Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:21:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818788.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_SRR1818788 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818788.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:21:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818788.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	767,140
Mapped reads	744,788 / 97.09%
Unmapped reads	22,352 / 2.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,672 / 0.74%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	218,153 / 28.44%
Duplication rate	26.41%
Clipped reads	740,743 / 96.56%

2.2. ACGT Content

Number/percentage of A's	14,195,319 / 28.05%
Number/percentage of C's	10,831,449 / 21.4%
Number/percentage of T's	14,663,166 / 28.98%
Number/percentage of G's	10,910,890 / 21.56%
Number/percentage of N's	3,003 / 0.01%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0164

Standard Deviation	0.2357

2.4. Mapping Quality

Mean Mapping Quality	47.74

2.5. Mismatches and indels

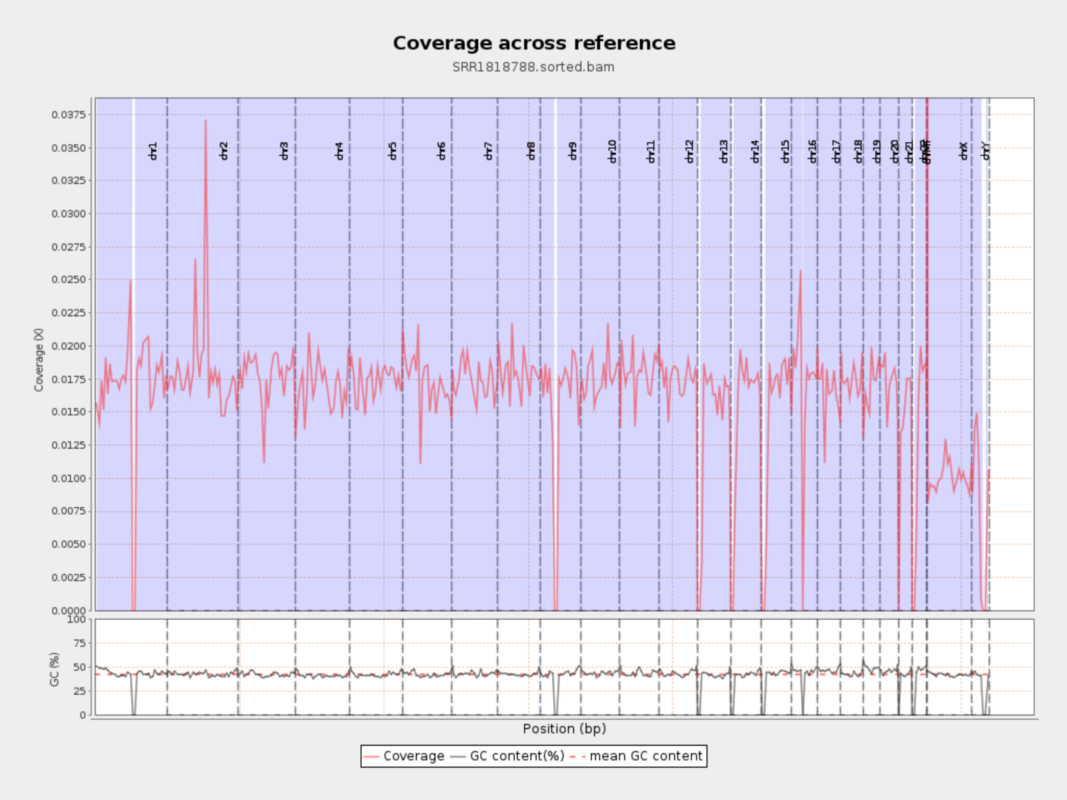
General error rate	0.55%
Mismatches	264,371
Insertions	6,428
Mapped reads with at least one insertion	0.85%
Deletions	13,125
Mapped reads with at least one deletion	1.74%
Homopolymer indels	38.52%

2.6. Chromosome stats

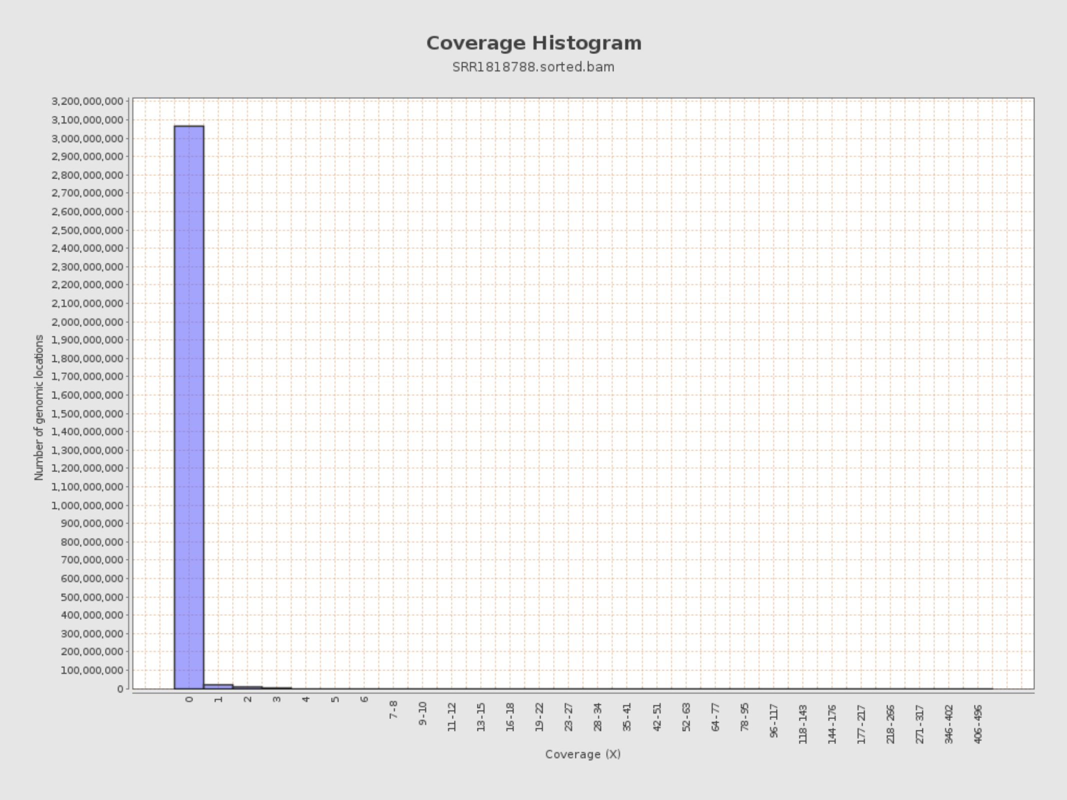
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4181677	0.0168	0.278
chr2	243199373	4443228	0.0183	0.3863
chr3	198022430	3533952	0.0178	0.1934
chr4	191154276	3233981	0.0169	0.2051
chr5	180915260	3147238	0.0174	0.2007
chr6	171115067	2961551	0.0173	0.2033
chr7	159138663	2778962	0.0175	0.2101

chr8	146364022	2640509	0.018	0.2094
chr9	141213431	2172692	0.0154	0.2012
chr10	135534747	2403834	0.0177	0.2524
chr11	135006516	2426387	0.018	0.2073
chr12	133851895	2344093	0.0175	0.1975
chr13	115169878	1612857	0.014	0.171
chr14	107349540	1571528	0.0146	0.1993
chr15	102531392	1459967	0.0142	0.1736
chr16	90354753	1533626	0.017	0.262
chr17	81195210	1337048	0.0165	0.1938
chr18	78077248	1363502	0.0175	0.2505
chr19	59128983	1010228	0.0171	0.2468
chr20	63025520	1095450	0.0174	0.2022
chr21	48129895	684315	0.0142	0.1807
chr22	51304566	635460	0.0124	0.1727
chrMT	16571	48391	2.9202	3.3998
chrX	155270560	1560178	0.01	0.1541
chrY	59373566	444307	0.0075	0.4019

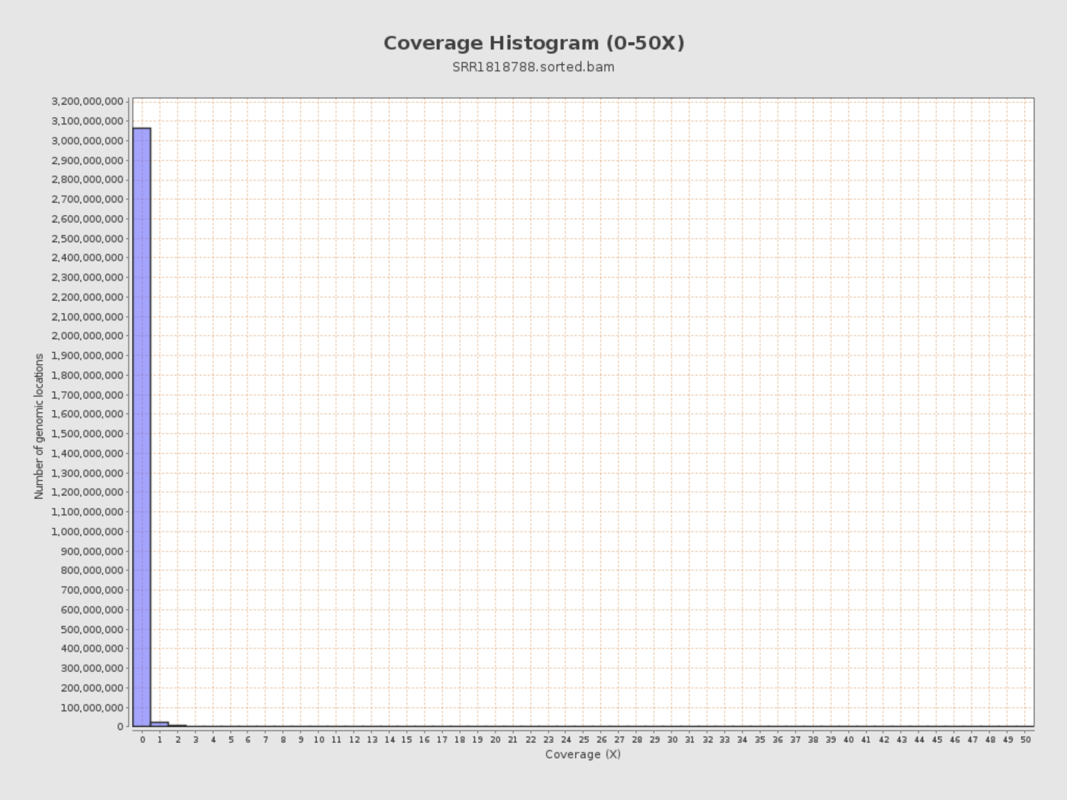
3. Results : Coverage across reference



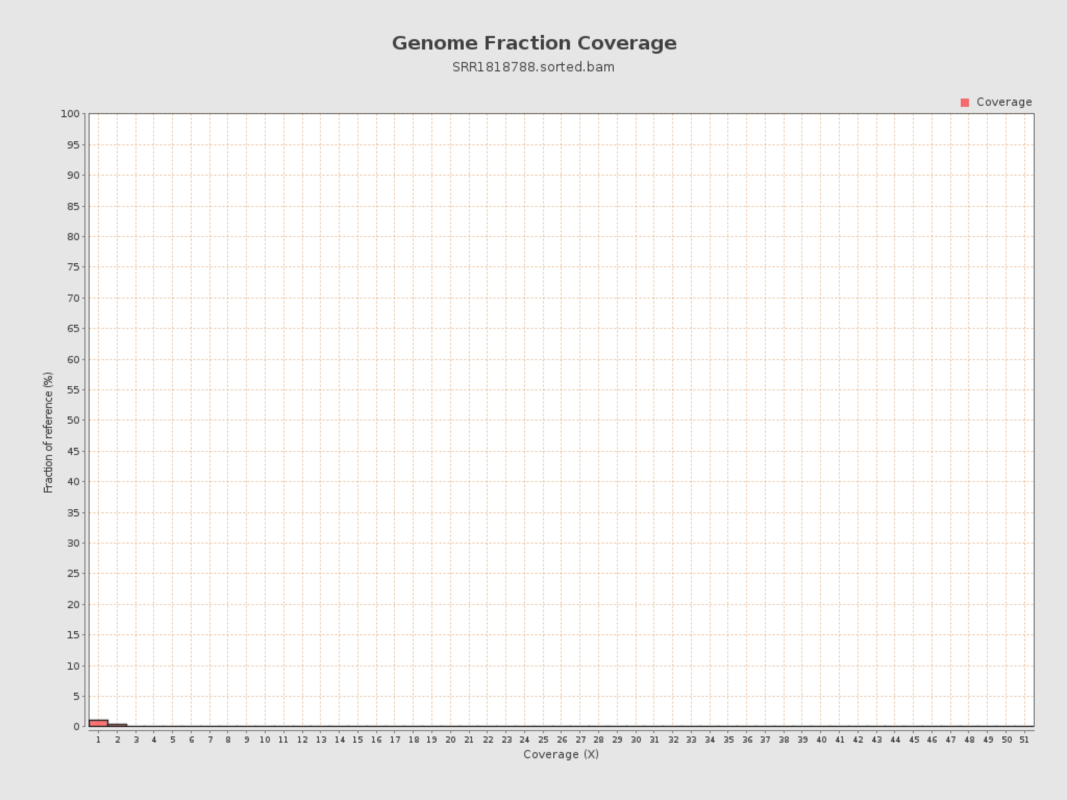
4. Results : Coverage Histogram



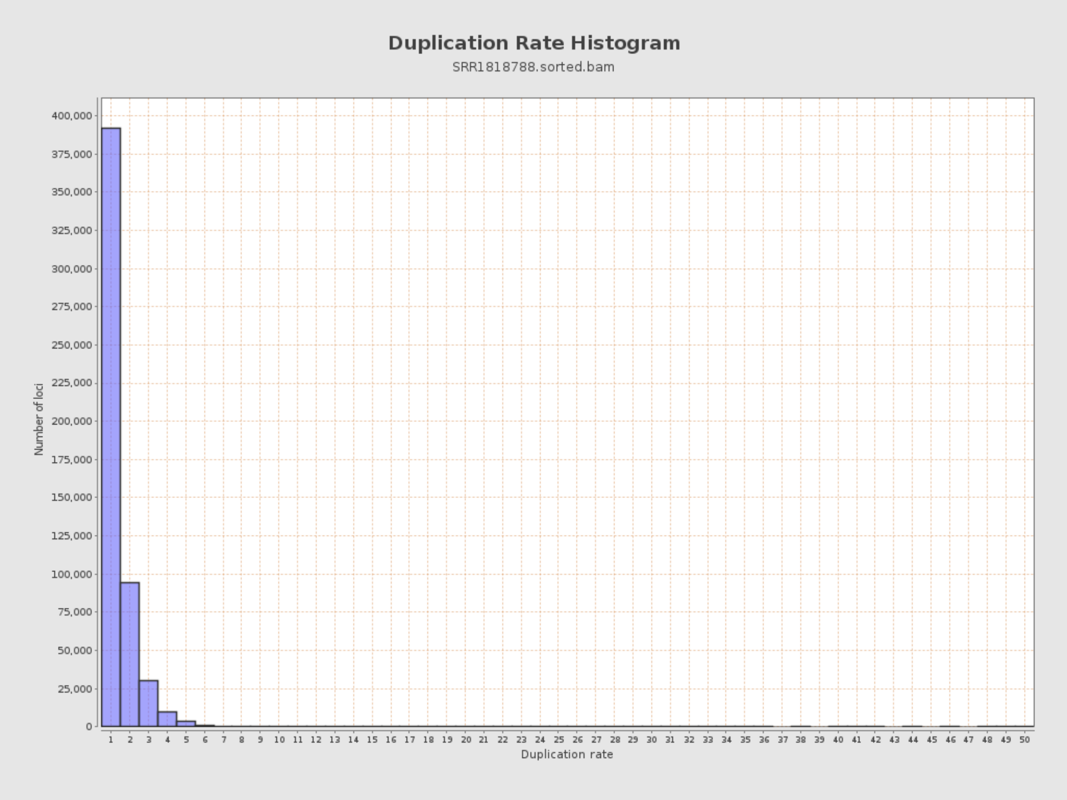
5. Results : Coverage Histogram (0-50X)



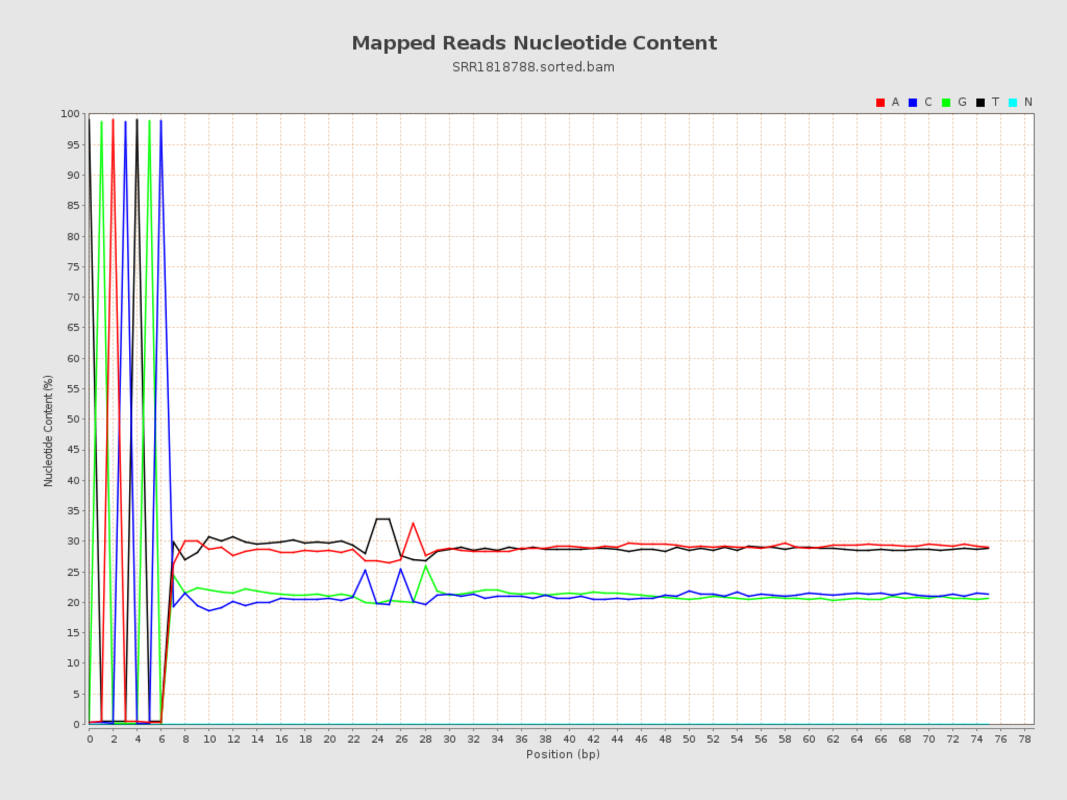
6. Results : Genome Fraction Coverage



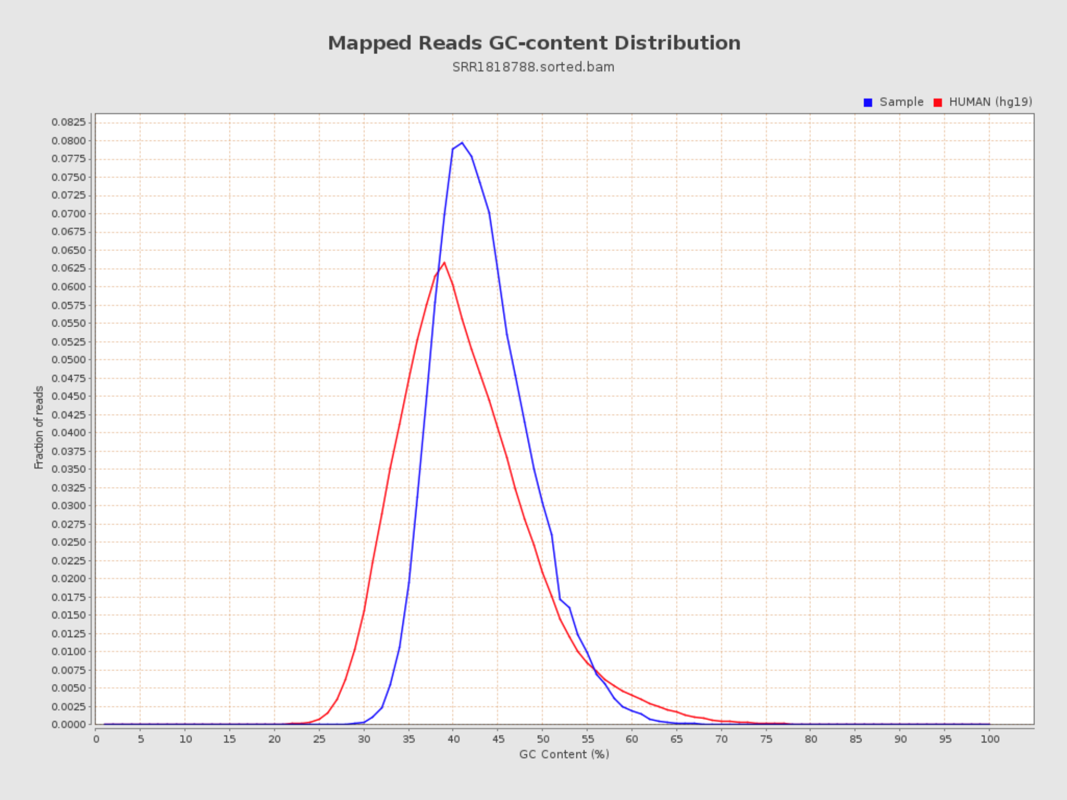
7. Results : Duplication Rate Histogram



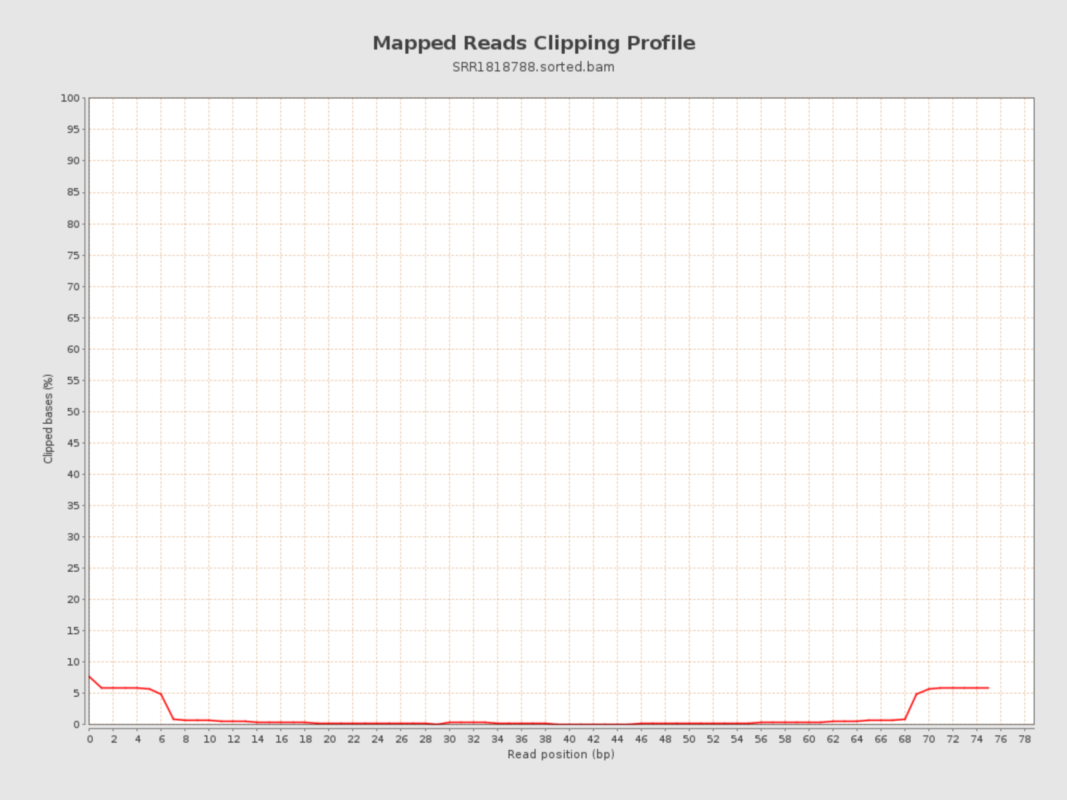
8. Results : Mapped Reads Nucleotide Content



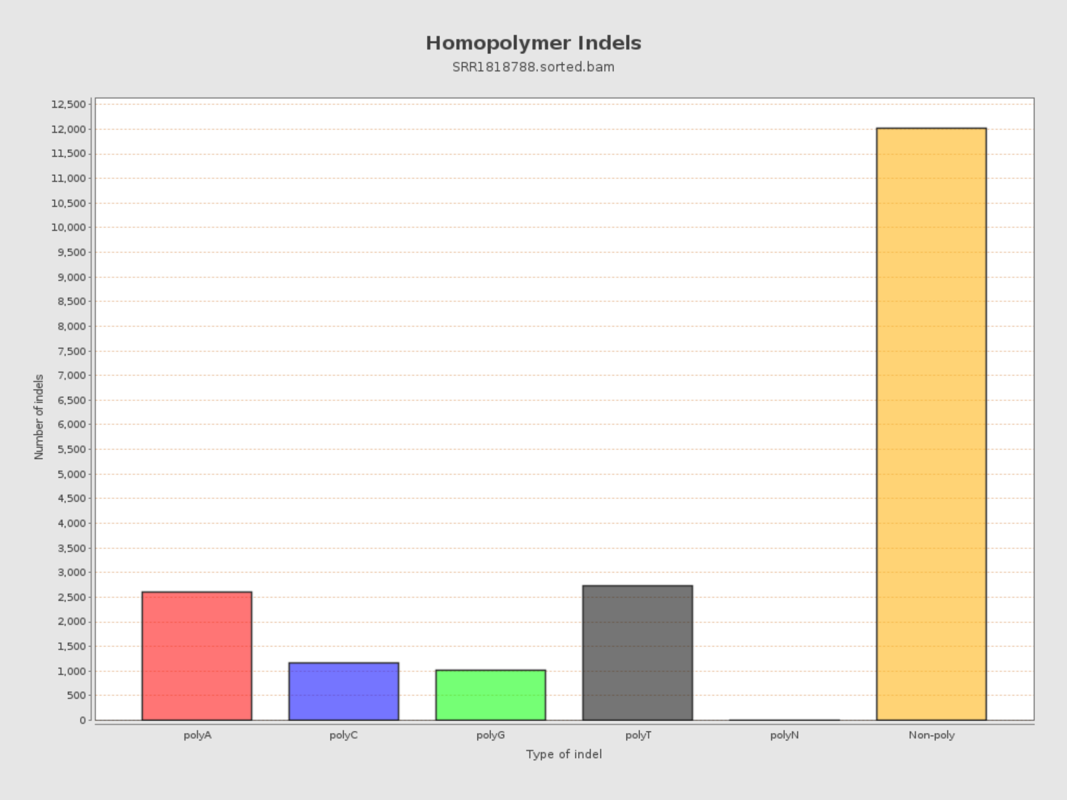
9. Results : Mapped Reads GC-content Distribution



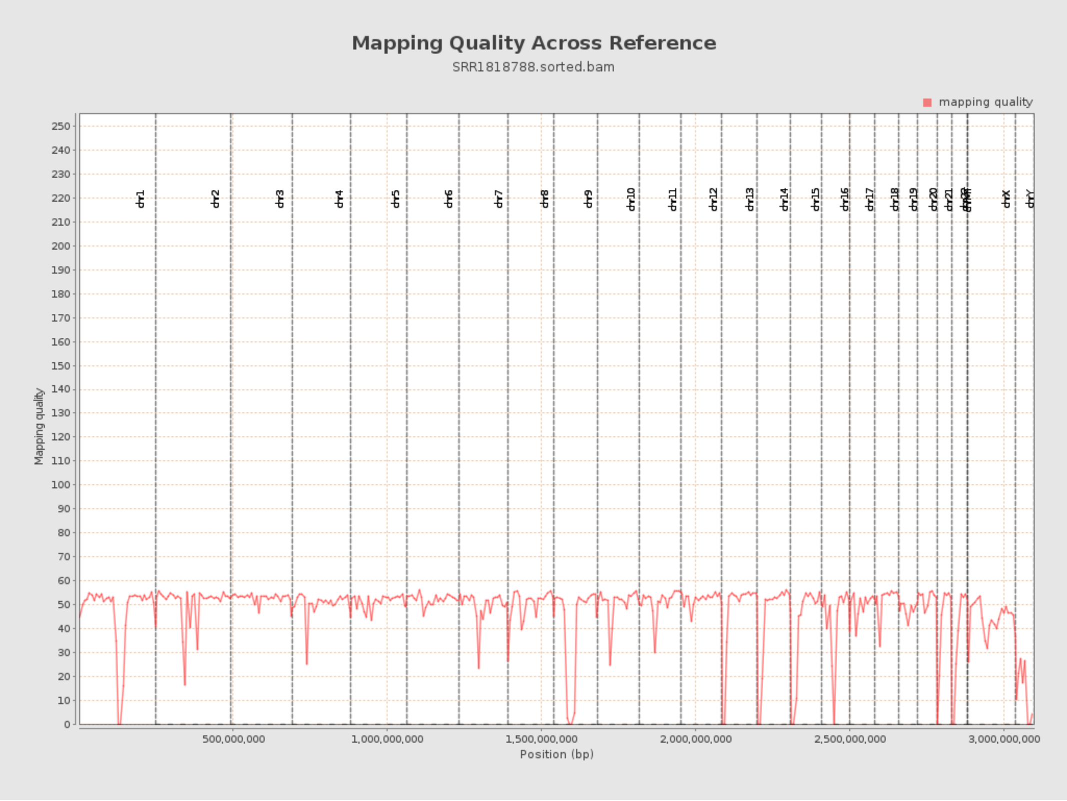
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram