Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:09:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818998.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_SRR1818998 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818998.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:08:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818998.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,173,639
Mapped reads	2,143,287 / 98.6%
Unmapped reads	30,352 / 1.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,396 / 1.4%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	1,146,342 / 52.74%
Duplication rate	44.28%
Clipped reads	2,131,789 / 98.07%

2.2. ACGT Content

Number/percentage of A's	57,351,665 / 28.87%
Number/percentage of C's	40,385,604 / 20.33%
Number/percentage of T's	56,621,854 / 28.5%
Number/percentage of G's	44,319,189 / 22.31%
Number/percentage of N's	9,561 / 0%
GC Percentage	42.63%

2.3. Coverage

Mean	0.0642

Standard Deviation	0.7821

2.4. Mapping Quality

Mean Mapping Quality	49.24

2.5. Mismatches and indels

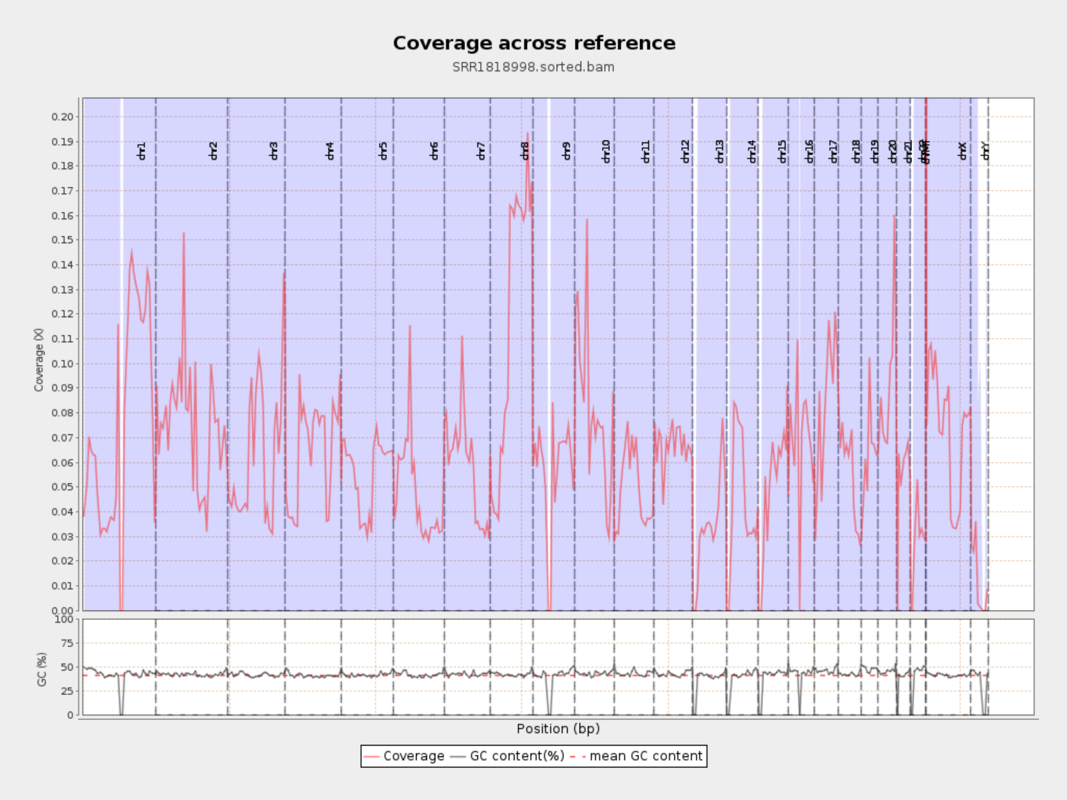
General error rate	0.68%
Mismatches	1,285,910
Insertions	34,223
Mapped reads with at least one insertion	1.56%
Deletions	62,791
Mapped reads with at least one deletion	2.87%
Homopolymer indels	39.95%

2.6. Chromosome stats

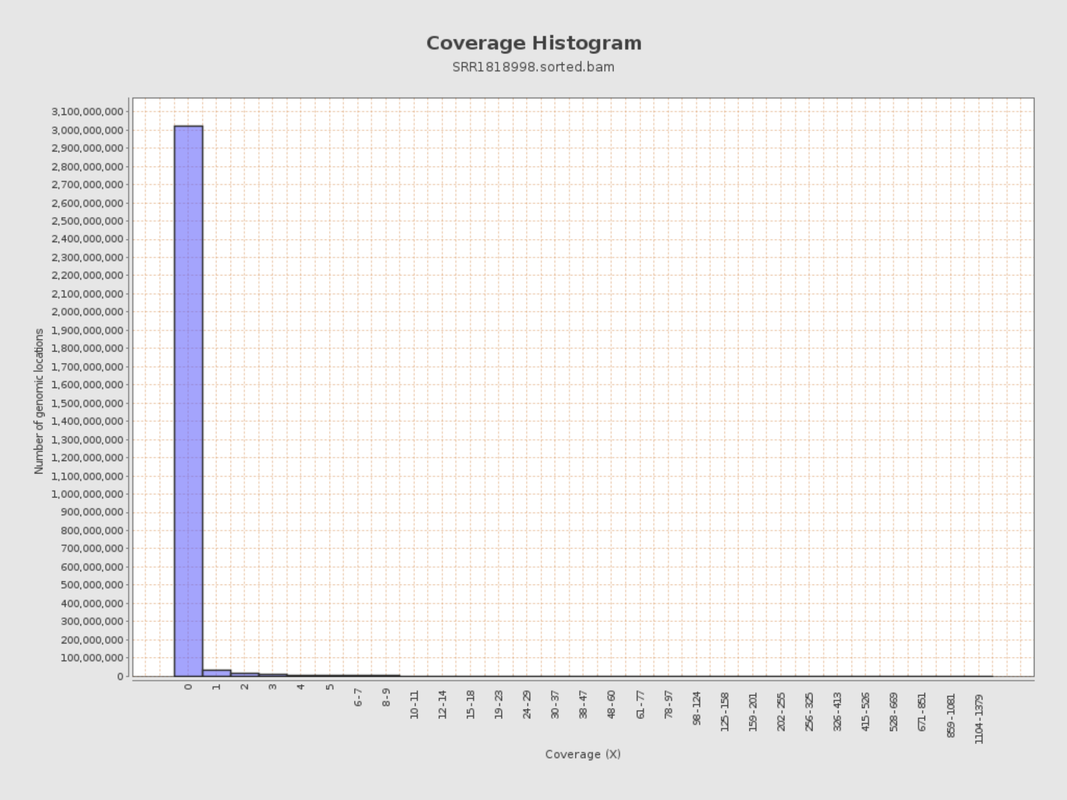
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18741622	0.0752	1.2724
chr2	243199373	18392231	0.0756	1.0761
chr3	198022430	12533457	0.0633	0.5334
chr4	191154276	12492844	0.0654	0.5904
chr5	180915260	10092979	0.0558	0.5136
chr6	171115067	8068211	0.0472	0.624
chr7	159138663	9309798	0.0585	0.84

chr8	146364022	17561534	0.12	0.8323
chr9	141213431	8010135	0.0567	0.7212
chr10	135534747	10902678	0.0804	0.994
chr11	135006516	6620249	0.049	0.5501
chr12	133851895	8989132	0.0672	0.5673
chr13	115169878	4034452	0.035	0.4011
chr14	107349540	4848602	0.0452	0.4696
chr15	102531392	4909058	0.0479	0.4819
chr16	90354753	6090149	0.0674	0.8503
chr17	81195210	6799204	0.0837	0.7211
chr18	78077248	4409529	0.0565	0.8613
chr19	59128983	3722886	0.063	1.1764
chr20	63025520	5892996	0.0935	0.6879
chr21	48129895	2647445	0.055	0.5267
chr22	51304566	1393364	0.0272	0.3805
chrMT	16571	123410	7.4473	6.9496
chrX	155270560	11514574	0.0742	0.6654
chrY	59373566	701952	0.0118	0.7187

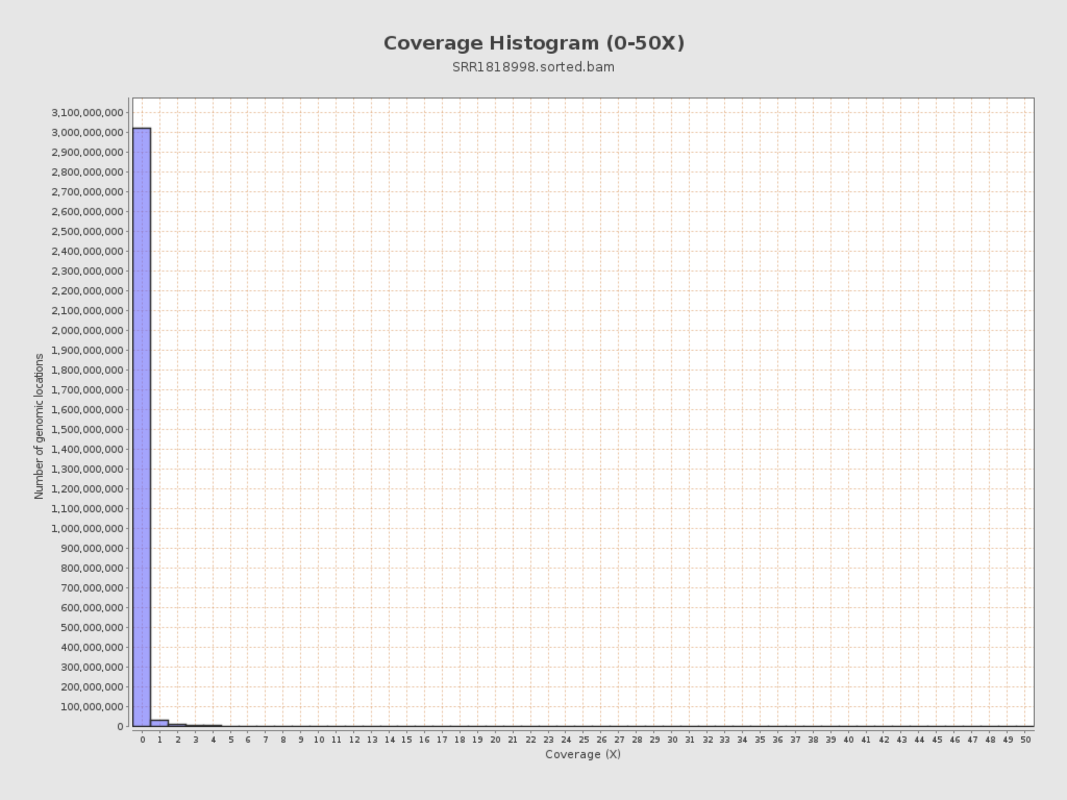
3. Results : Coverage across reference



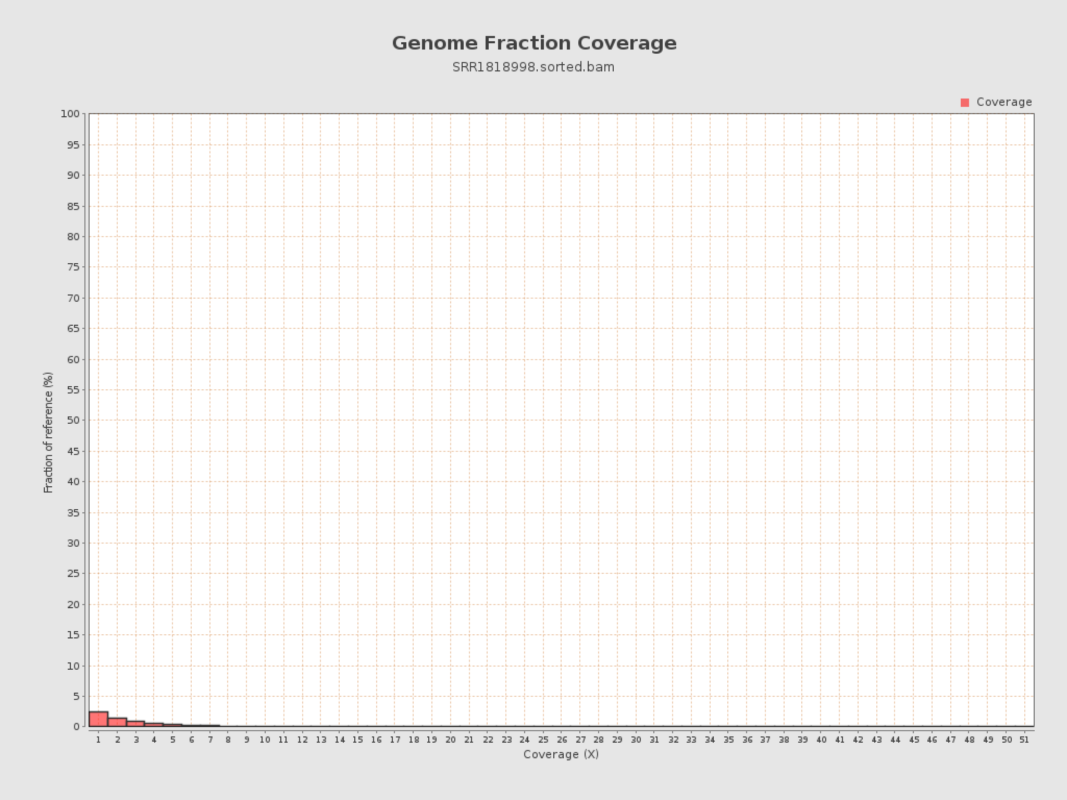
4. Results : Coverage Histogram



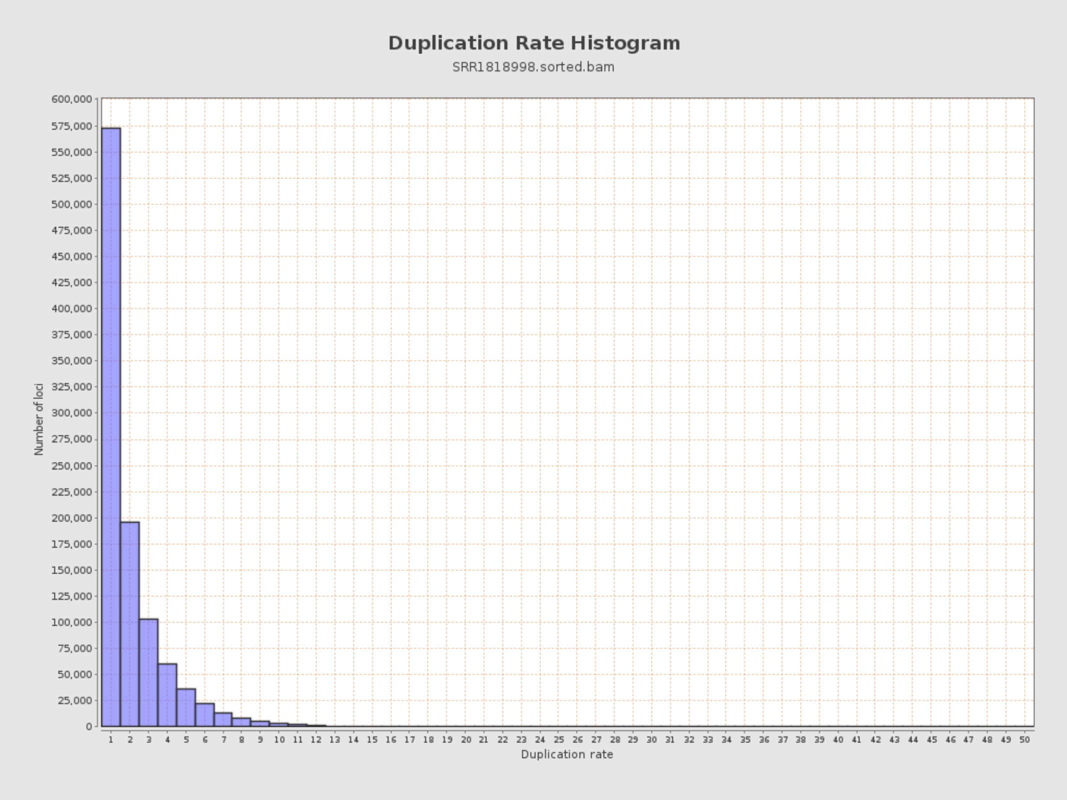
5. Results : Coverage Histogram (0-50X)



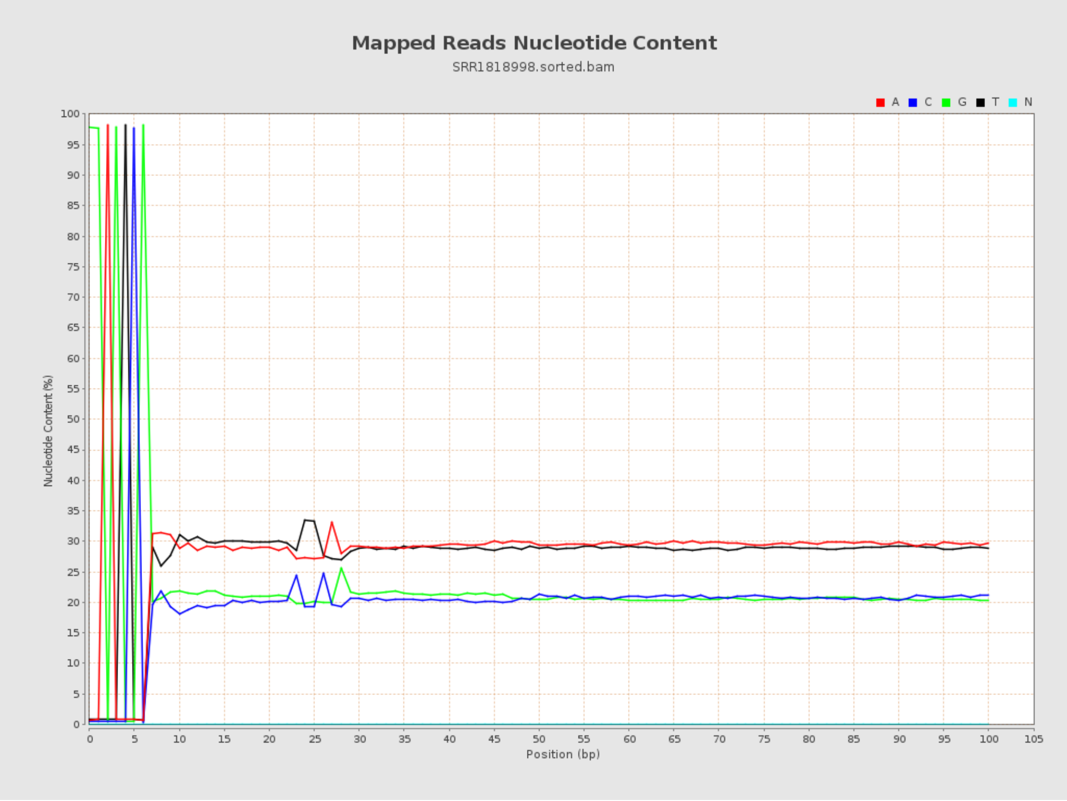
6. Results : Genome Fraction Coverage



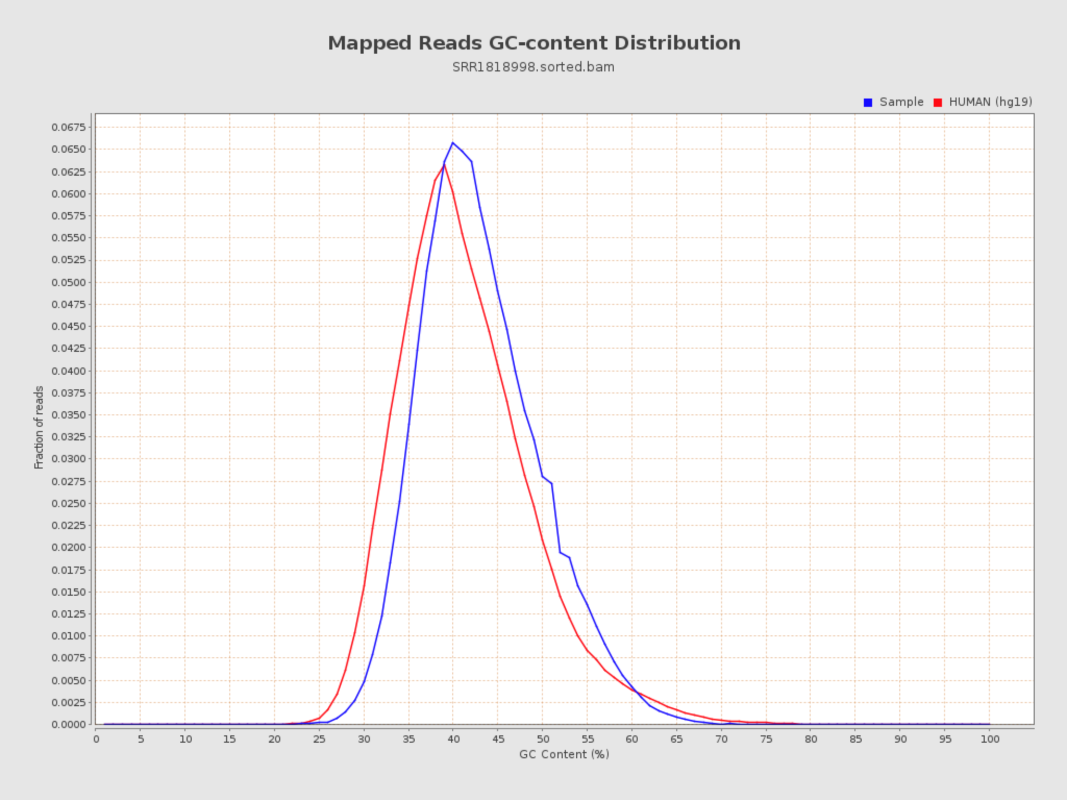
7. Results : Duplication Rate Histogram



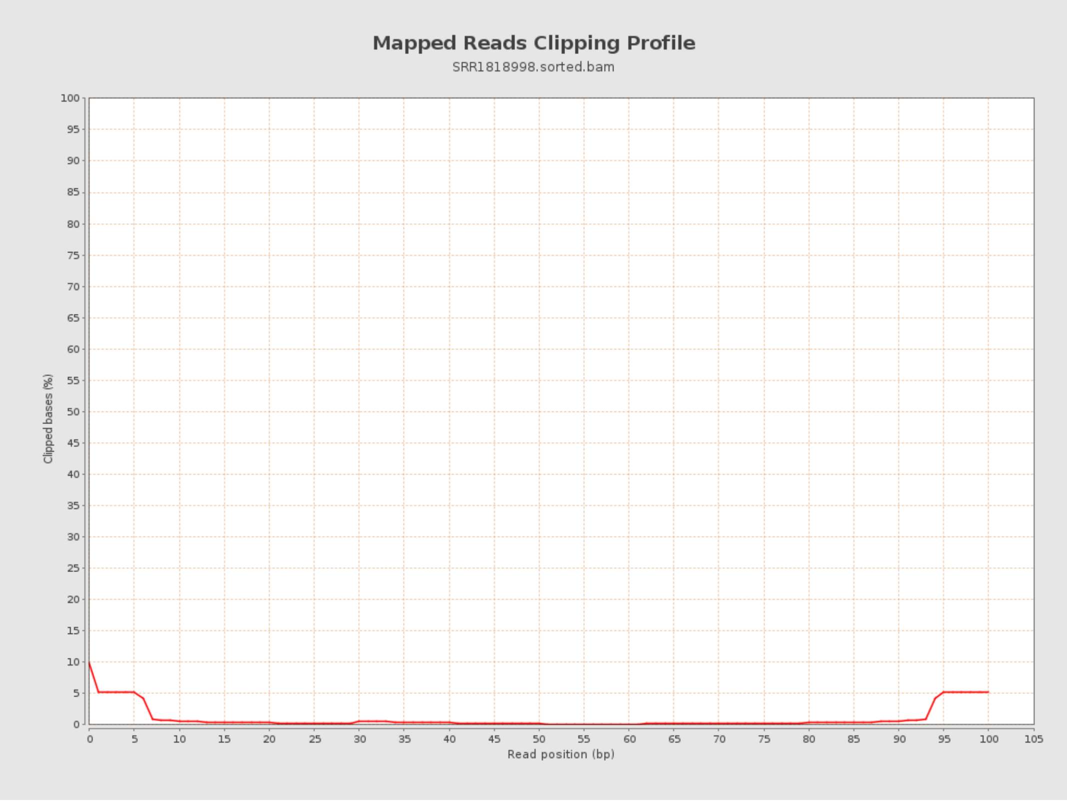
8. Results : Mapped Reads Nucleotide Content



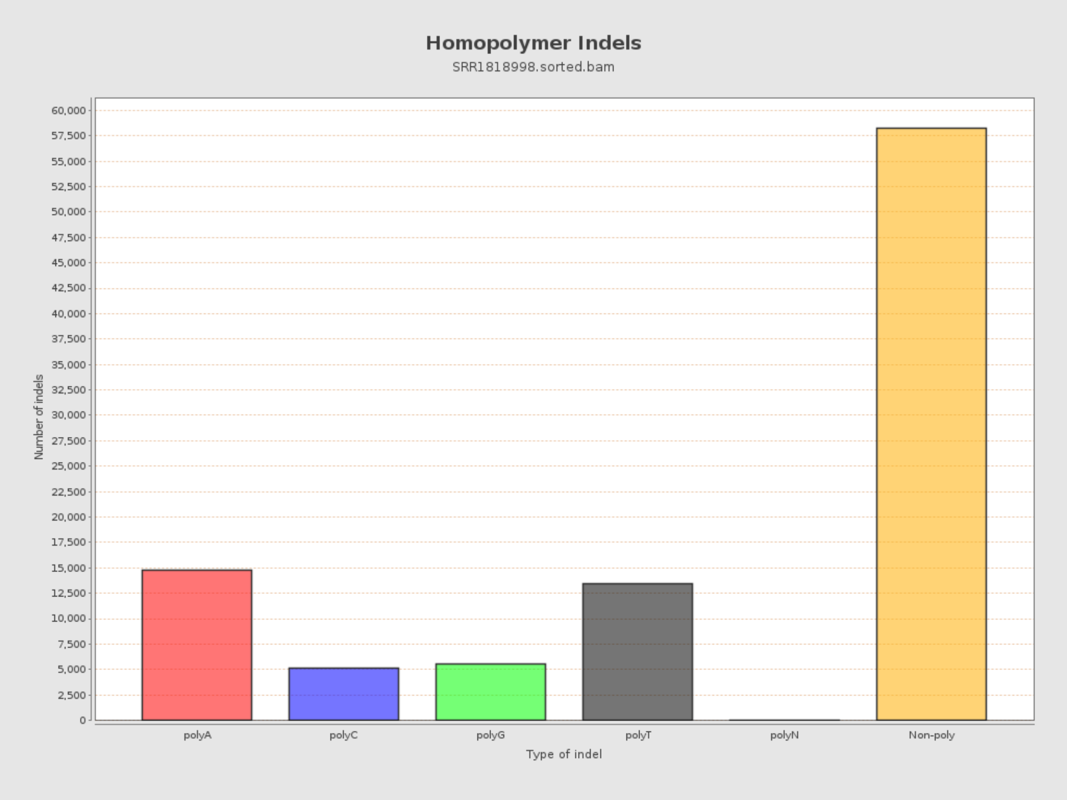
9. Results : Mapped Reads GC-content Distribution



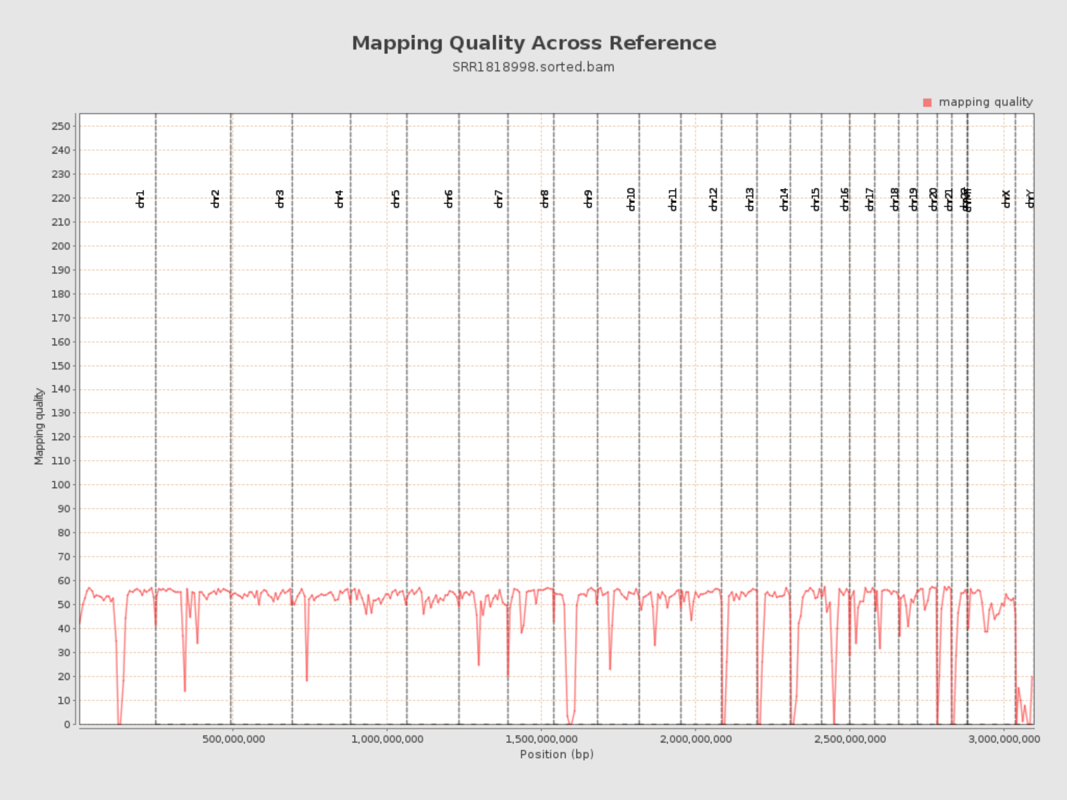
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram