Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:13:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818883.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_SRR1818883 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818883.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:13:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818883.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,818,296
Mapped reads	1,795,078 / 98.72%
Unmapped reads	23,218 / 1.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,277 / 1.5%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	345,045 / 18.98%
Duplication rate	16.02%
Clipped reads	1,797,848 / 98.88%

2.2. ACGT Content

Number/percentage of A's	47,188,813 / 28.4%
Number/percentage of C's	35,066,724 / 21.1%
Number/percentage of T's	47,909,384 / 28.83%
Number/percentage of G's	36,012,189 / 21.67%
Number/percentage of N's	2,385 / 0%
GC Percentage	42.77%

2.3. Coverage

Mean	0.0537

Standard Deviation	0.6581

2.4. Mapping Quality

Mean Mapping Quality	49.23

2.5. Mismatches and indels

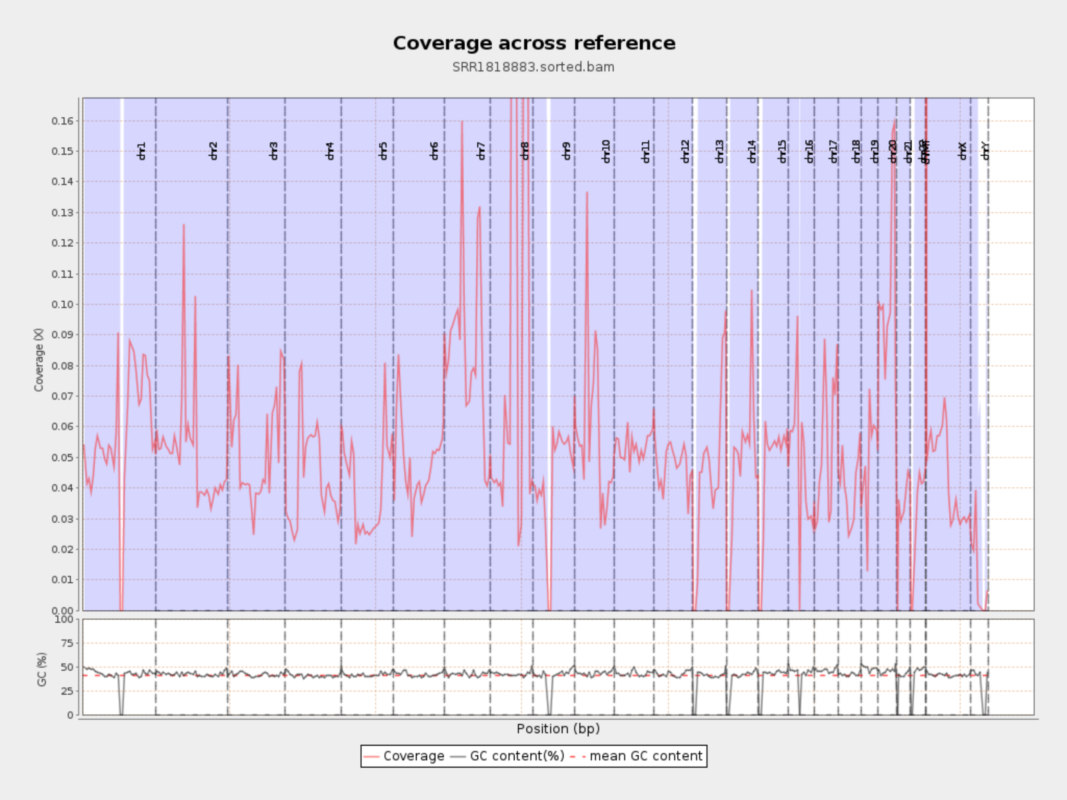
General error rate	0.66%
Mismatches	1,034,303
Insertions	24,596
Mapped reads with at least one insertion	1.33%
Deletions	53,783
Mapped reads with at least one deletion	2.92%
Homopolymer indels	39.64%

2.6. Chromosome stats

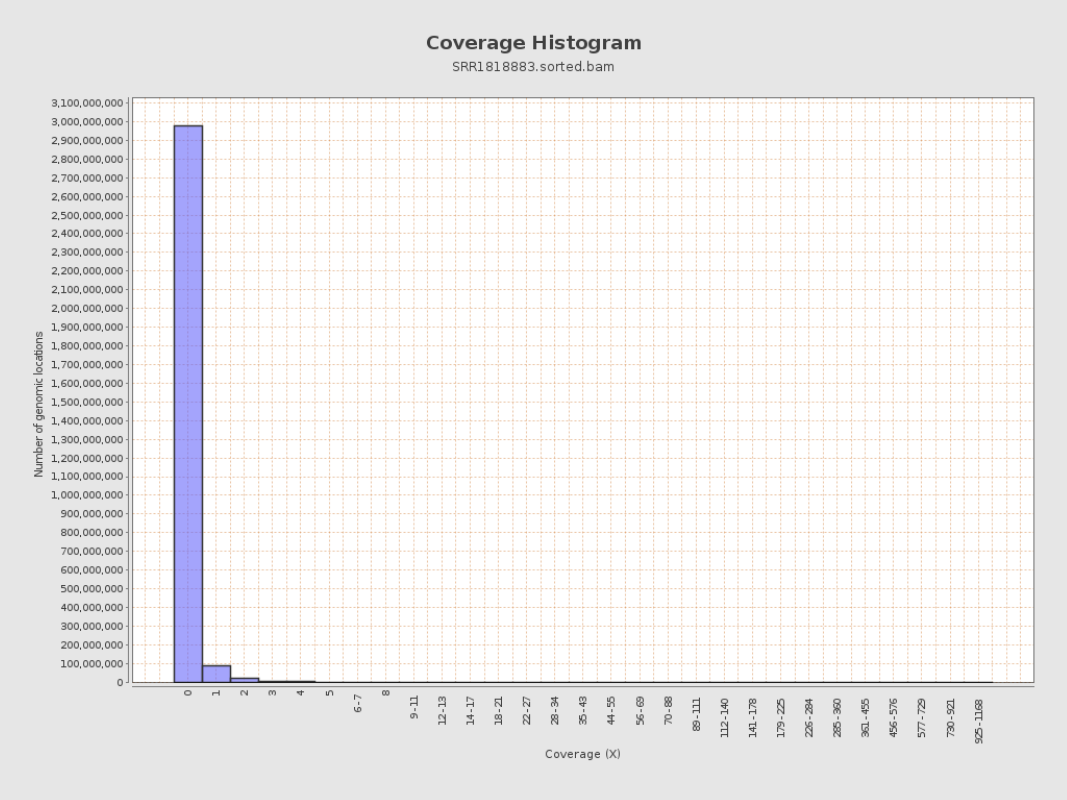
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14374163	0.0577	0.947
chr2	243199373	12566647	0.0517	0.9643
chr3	198022430	10565839	0.0534	0.3011
chr4	191154276	8372425	0.0438	0.3882
chr5	180915260	7306118	0.0404	0.2788
chr6	171115067	8201435	0.0479	0.3242
chr7	159138663	13664001	0.0859	1.4769

chr8	146364022	16527542	0.1129	0.5968
chr9	141213431	6055256	0.0429	0.5425
chr10	135534747	7744337	0.0571	0.8561
chr11	135006516	7209737	0.0534	0.3923
chr12	133851895	6390149	0.0477	0.2848
chr13	115169878	5255112	0.0456	0.2756
chr14	107349540	5164886	0.0481	0.3145
chr15	102531392	4614775	0.045	0.2742
chr16	90354753	4219755	0.0467	0.6963
chr17	81195210	4290252	0.0528	0.4168
chr18	78077248	3144688	0.0403	0.6253
chr19	59128983	2913711	0.0493	0.8309
chr20	63025520	6834701	0.1084	0.4696
chr21	48129895	1623366	0.0337	0.2984
chr22	51304566	1507438	0.0294	0.2535
chrMT	16571	285966	17.257	10.6489
chrX	155270560	6805502	0.0438	0.3445
chrY	59373566	647787	0.0109	0.7798

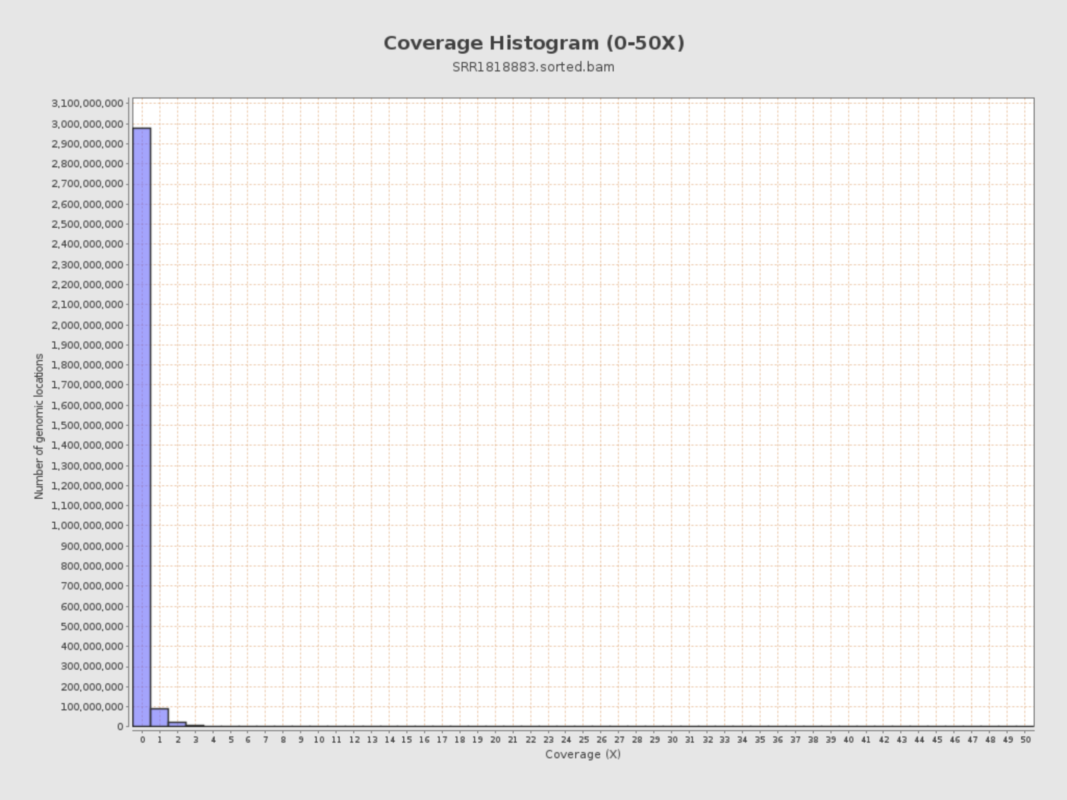
3. Results : Coverage across reference



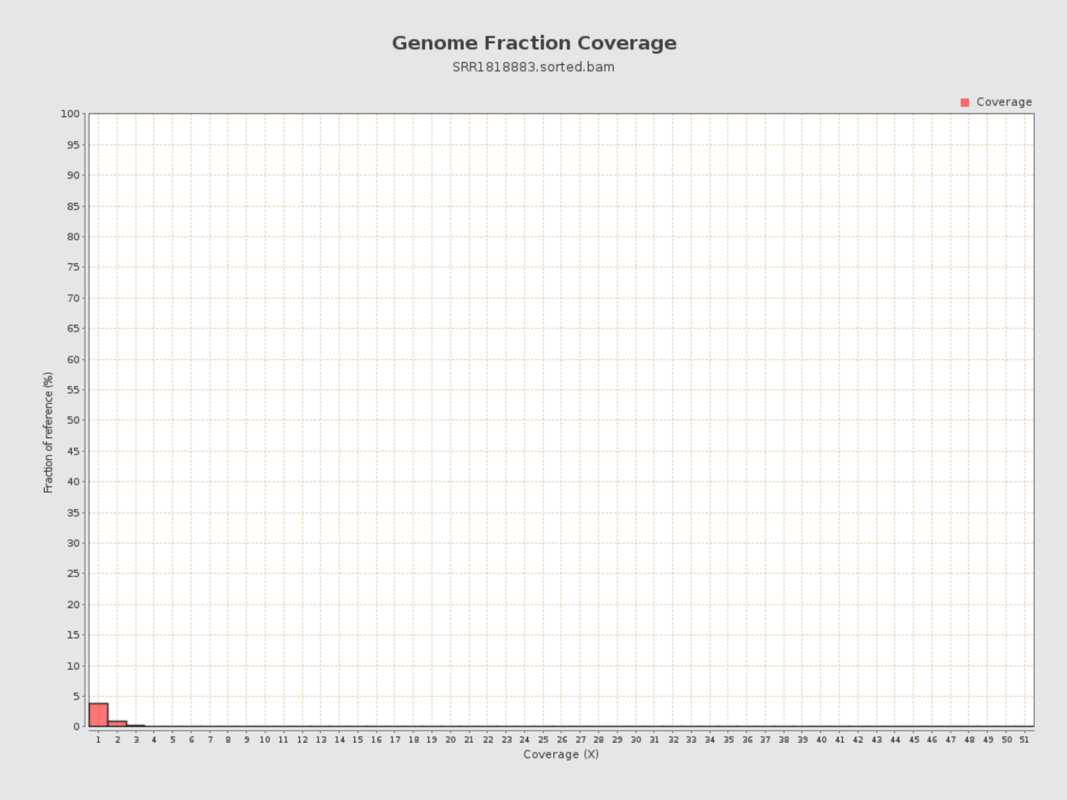
4. Results : Coverage Histogram



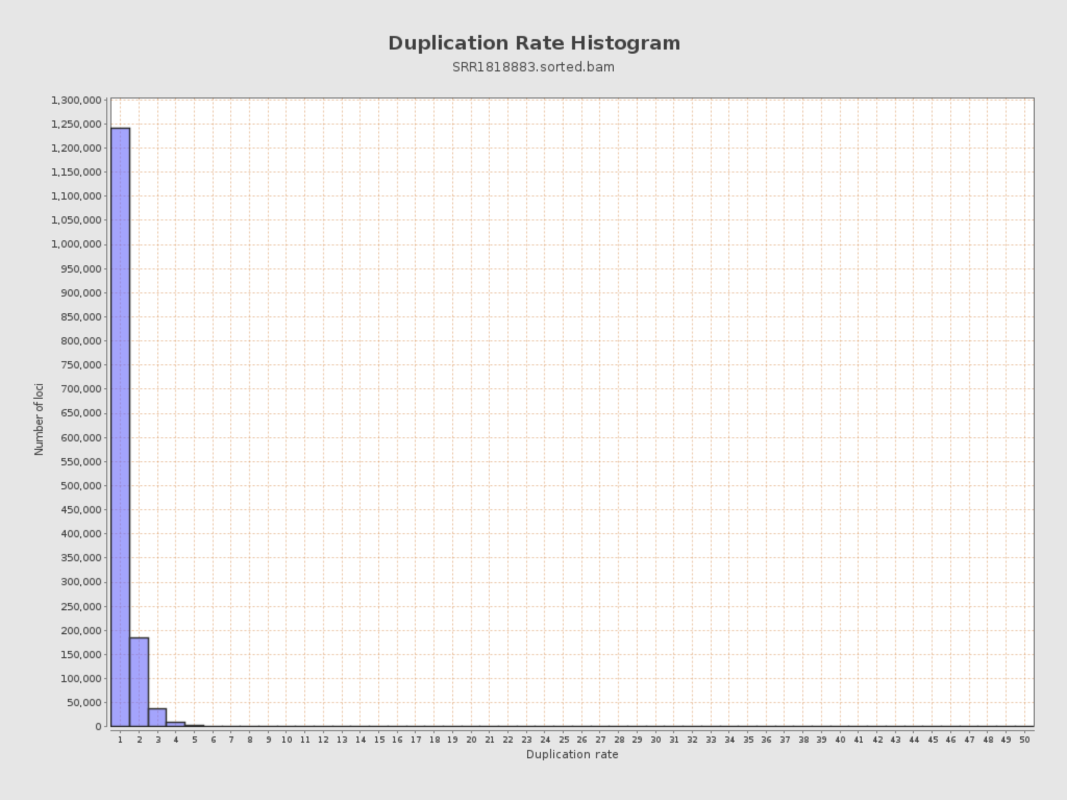
5. Results : Coverage Histogram (0-50X)



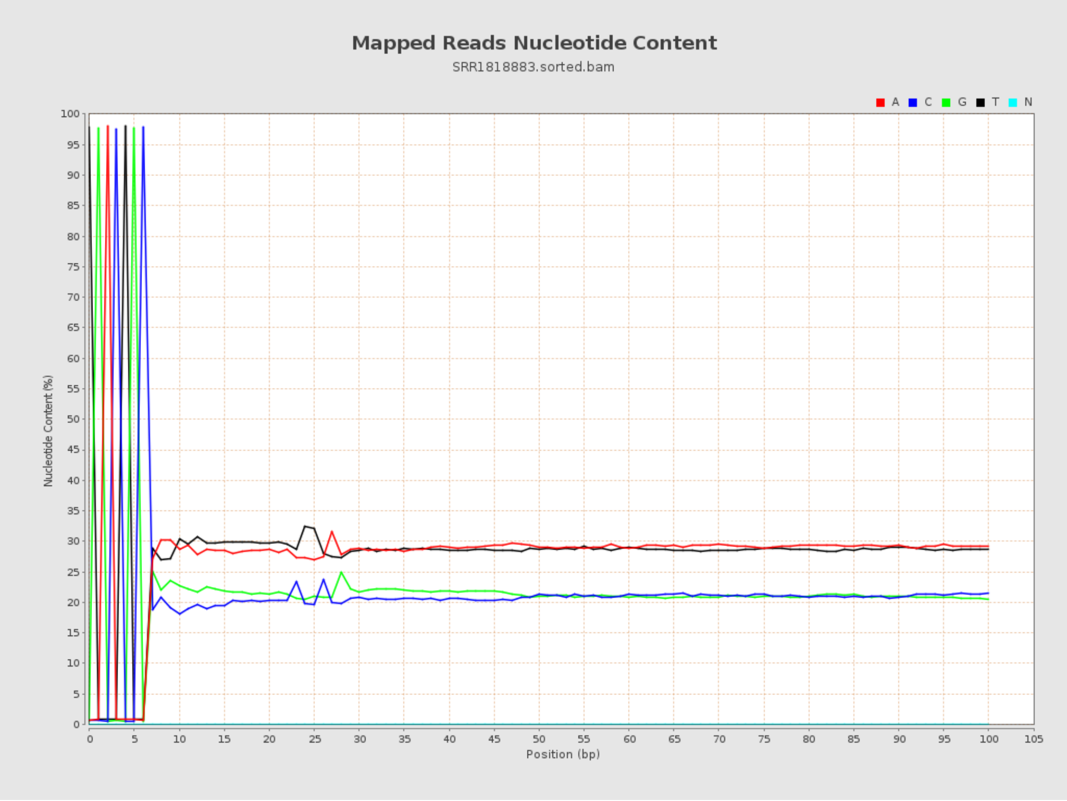
6. Results : Genome Fraction Coverage



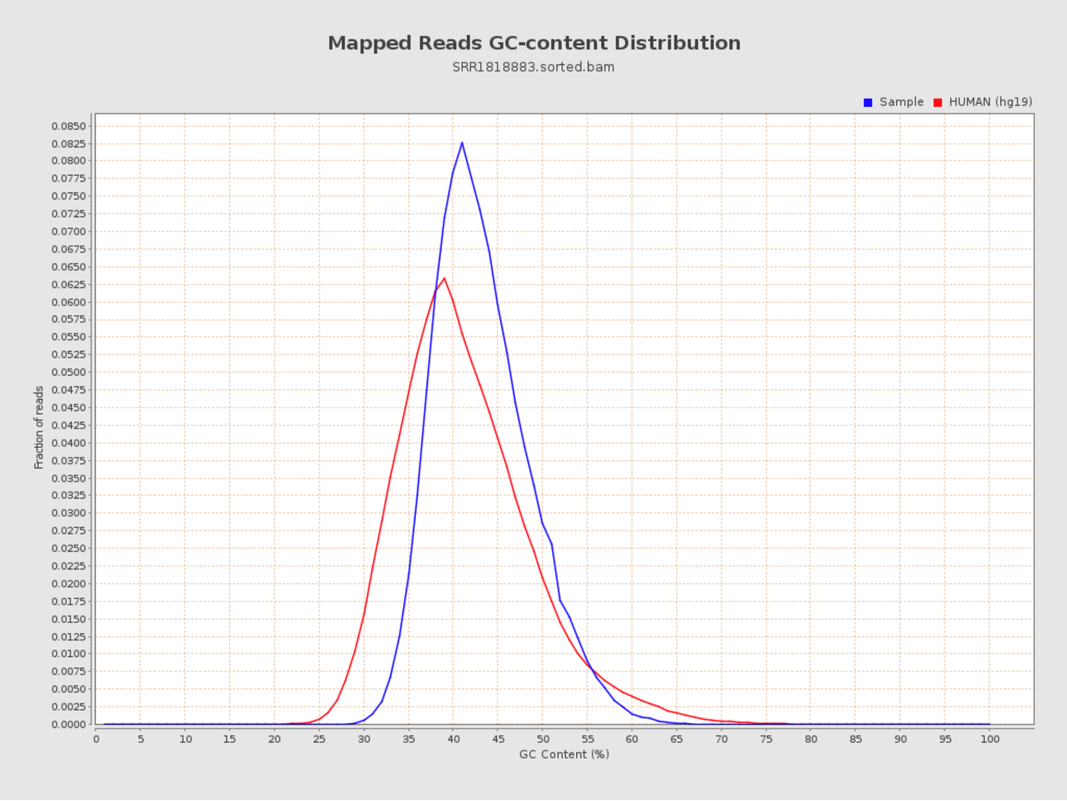
7. Results : Duplication Rate Histogram



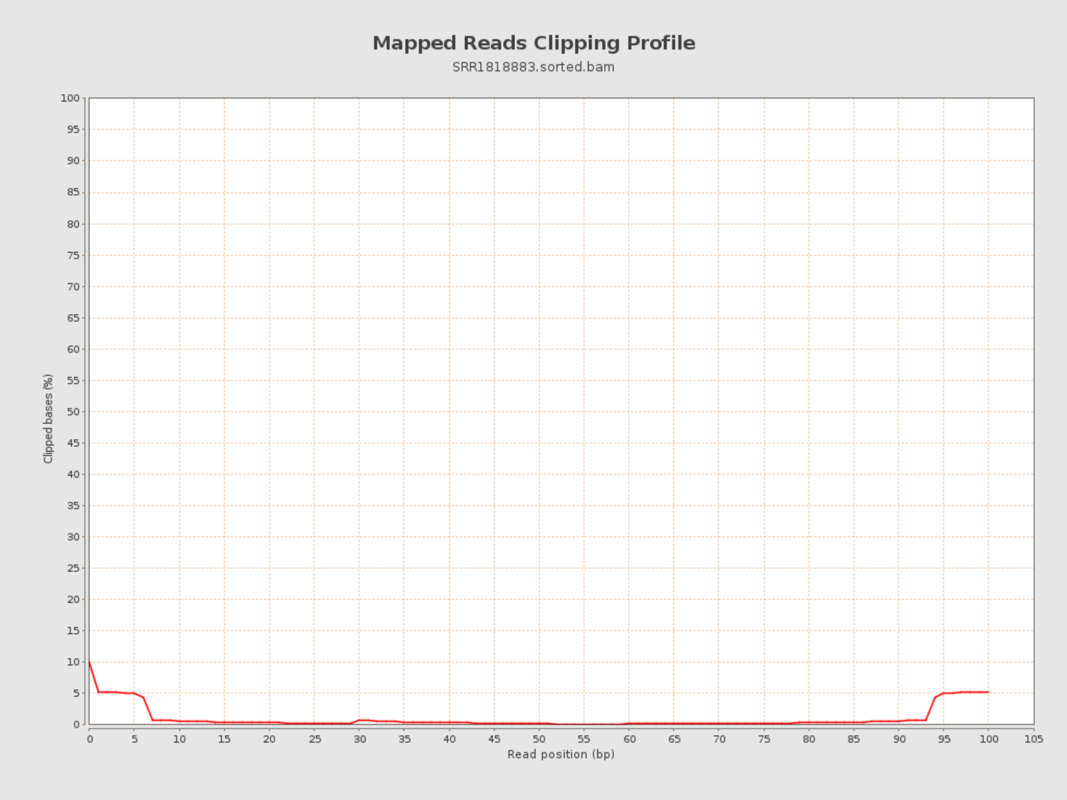
8. Results : Mapped Reads Nucleotide Content



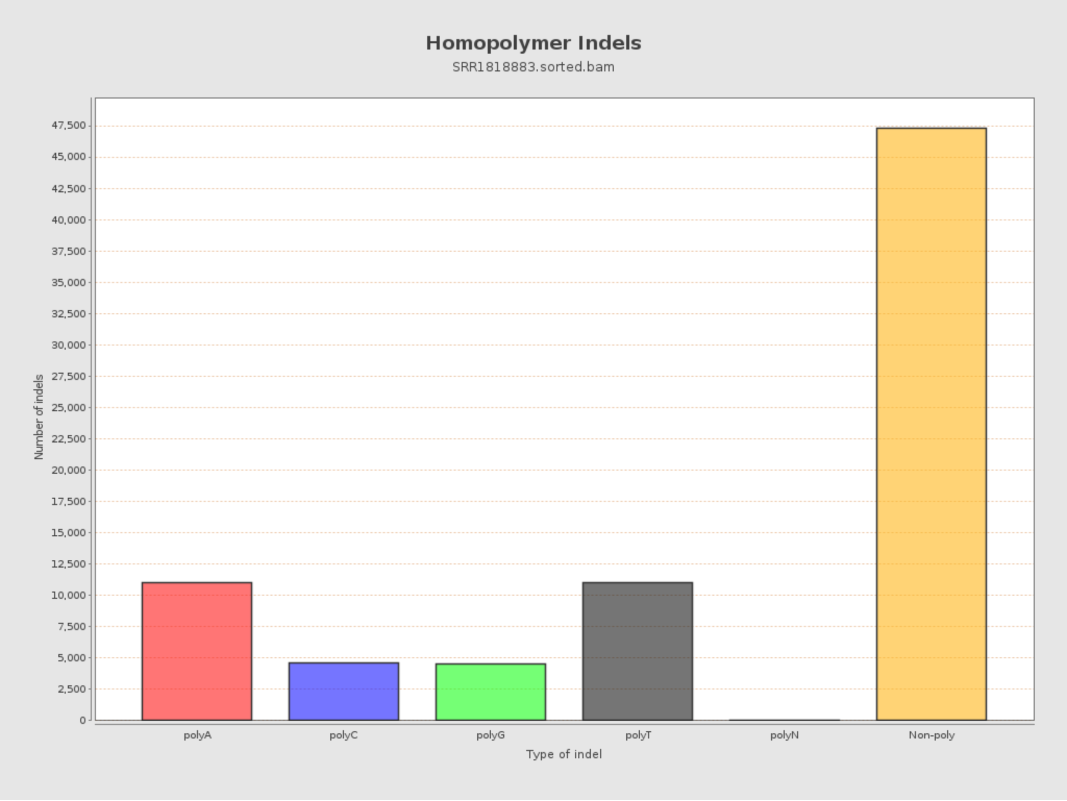
9. Results : Mapped Reads GC-content Distribution



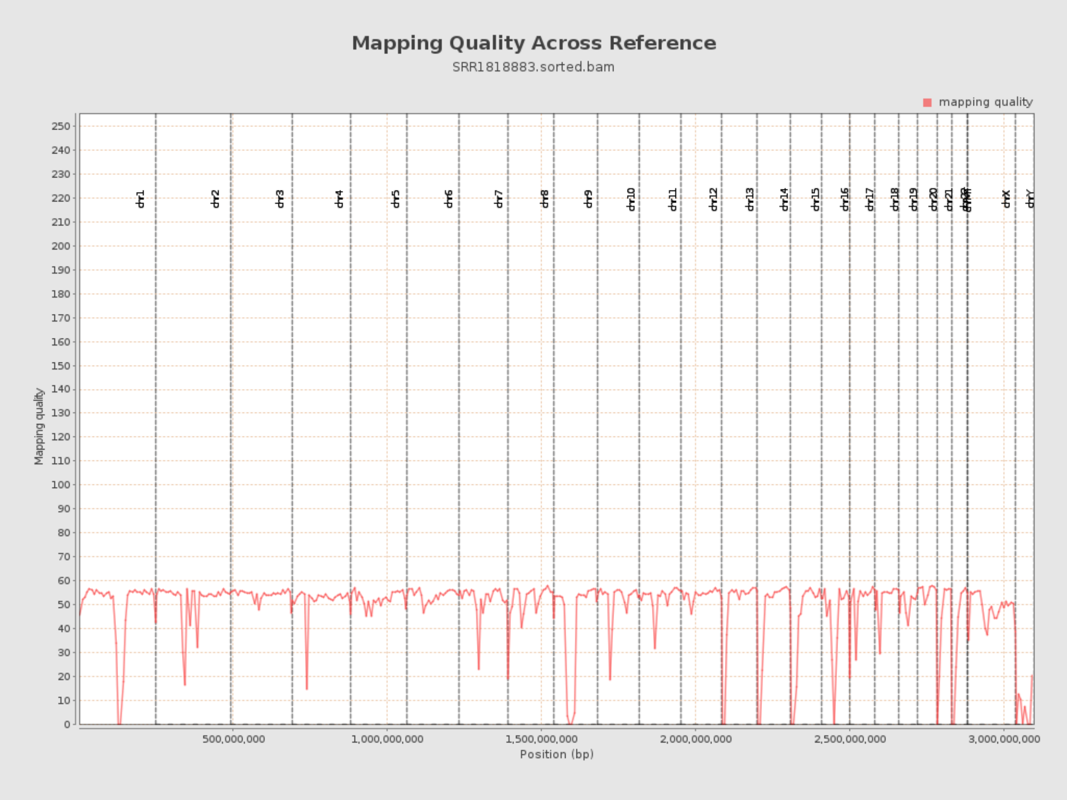
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram