Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:30:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818911.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_SRR1818911 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818911.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:30:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818911.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,656,723
Mapped reads	1,633,263 / 98.58%
Unmapped reads	23,460 / 1.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,402 / 1.47%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	382,853 / 23.11%
Duplication rate	19.69%
Clipped reads	1,648,642 / 99.51%

2.2. ACGT Content

Number/percentage of A's	44,798,915 / 29.66%
Number/percentage of C's	31,704,534 / 20.99%
Number/percentage of T's	41,940,264 / 27.77%
Number/percentage of G's	32,596,422 / 21.58%
Number/percentage of N's	2,262 / 0%
GC Percentage	42.57%

2.3. Coverage

Mean	0.0488

Standard Deviation	0.6269

2.4. Mapping Quality

Mean Mapping Quality	49.22

2.5. Mismatches and indels

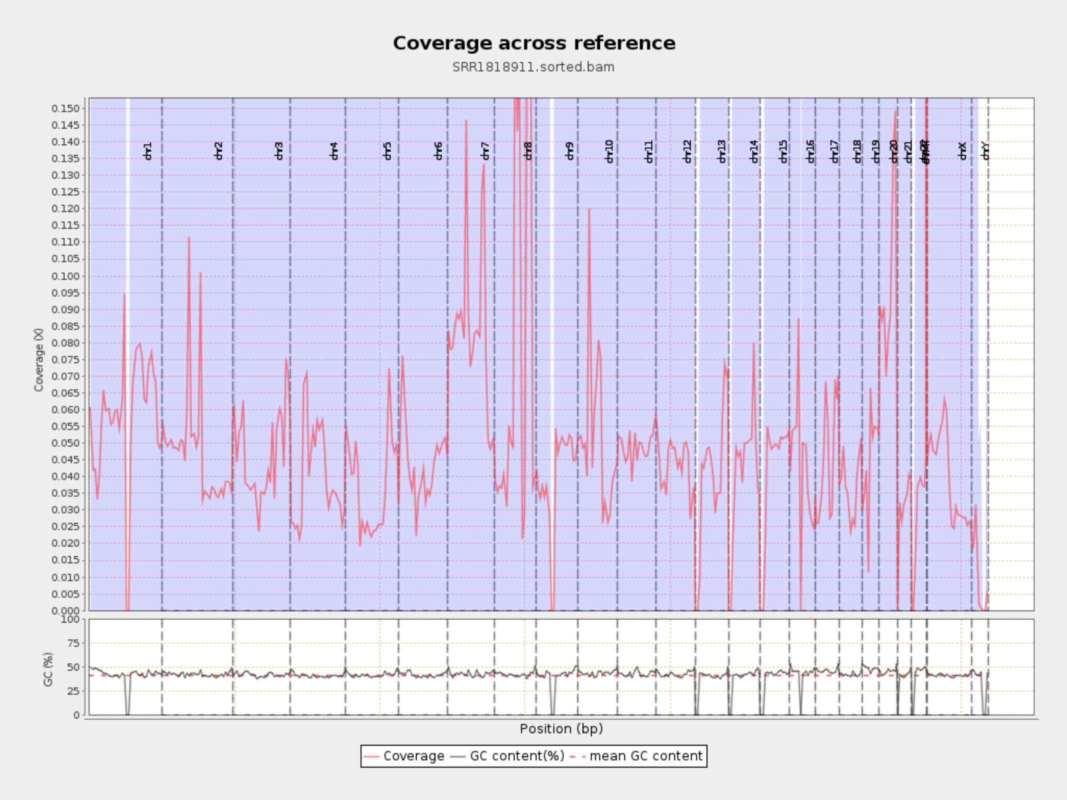
General error rate	0.65%
Mismatches	919,237
Insertions	22,469
Mapped reads with at least one insertion	1.33%
Deletions	49,762
Mapped reads with at least one deletion	2.97%
Homopolymer indels	40.18%

2.6. Chromosome stats

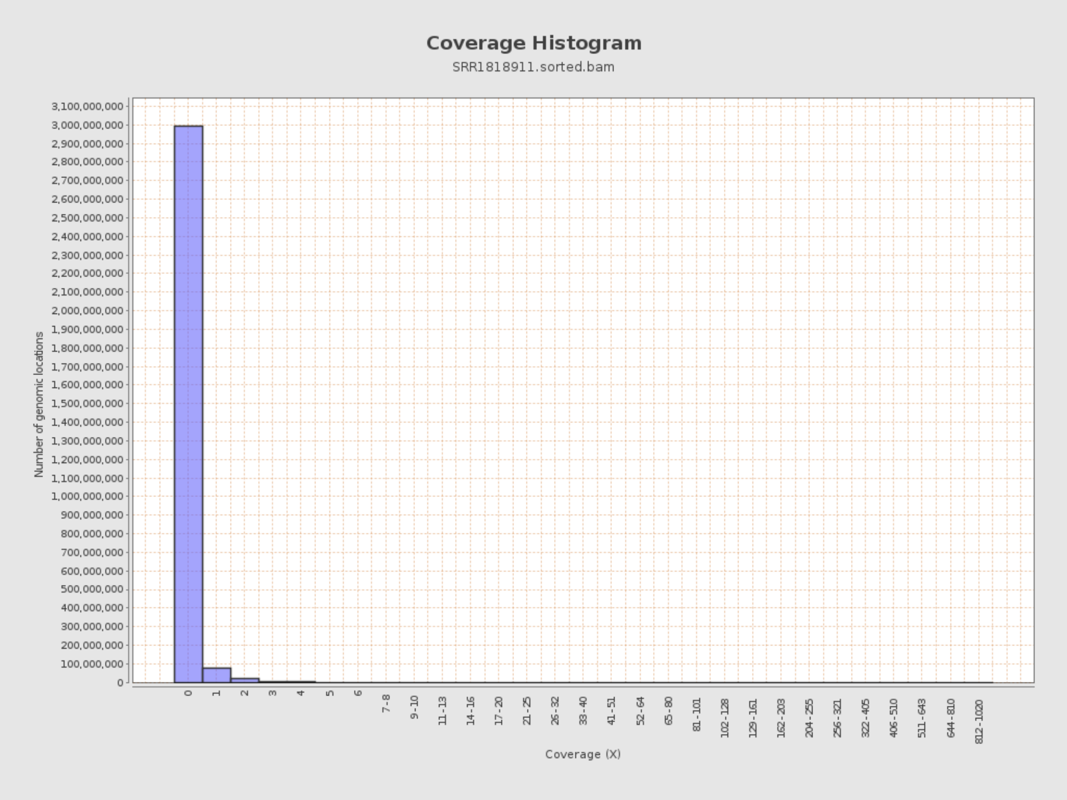
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14372404	0.0577	0.9066
chr2	243199373	11621166	0.0478	0.9675
chr3	198022430	9211020	0.0465	0.2934
chr4	191154276	7567205	0.0396	0.3622
chr5	180915260	6678057	0.0369	0.284
chr6	171115067	7510818	0.0439	0.3097
chr7	159138663	13569532	0.0853	1.3747

chr8	146364022	13174992	0.09	0.5077
chr9	141213431	5521656	0.0391	0.4841
chr10	135534747	6990687	0.0516	0.7969
chr11	135006516	6604415	0.0489	0.3615
chr12	133851895	5868046	0.0438	0.2906
chr13	115169878	4630797	0.0402	0.2728
chr14	107349540	4448341	0.0414	0.3087
chr15	102531392	4243171	0.0414	0.2848
chr16	90354753	3810227	0.0422	0.6685
chr17	81195210	3733858	0.046	0.3773
chr18	78077248	2896028	0.0371	0.5637
chr19	59128983	2635361	0.0446	0.8131
chr20	63025520	6224888	0.0988	0.4645
chr21	48129895	1478602	0.0307	0.2951
chr22	51304566	1372776	0.0268	0.2538
chrMT	16571	206614	12.4684	8.0922
chrX	155270560	6209034	0.04	0.3295
chrY	59373566	561222	0.0095	0.8112

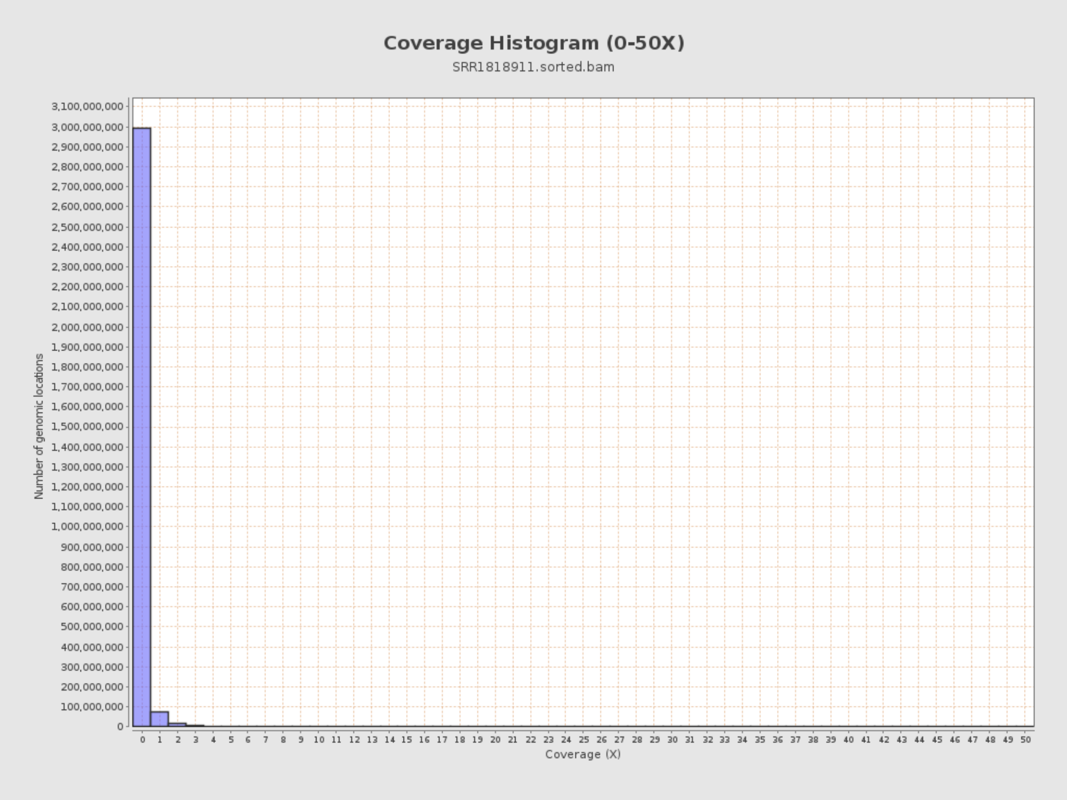
3. Results : Coverage across reference



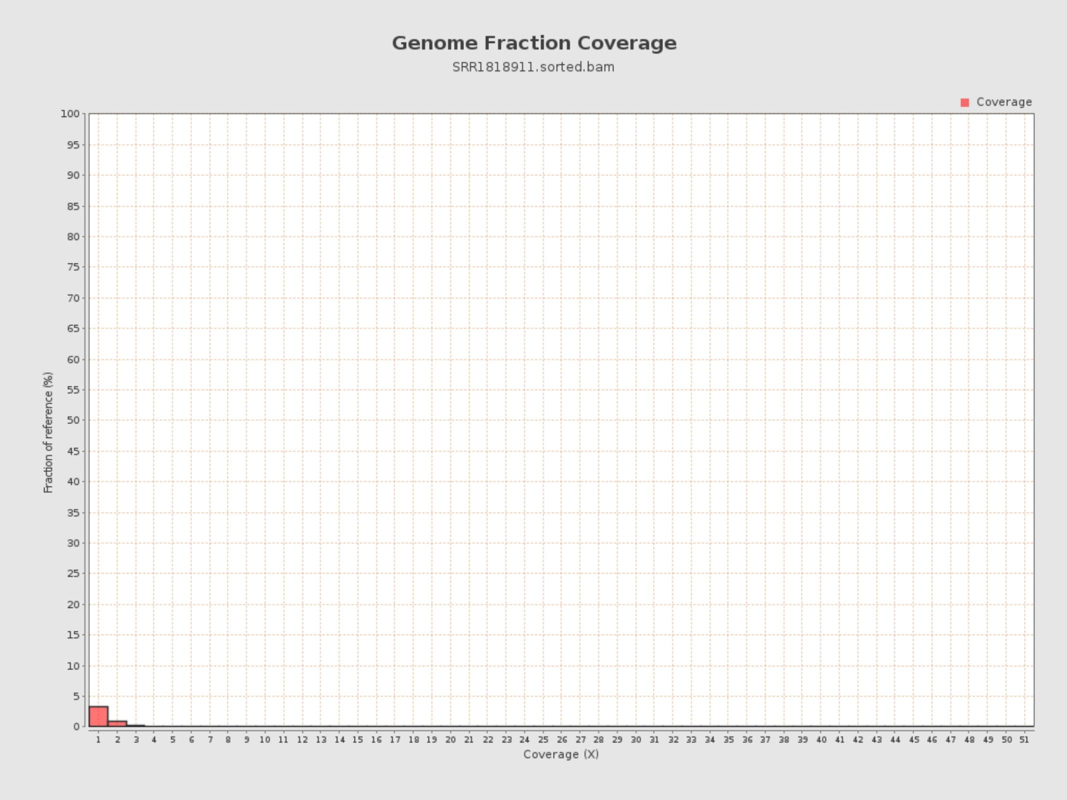
4. Results : Coverage Histogram



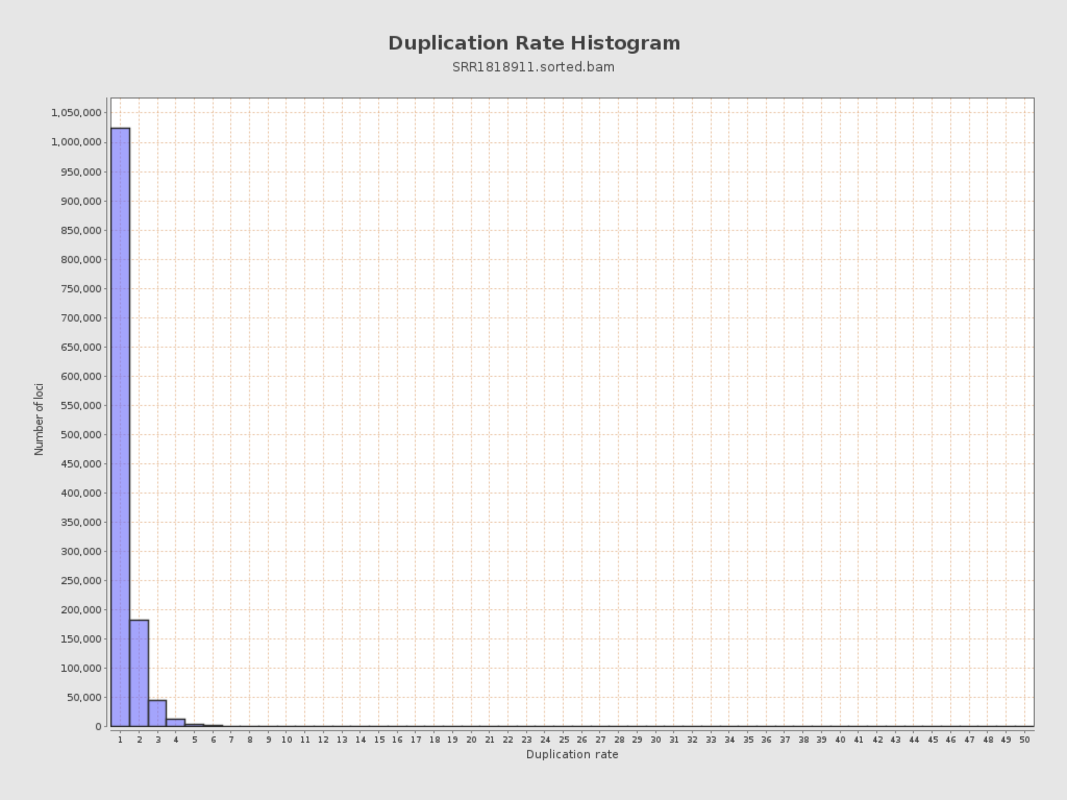
5. Results : Coverage Histogram (0-50X)



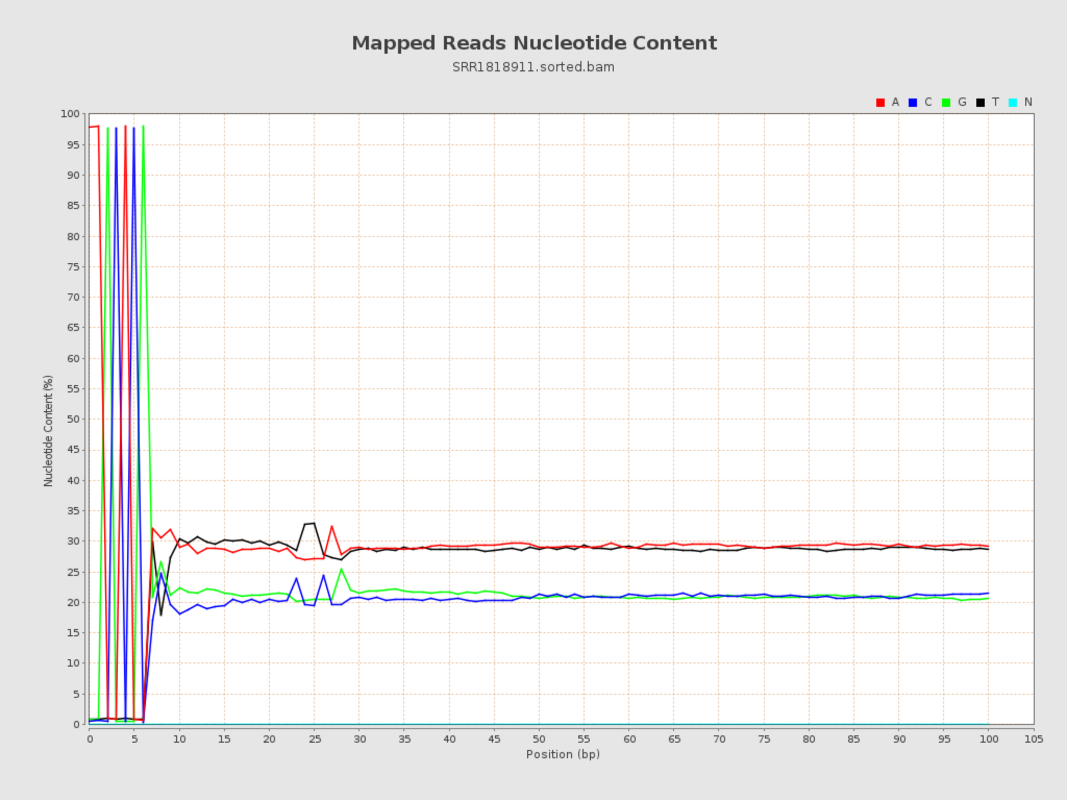
6. Results : Genome Fraction Coverage



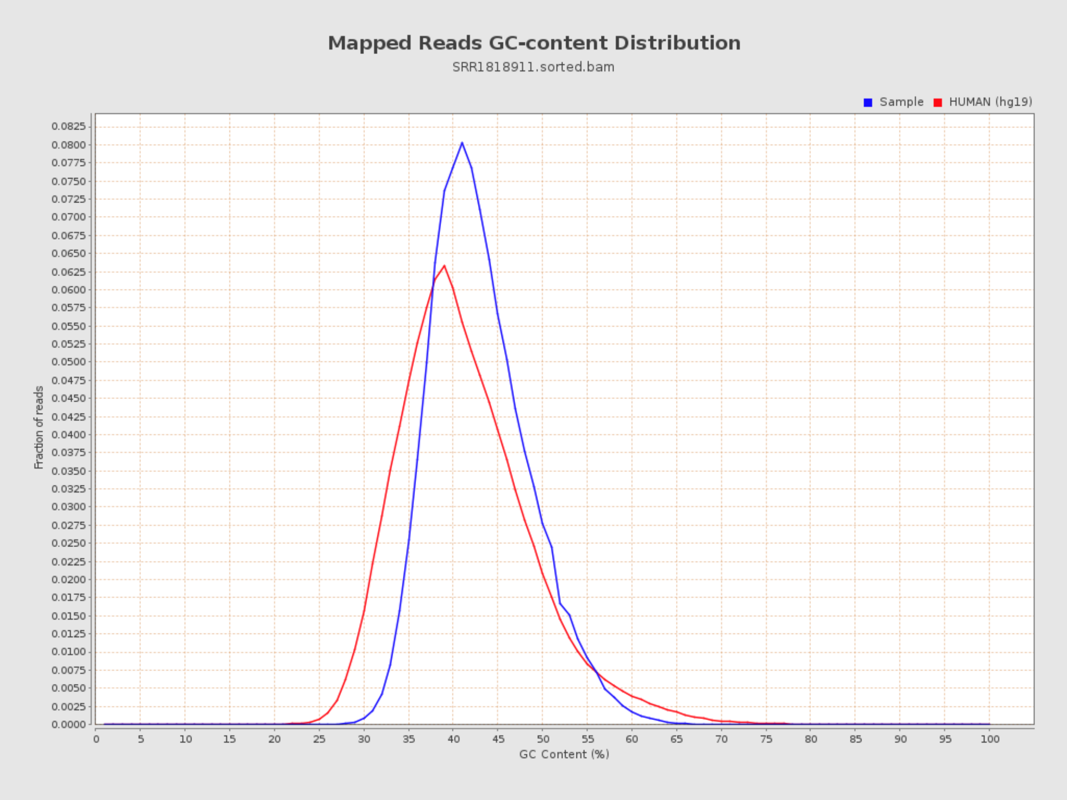
7. Results : Duplication Rate Histogram



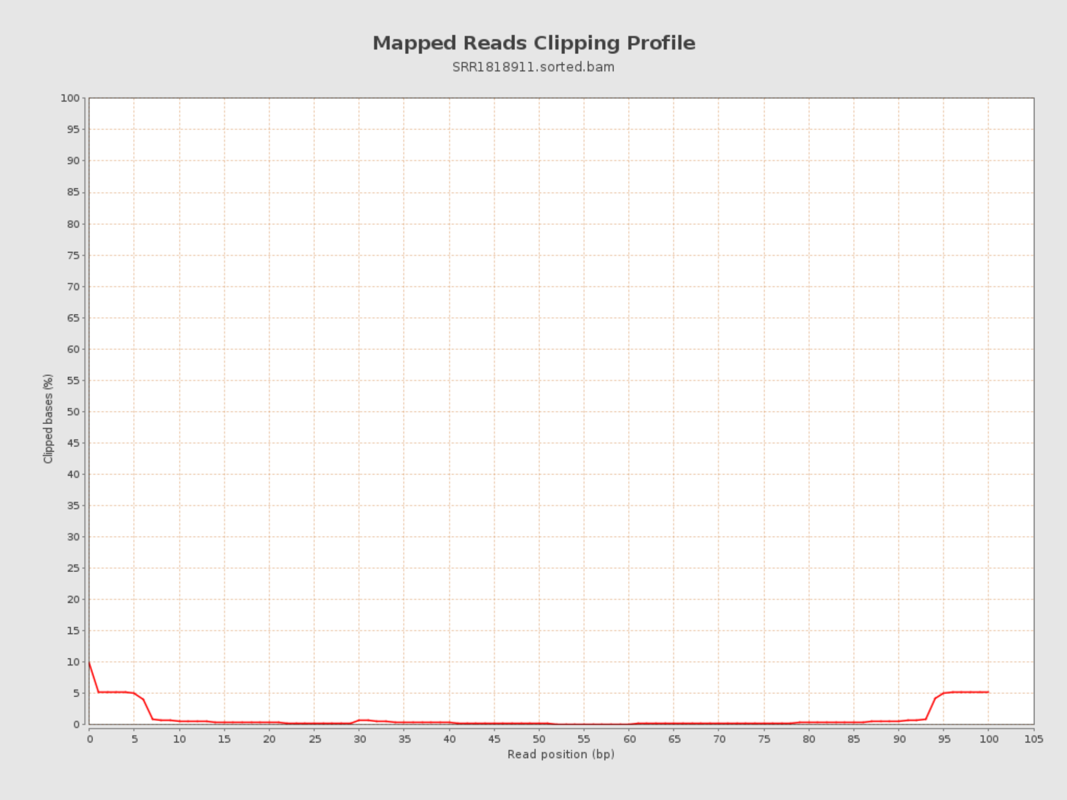
8. Results : Mapped Reads Nucleotide Content



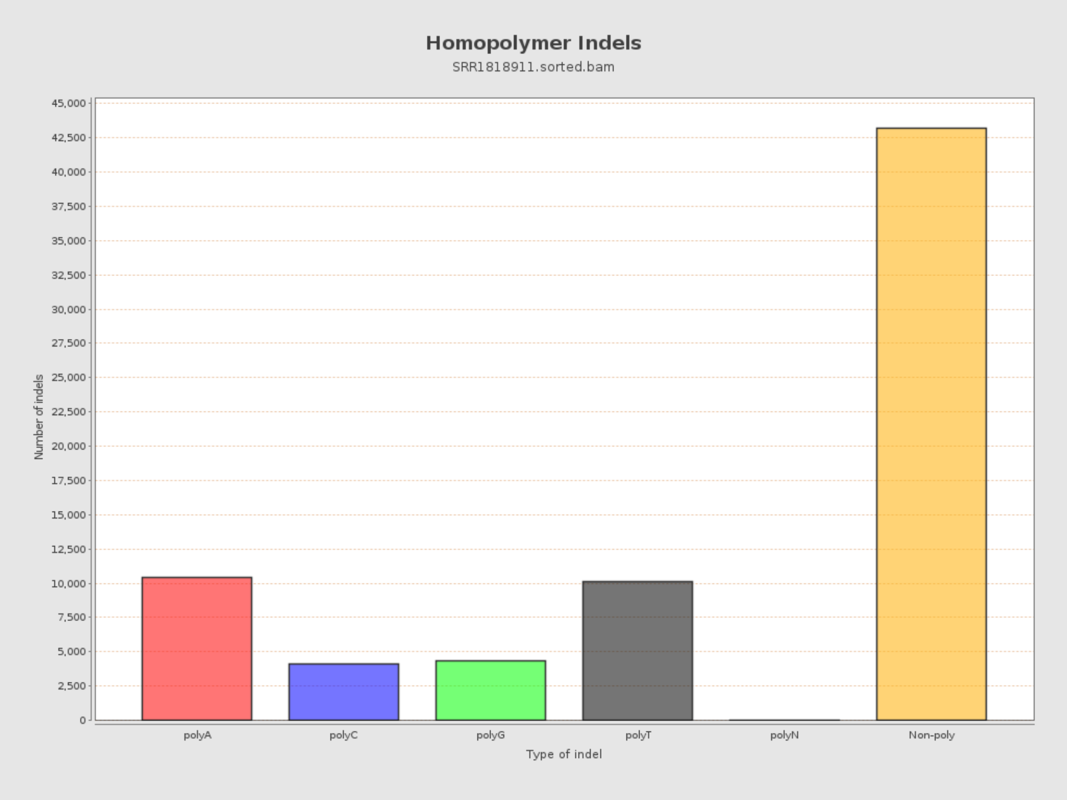
9. Results : Mapped Reads GC-content Distribution



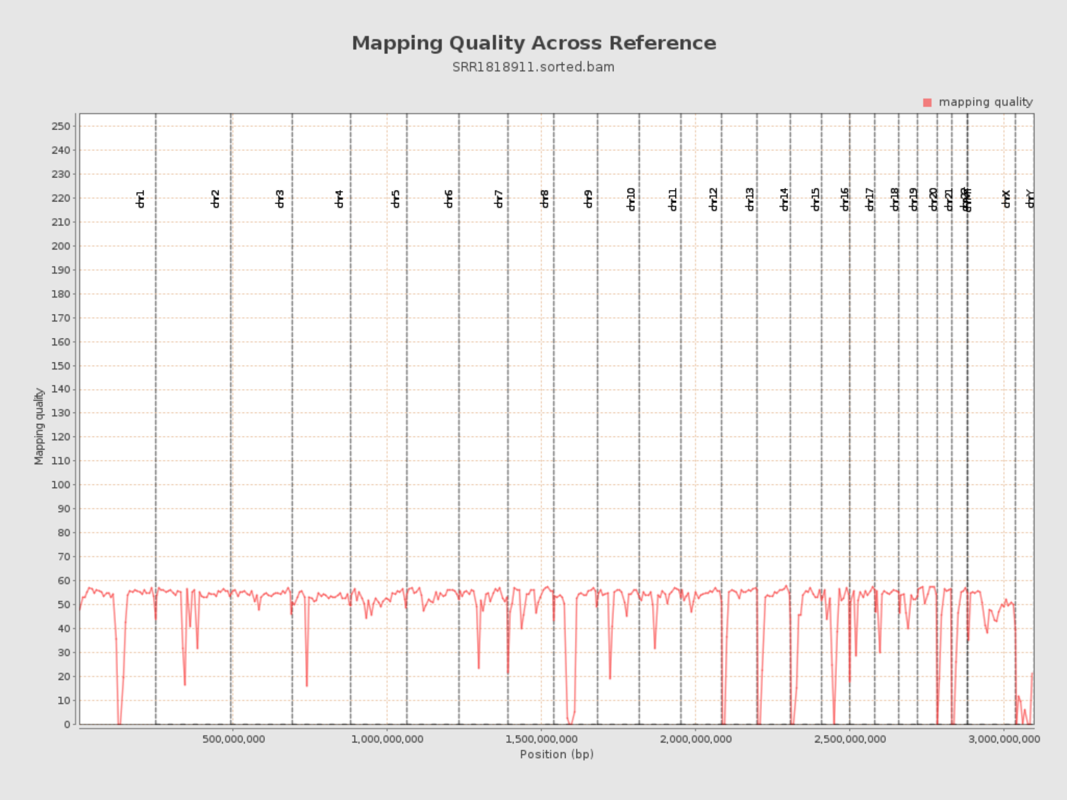
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram