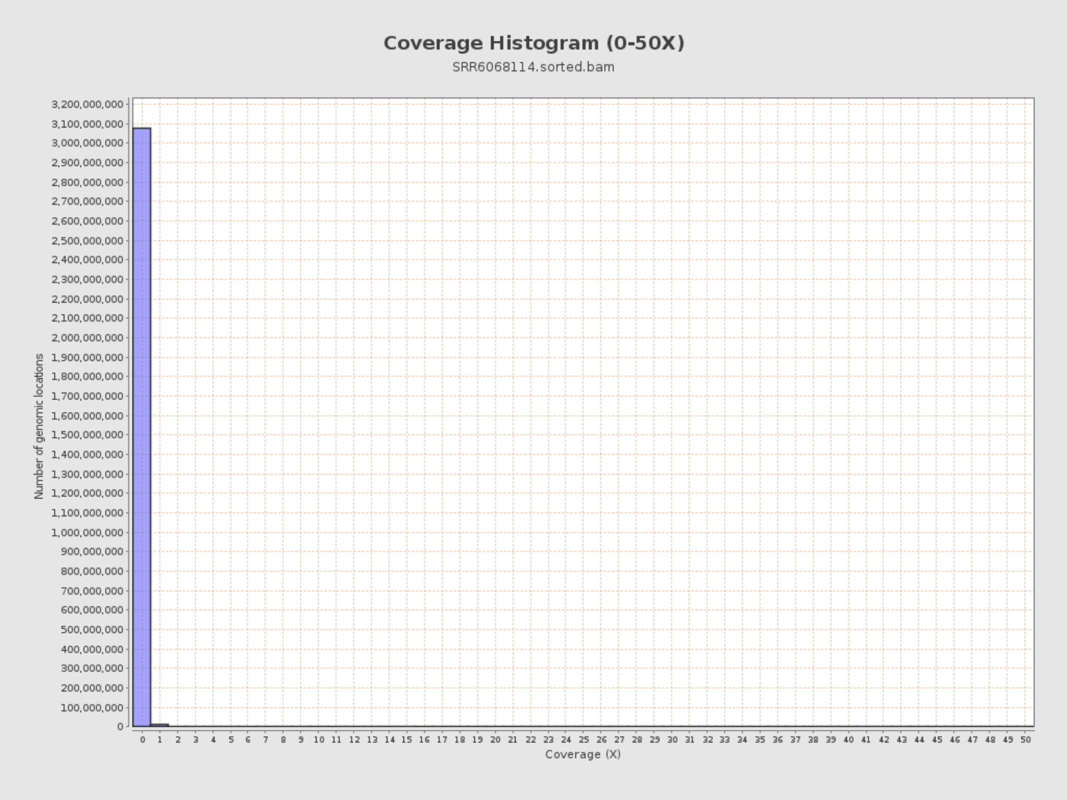
3. Results : Coverage across reference



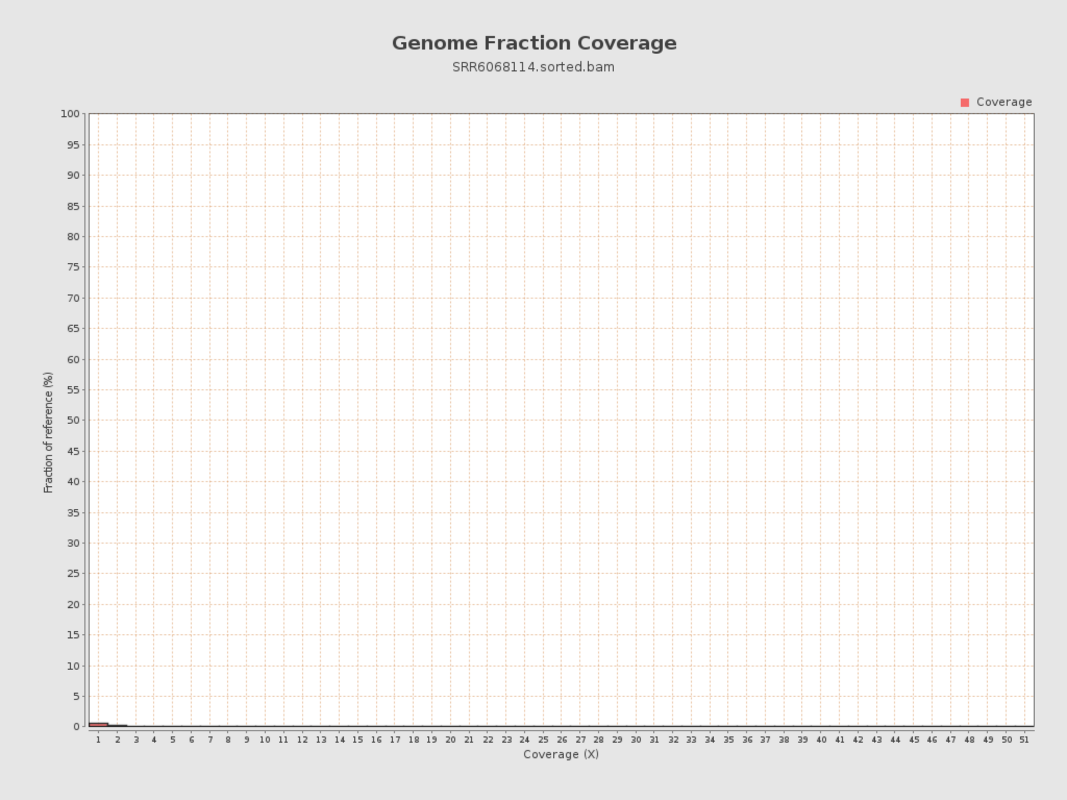
4. Results : Coverage Histogram



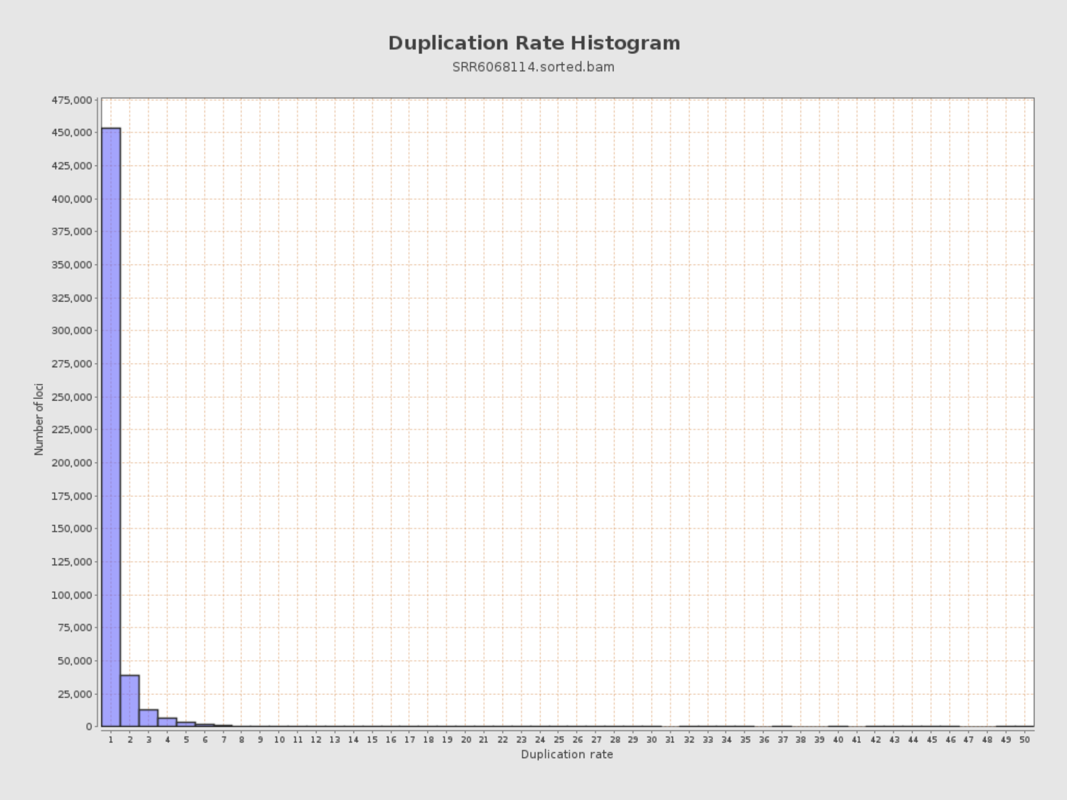
5. Results : Coverage Histogram (0-50X)



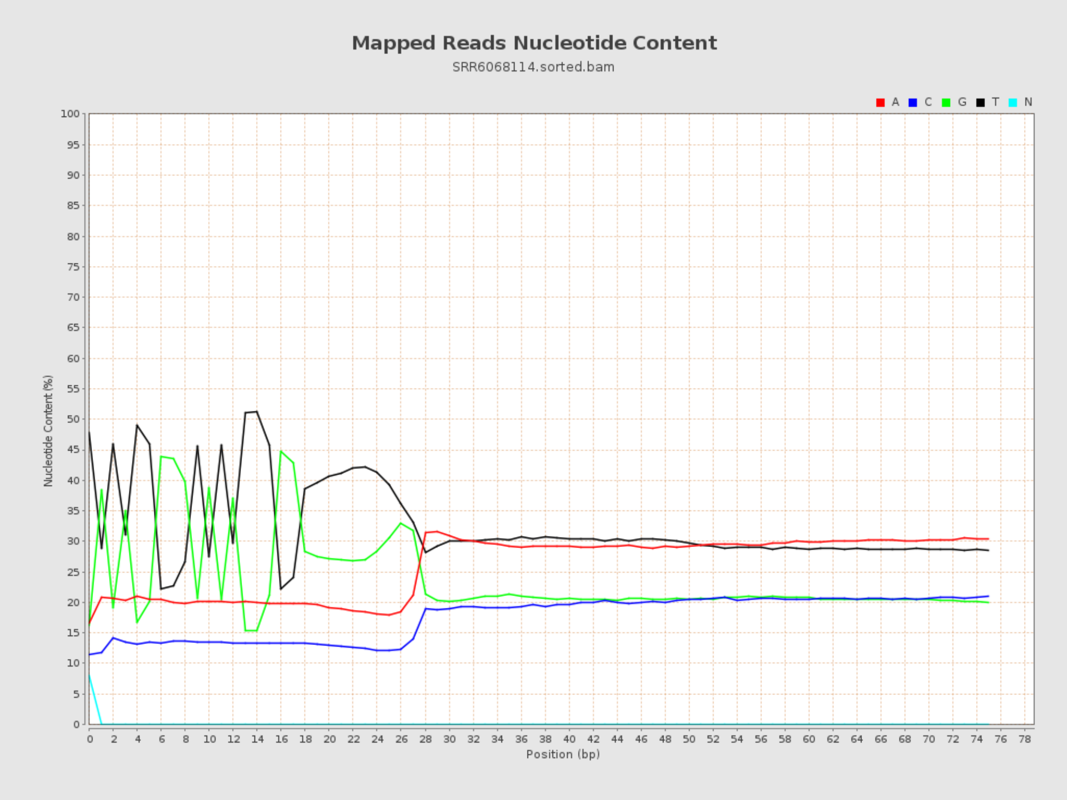
6. Results : Genome Fraction Coverage



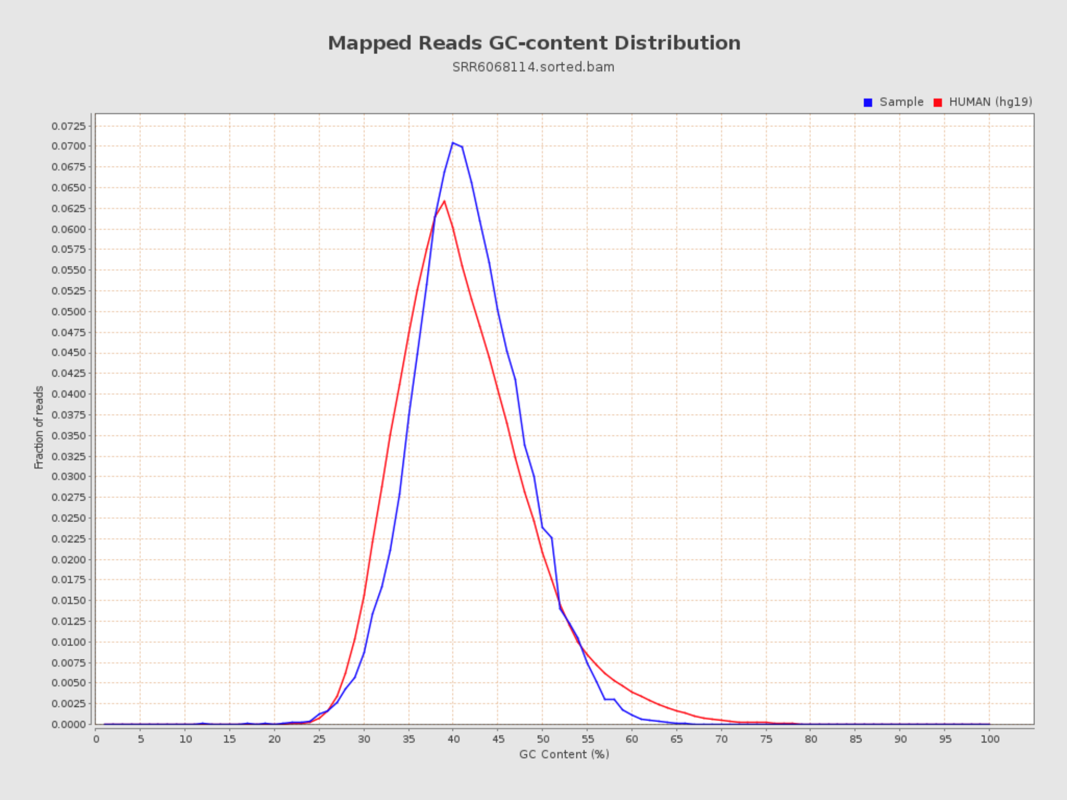
7. Results : Duplication Rate Histogram



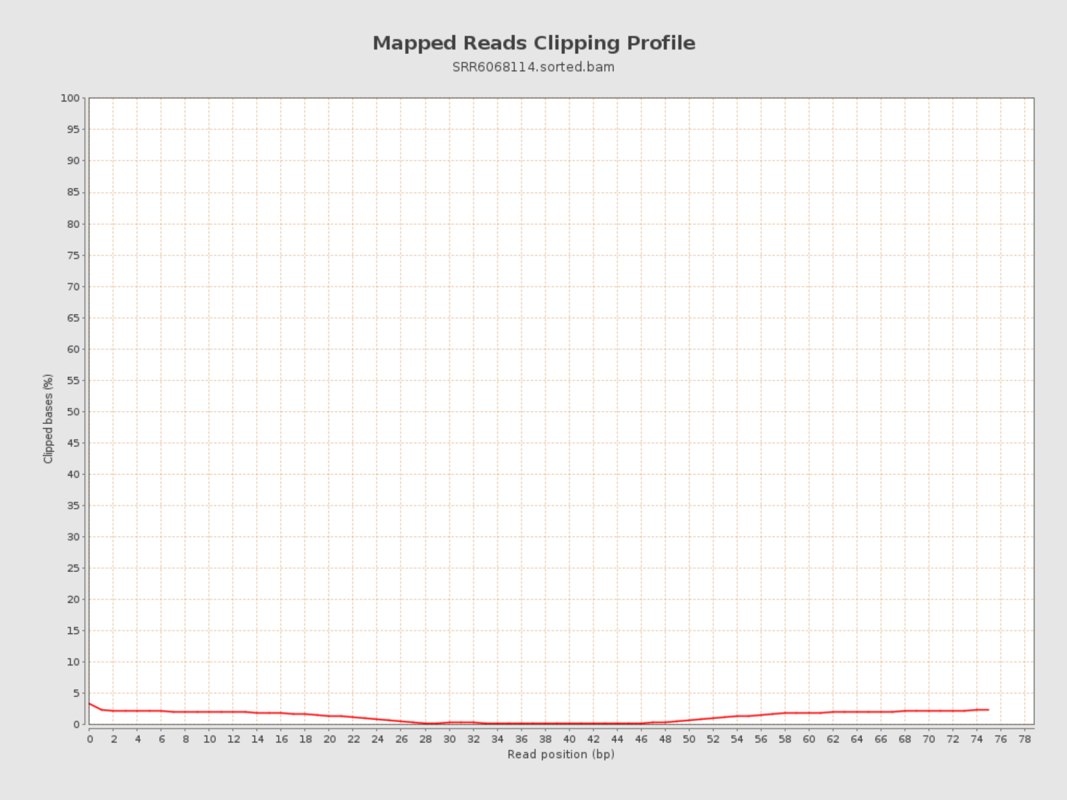
8. Results : Mapped Reads Nucleotide Content



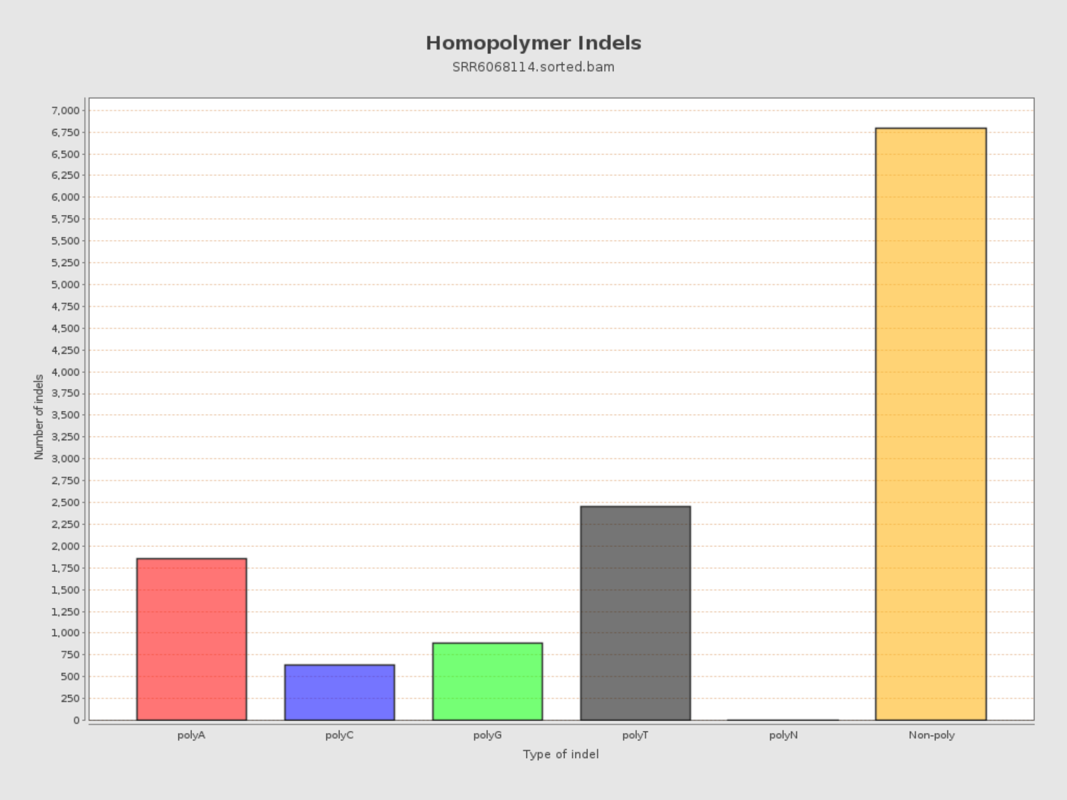
9. Results : Mapped Reads GC-content Distribution



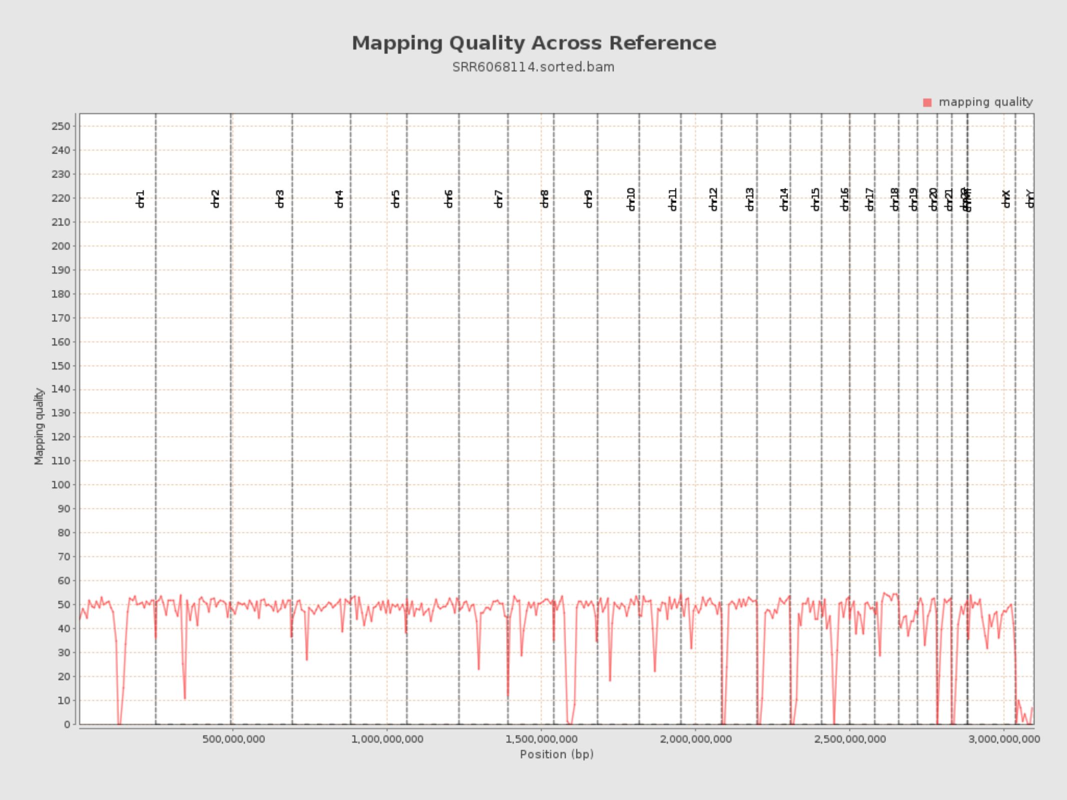
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram