Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:44:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085114.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_SRR3085114 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:43:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,192,137
Mapped reads	988,428 / 82.91%
Unmapped reads	203,709 / 17.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,748 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	17,412 / 1.46%
Duplication rate	1.47%
Clipped reads	564,571 / 47.36%

2.2. ACGT Content

Number/percentage of A's	18,839,937 / 29.83%
Number/percentage of C's	12,118,071 / 19.19%
Number/percentage of T's	18,334,631 / 29.03%
Number/percentage of G's	13,866,016 / 21.95%
Number/percentage of N's	1,277 / 0%
GC Percentage	41.14%

2.3. Coverage

Mean	0.0204

Standard Deviation	0.1818

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

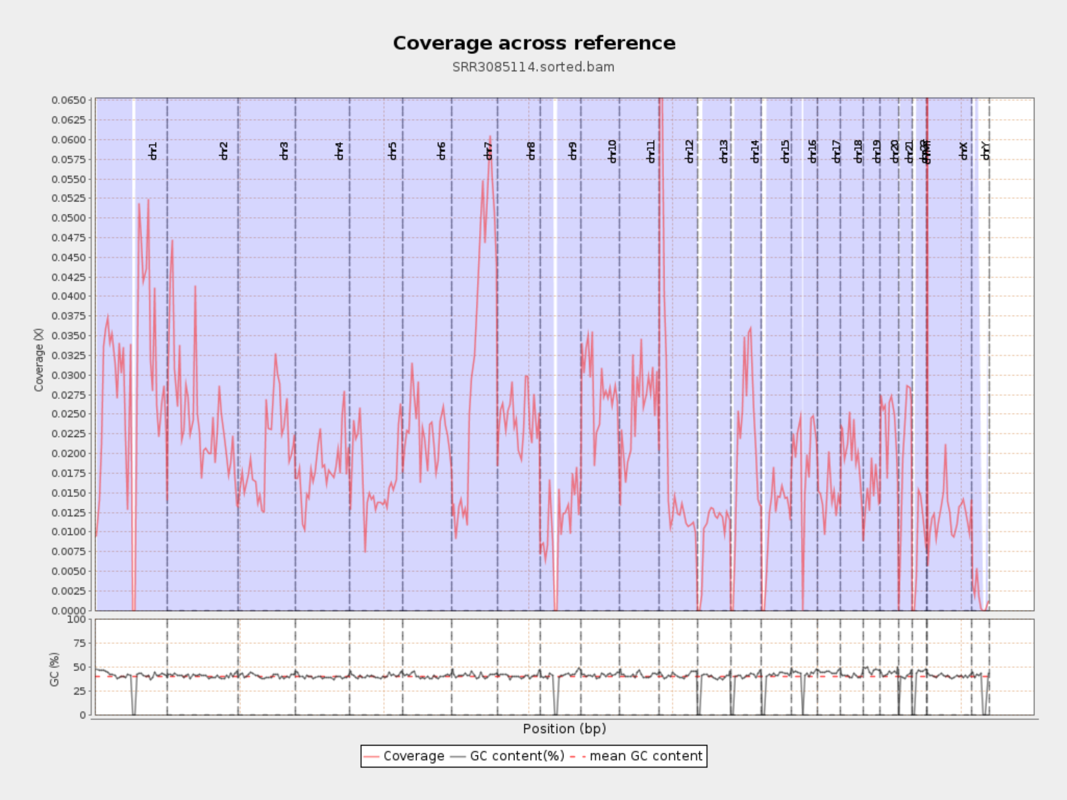
General error rate	0.92%
Mismatches	575,602
Insertions	4,978
Mapped reads with at least one insertion	0.5%
Deletions	14,032
Mapped reads with at least one deletion	1.4%
Homopolymer indels	45.18%

2.6. Chromosome stats

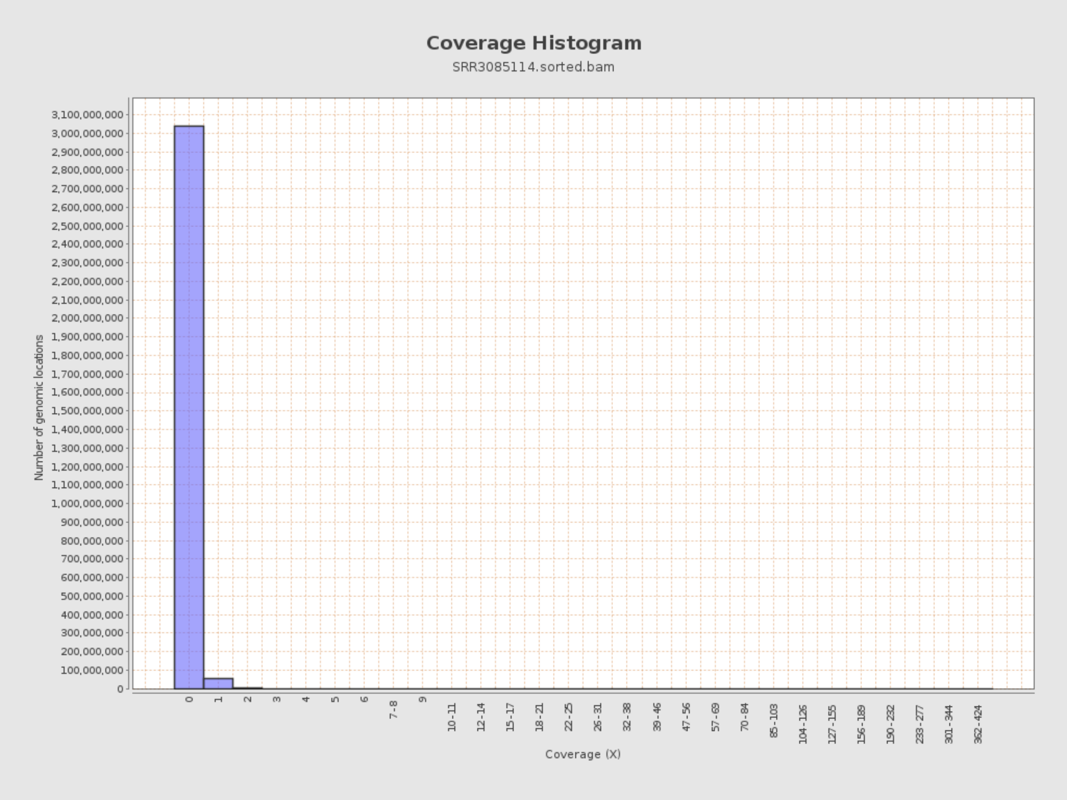
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7278923	0.0292	0.2743
chr2	243199373	6070038	0.025	0.2003
chr3	198022430	4046813	0.0204	0.1502
chr4	191154276	3453137	0.0181	0.1401
chr5	180915260	3091589	0.0171	0.1358
chr6	171115067	3871085	0.0226	0.1689
chr7	159138663	5219890	0.0328	0.2103

chr8	146364022	3597012	0.0246	0.2925
chr9	141213431	1514966	0.0107	0.1355
chr10	135534747	3811843	0.0281	0.2235
chr11	135006516	3475606	0.0257	0.194
chr12	133851895	2887094	0.0216	0.1563
chr13	115169878	1141572	0.0099	0.1029
chr14	107349540	2236793	0.0208	0.1516
chr15	102531392	1181410	0.0115	0.1111
chr16	90354753	1737023	0.0192	0.1482
chr17	81195210	1161611	0.0143	0.1317
chr18	78077248	1599807	0.0205	0.2243
chr19	59128983	886626	0.015	0.1835
chr20	63025520	1504768	0.0239	0.1618
chr21	48129895	975285	0.0203	0.1495
chr22	51304566	445020	0.0087	0.0962
chrMT	16571	5271	0.3181	0.6336
chrX	155270560	1889612	0.0122	0.1235
chrY	59373566	99867	0.0017	0.0467

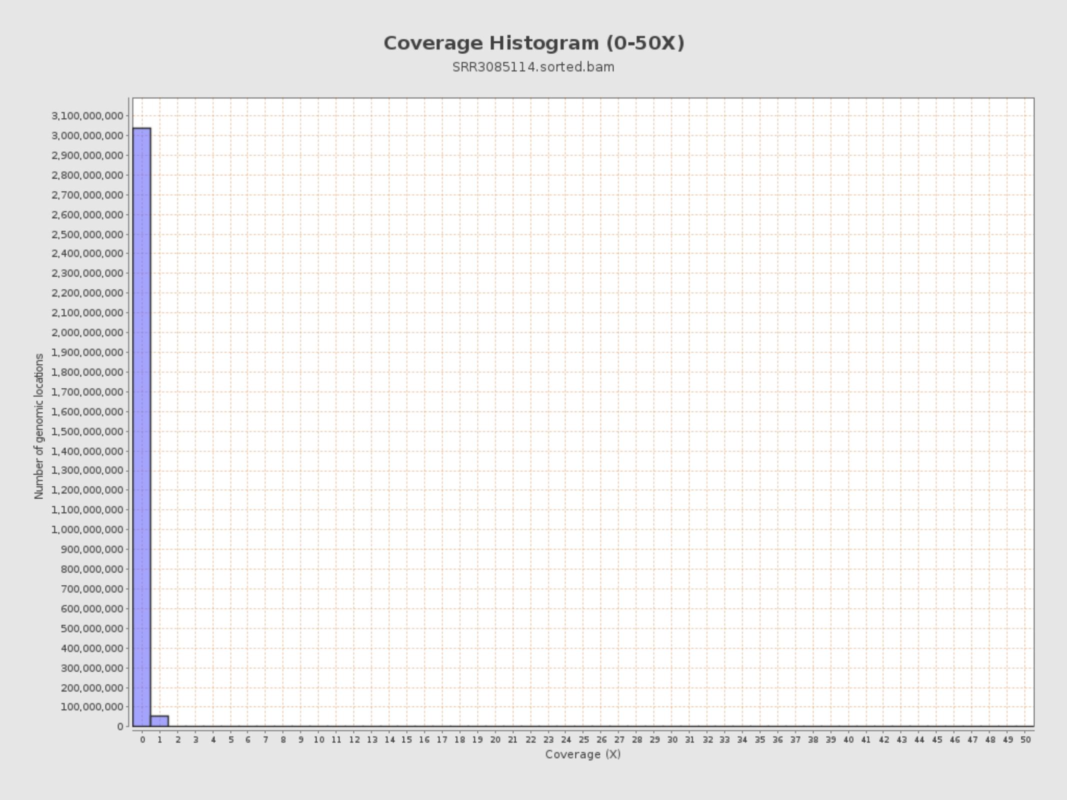
3. Results : Coverage across reference



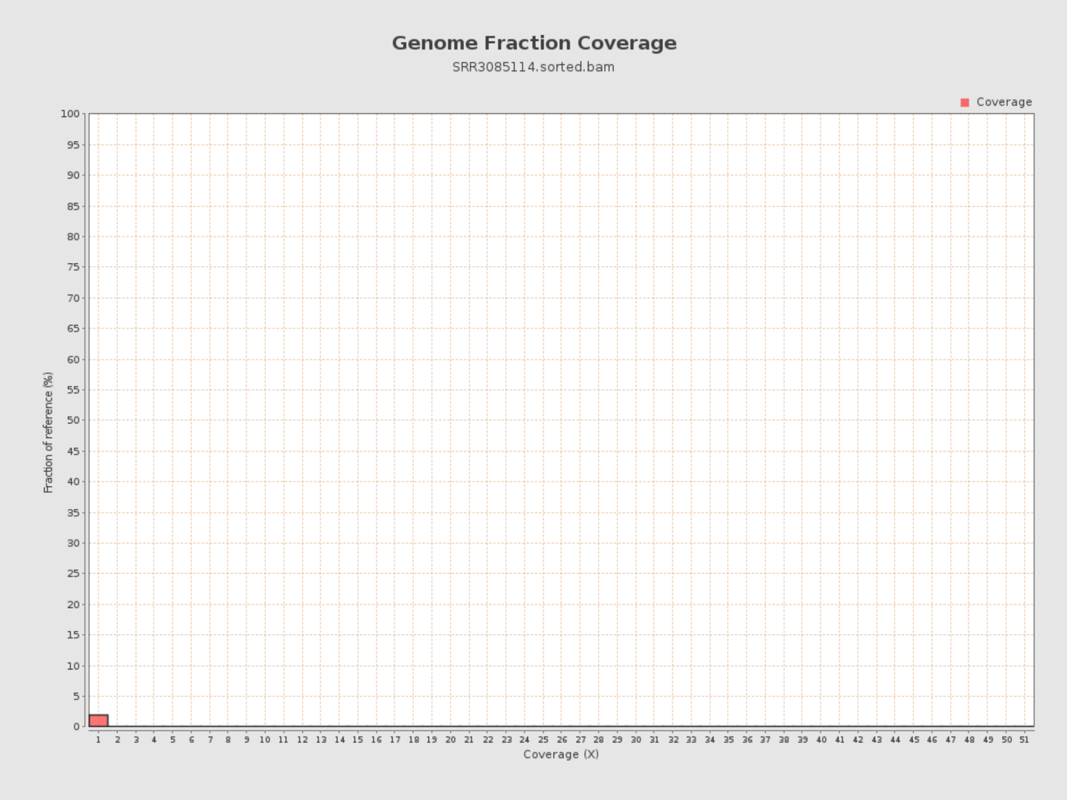
4. Results : Coverage Histogram



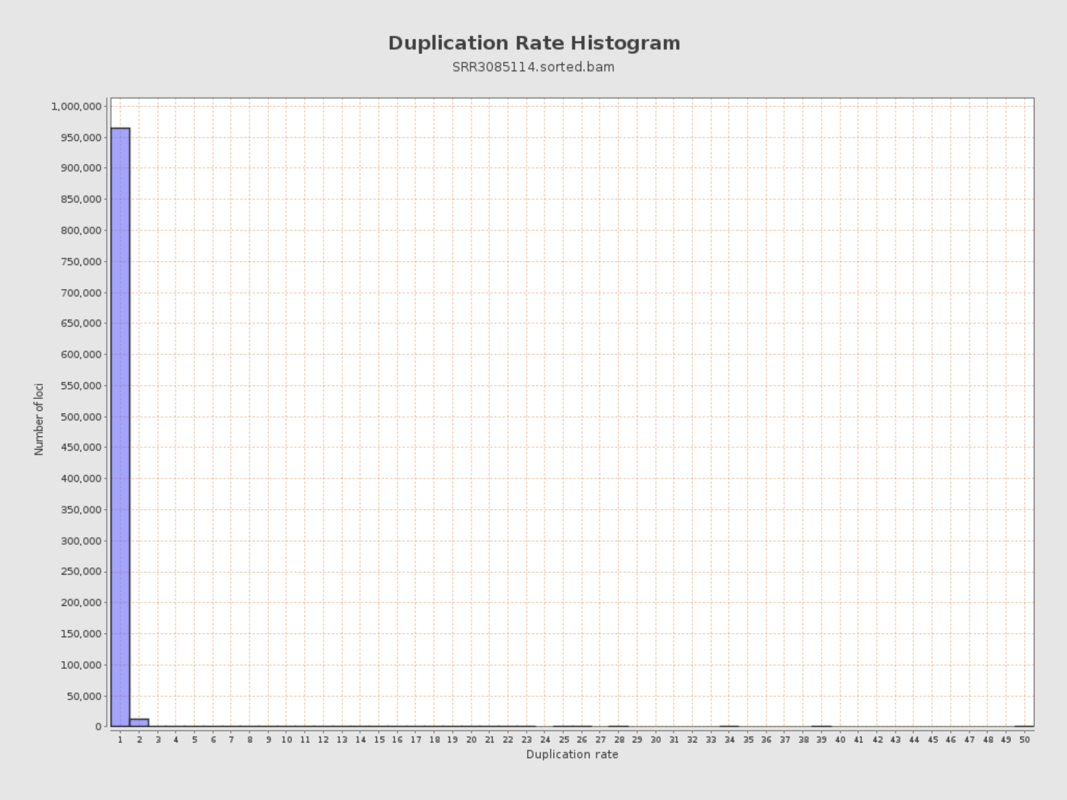
5. Results : Coverage Histogram (0-50X)



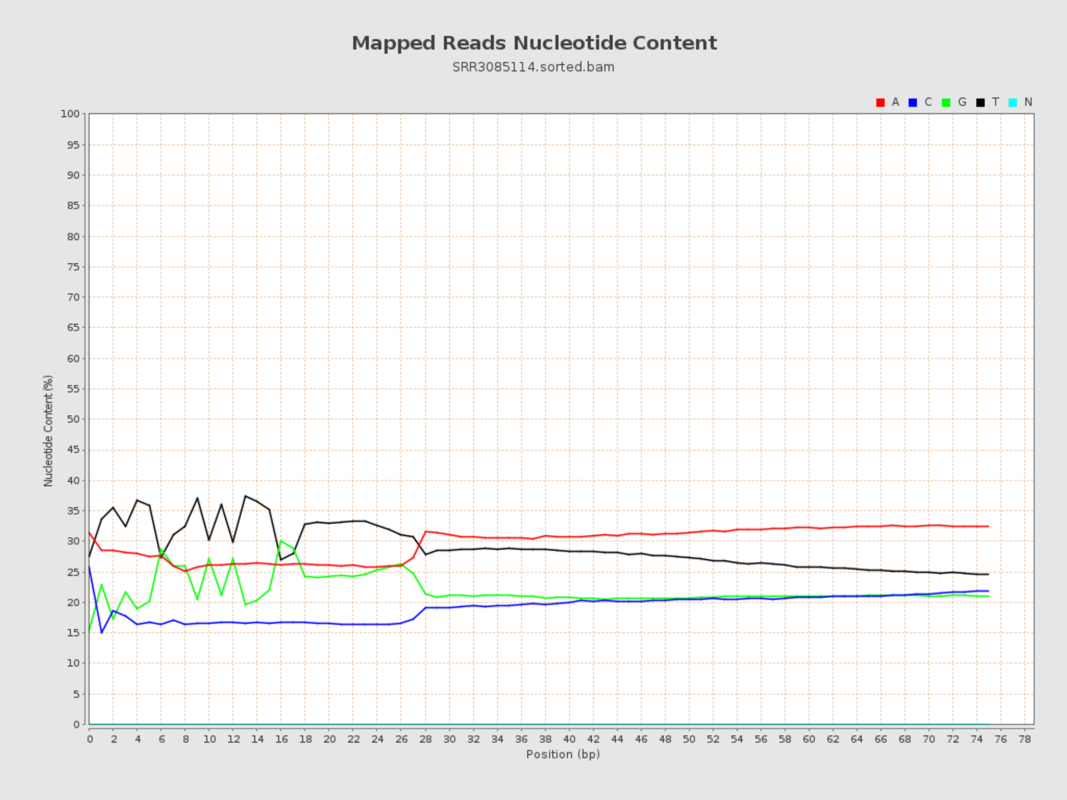
6. Results : Genome Fraction Coverage



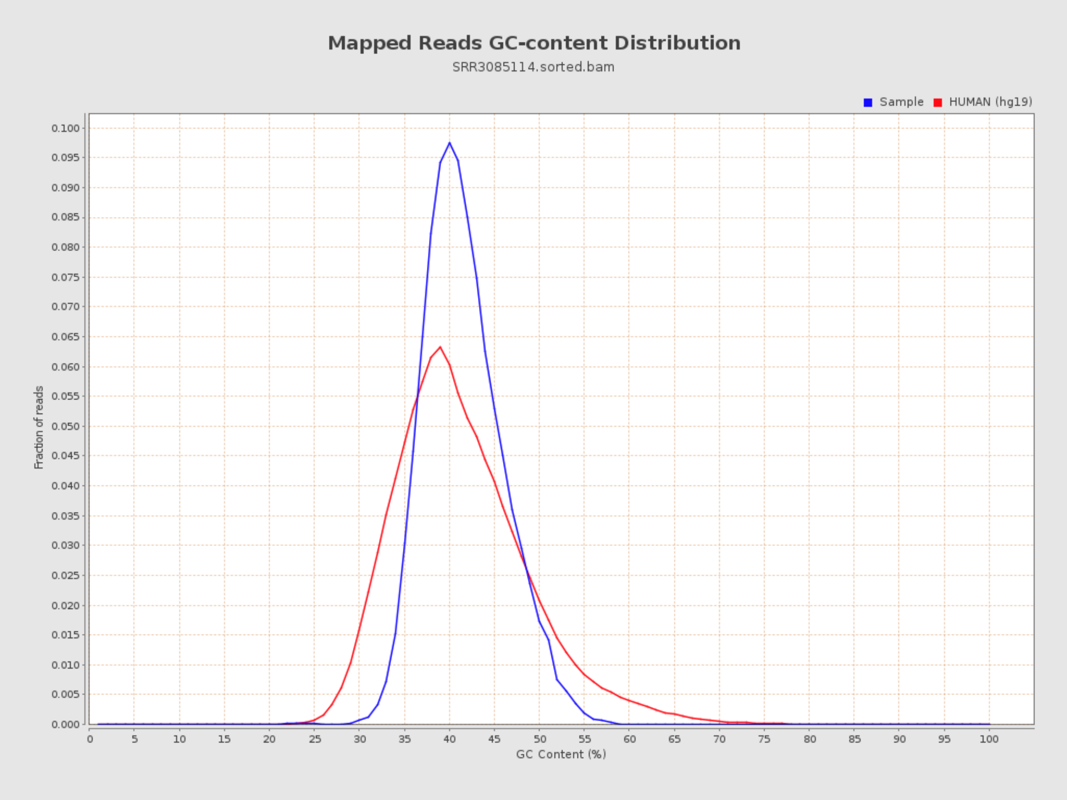
7. Results : Duplication Rate Histogram



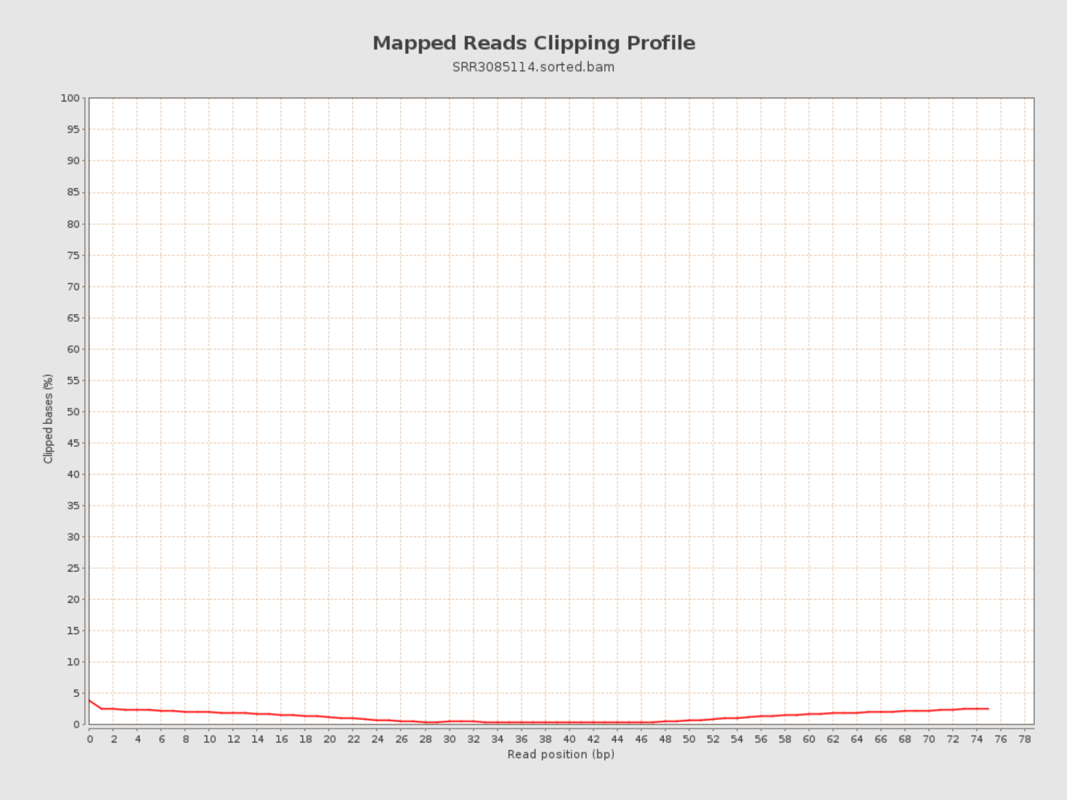
8. Results : Mapped Reads Nucleotide Content



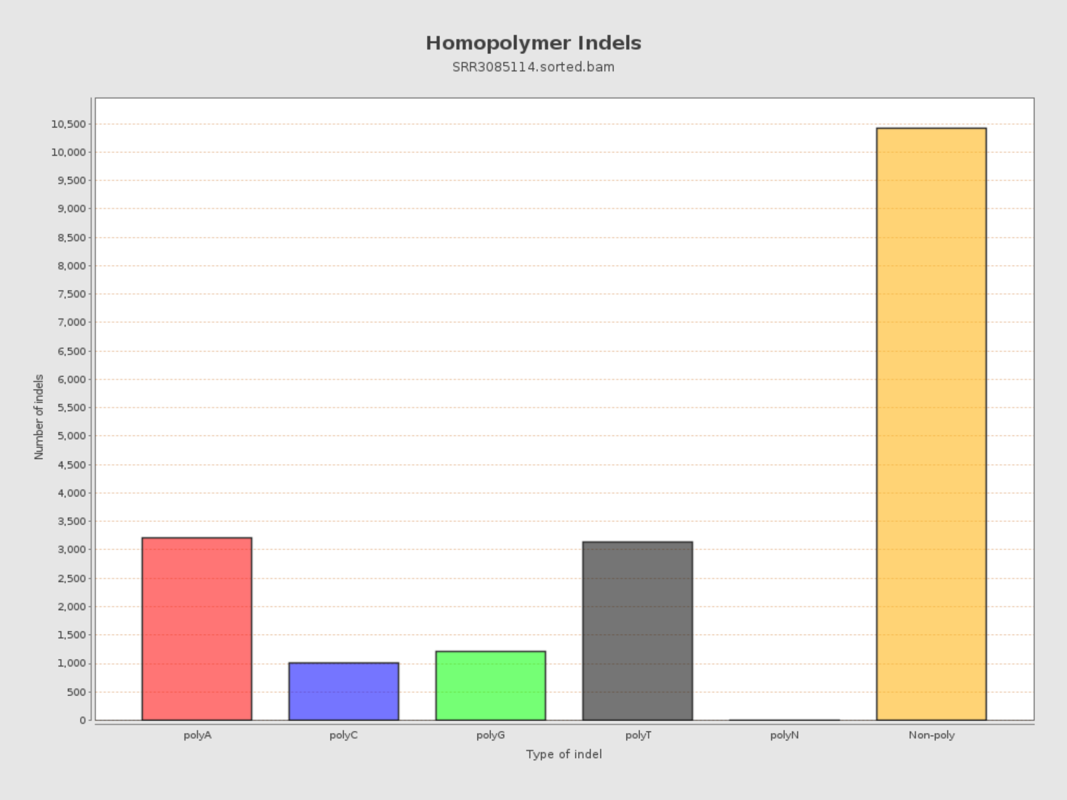
9. Results : Mapped Reads GC-content Distribution



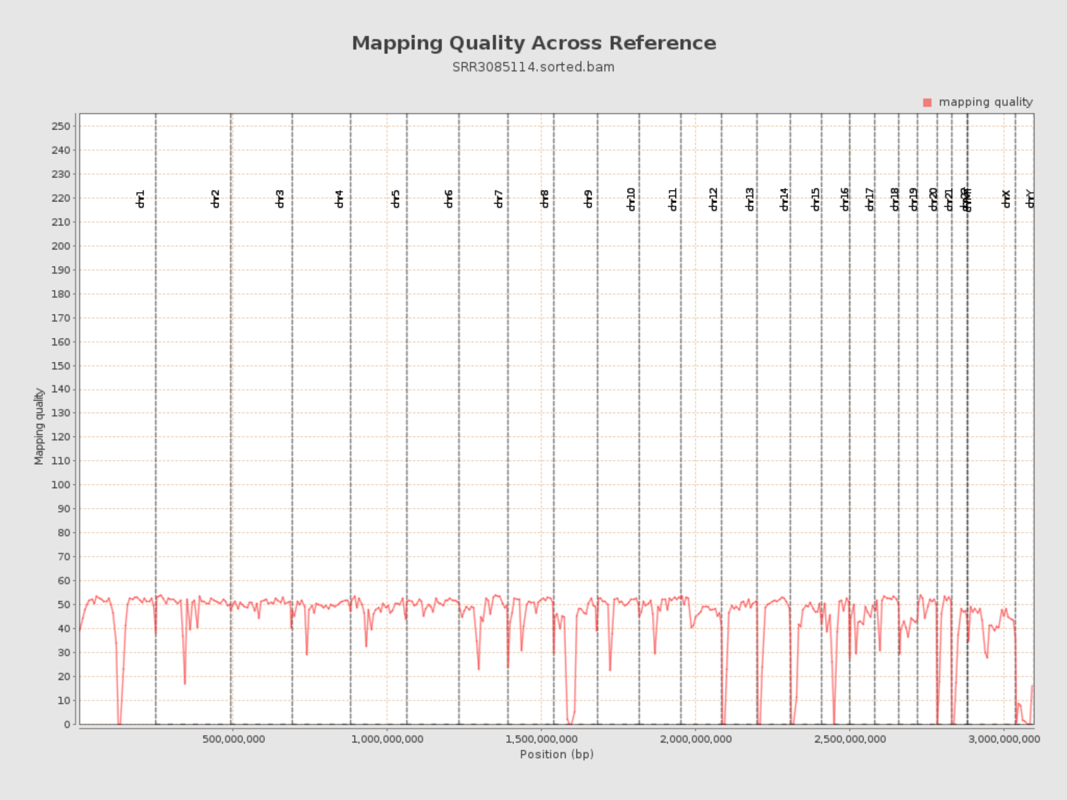
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram