Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:04:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818997.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_SRR1818997 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818997.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:04:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818997.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,865,374
Mapped reads	2,594,773 / 90.56%
Unmapped reads	270,601 / 9.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,301 / 1.27%
Read min/max/mean length	30 / 101 / 101.49
Duplicated reads (estimated)	1,288,062 / 44.95%
Duplication rate	41.15%
Clipped reads	2,621,364 / 91.48%

2.2. ACGT Content

Number/percentage of A's	70,024,104 / 29.15%
Number/percentage of C's	49,307,527 / 20.52%
Number/percentage of T's	67,928,001 / 28.27%
Number/percentage of G's	52,976,133 / 22.05%
Number/percentage of N's	11,986 / 0%
GC Percentage	42.57%

2.3. Coverage

Mean	0.0777

Standard Deviation	0.9446

2.4. Mapping Quality

Mean Mapping Quality	49.2

2.5. Mismatches and indels

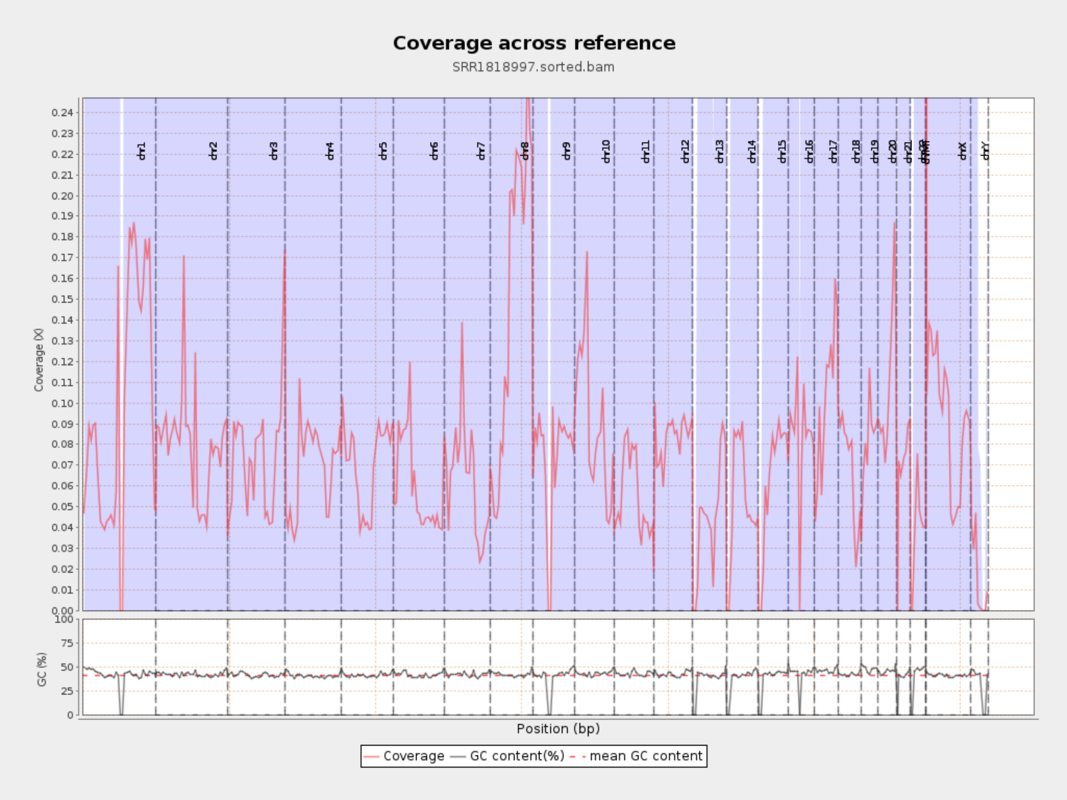
General error rate	0.65%
Mismatches	1,479,437
Insertions	32,719
Mapped reads with at least one insertion	1.22%
Deletions	75,657
Mapped reads with at least one deletion	2.85%
Homopolymer indels	42.49%

2.6. Chromosome stats

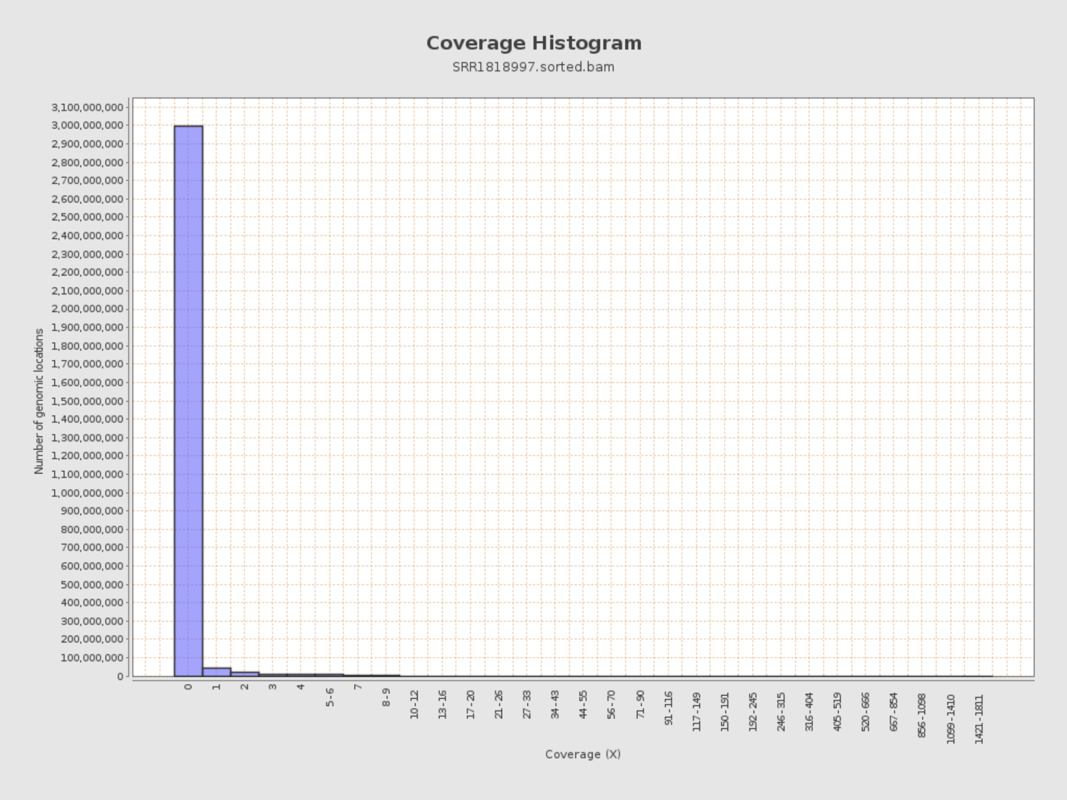
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24511244	0.0983	1.7169
chr2	243199373	19656087	0.0808	1.2947
chr3	198022430	14754568	0.0745	0.5503
chr4	191154276	13260502	0.0694	0.6156
chr5	180915260	12869202	0.0711	0.5547
chr6	171115067	10212048	0.0597	0.6303
chr7	159138663	10101509	0.0635	1.1114

chr8	146364022	22632775	0.1546	0.9059
chr9	141213431	10417769	0.0738	0.8957
chr10	135534747	12167189	0.0898	1.1794
chr11	135006516	7509417	0.0556	0.574
chr12	133851895	11239662	0.084	0.6069
chr13	115169878	5196990	0.0451	0.428
chr14	107349540	5749456	0.0536	0.4943
chr15	102531392	6262432	0.0611	0.4964
chr16	90354753	7440236	0.0823	1.0794
chr17	81195210	8238489	0.1015	0.74
chr18	78077248	5294471	0.0678	1.0299
chr19	59128983	4919462	0.0832	1.5243
chr20	63025520	7098961	0.1126	0.7504
chr21	48129895	3374241	0.0701	0.5943
chr22	51304566	1925574	0.0375	0.4202
chrMT	16571	56915	3.4346	4.4318
chrX	155270560	14589797	0.094	0.7402
chrY	59373566	911341	0.0153	1.0069

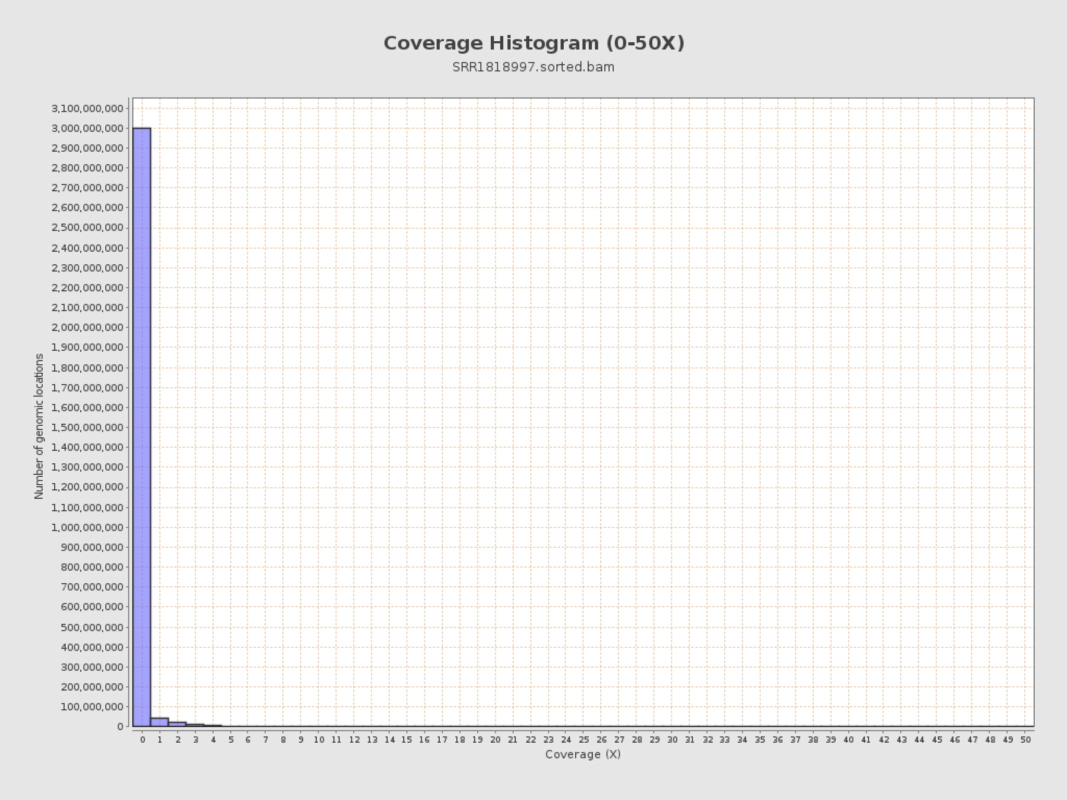
3. Results : Coverage across reference



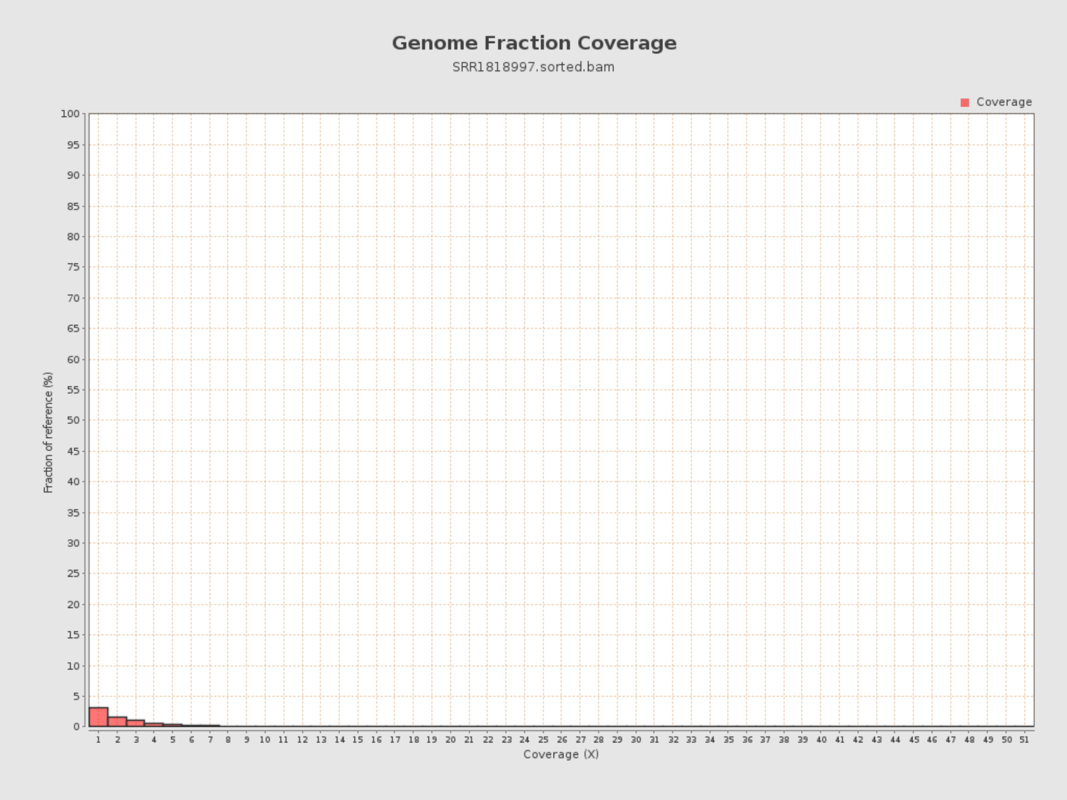
4. Results : Coverage Histogram



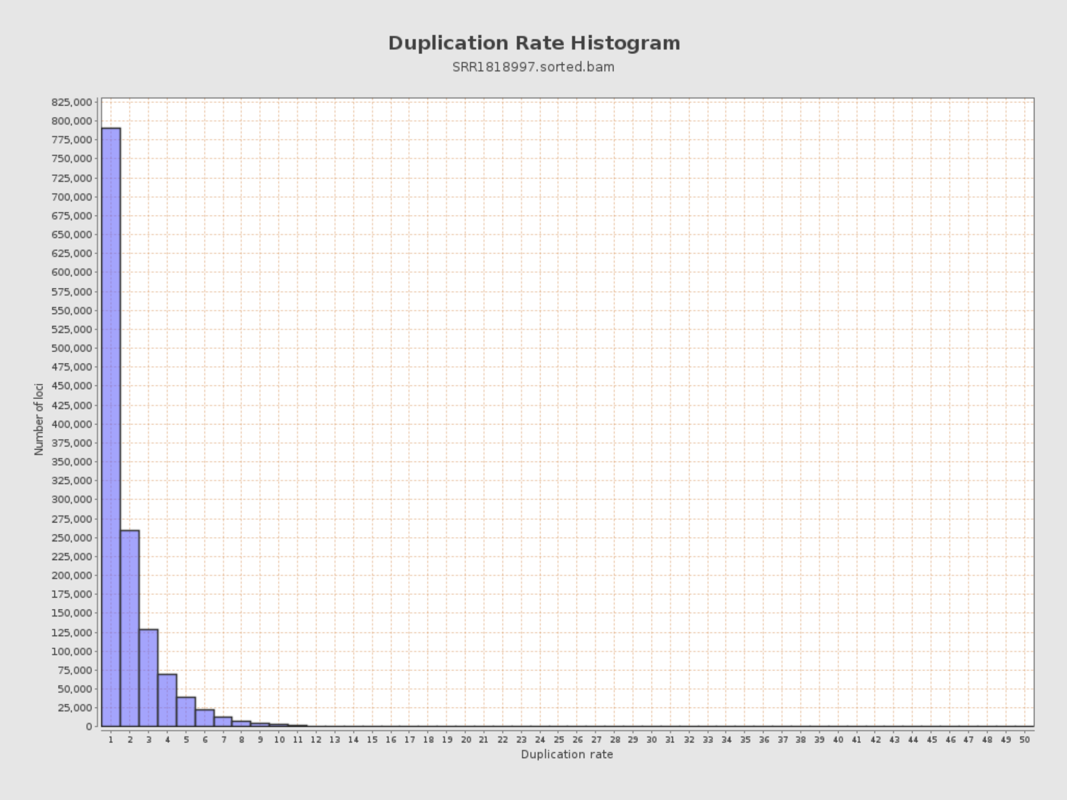
5. Results : Coverage Histogram (0-50X)



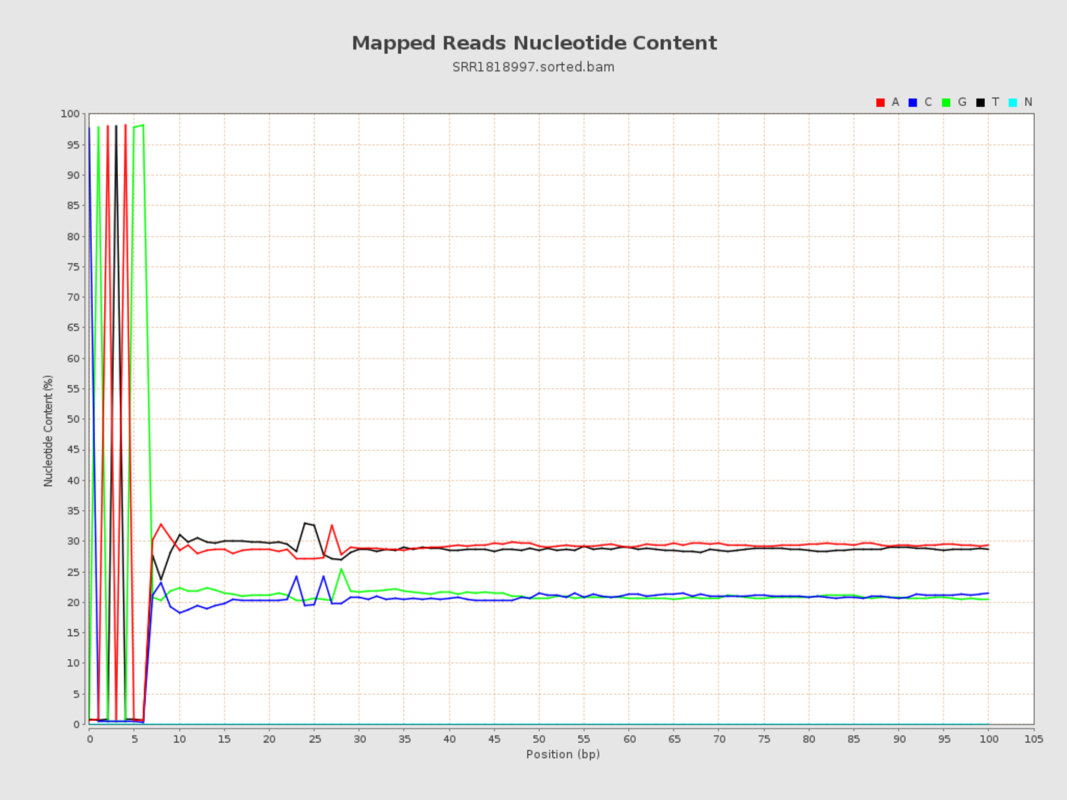
6. Results : Genome Fraction Coverage



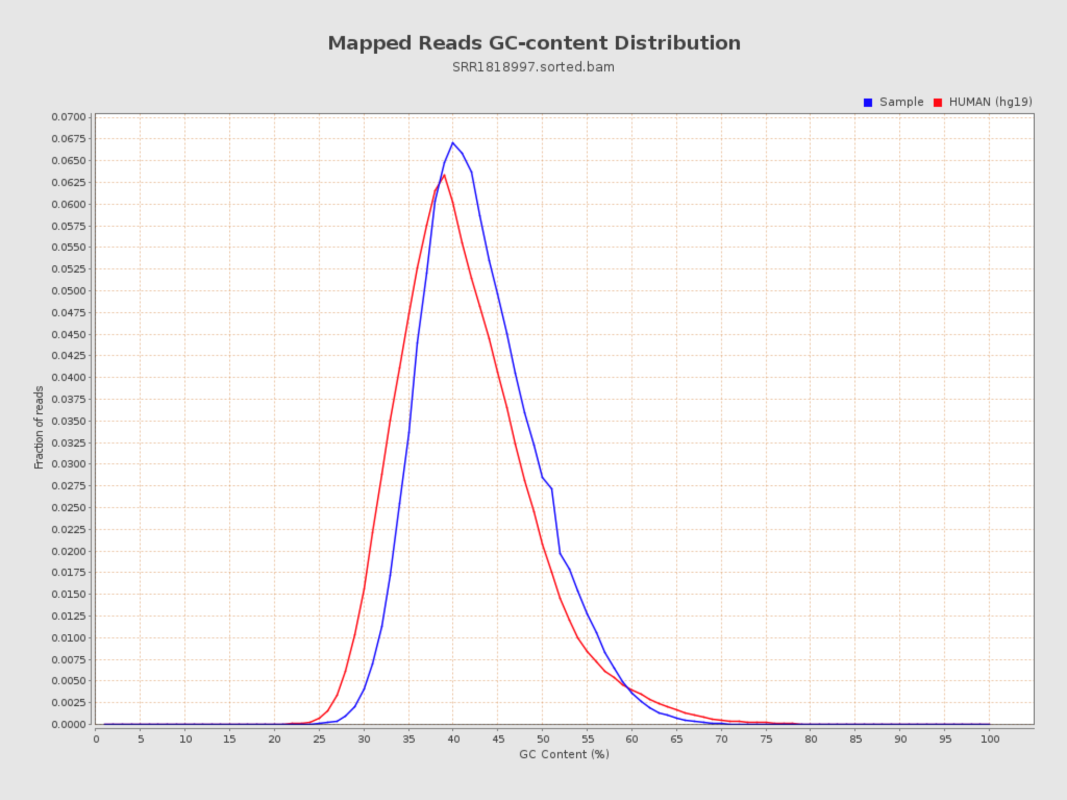
7. Results : Duplication Rate Histogram



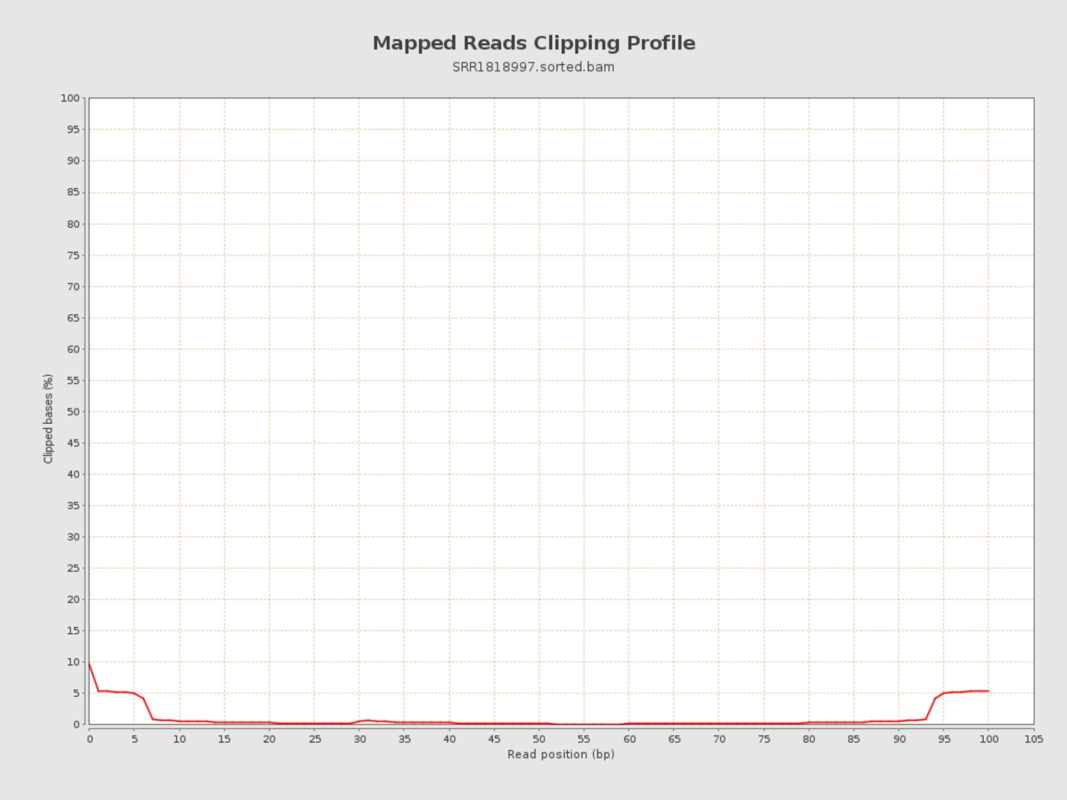
8. Results : Mapped Reads Nucleotide Content



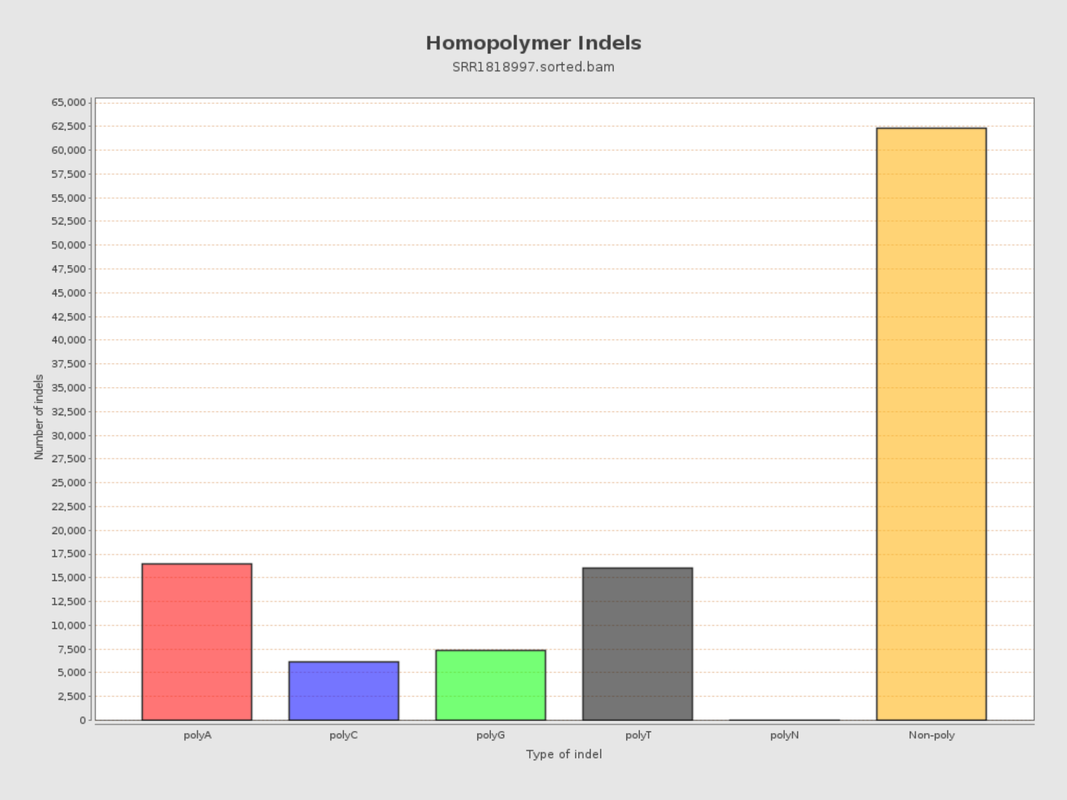
9. Results : Mapped Reads GC-content Distribution



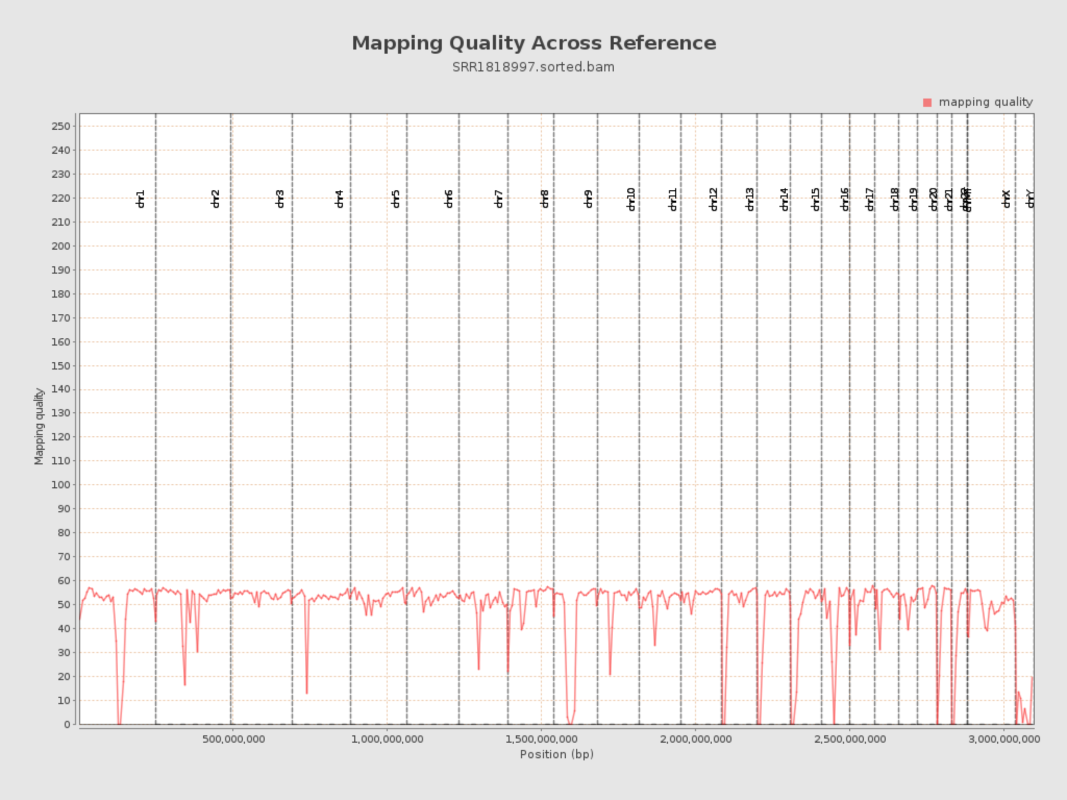
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram