Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:24:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818988.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_SRR1818988 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818988.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:24:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818988.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,596,453
Mapped reads	2,552,469 / 98.31%
Unmapped reads	43,984 / 1.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,701 / 1.57%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	1,658,672 / 63.88%
Duplication rate	50.57%
Clipped reads	2,577,219 / 99.26%

2.2. ACGT Content

Number/percentage of A's	68,009,090 / 28.84%
Number/percentage of C's	52,956,143 / 22.46%
Number/percentage of T's	67,940,858 / 28.81%
Number/percentage of G's	46,904,563 / 19.89%
Number/percentage of N's	11,288 / 0%
GC Percentage	42.35%

2.3. Coverage

Mean	0.0762

Standard Deviation	0.9402

2.4. Mapping Quality

Mean Mapping Quality	49.33

2.5. Mismatches and indels

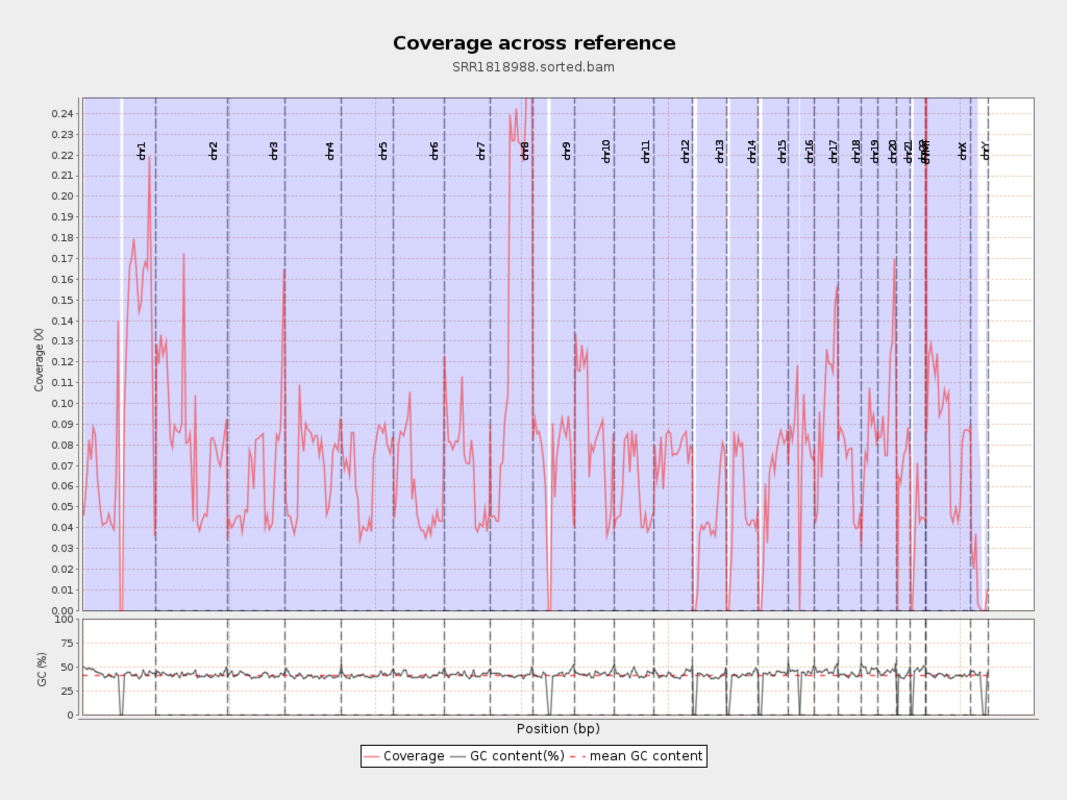
General error rate	0.67%
Mismatches	1,504,135
Insertions	37,638
Mapped reads with at least one insertion	1.44%
Deletions	78,350
Mapped reads with at least one deletion	3.01%
Homopolymer indels	43.48%

2.6. Chromosome stats

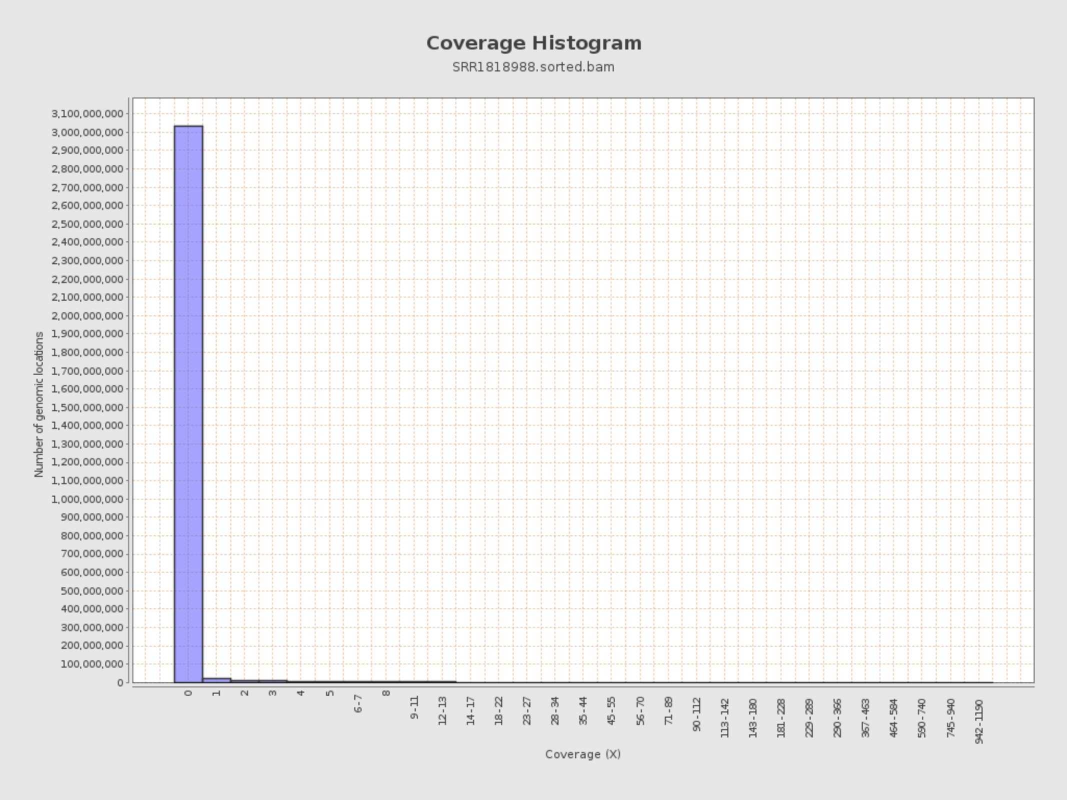
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24001139	0.0963	1.4072
chr2	243199373	20737726	0.0853	1.4255
chr3	198022430	12663959	0.064	0.6595
chr4	191154276	13464471	0.0704	0.7641
chr5	180915260	12297777	0.068	0.6988
chr6	171115067	9802457	0.0573	0.6953
chr7	159138663	11203251	0.0704	0.9285

chr8	146364022	24088052	0.1646	1.1492
chr9	141213431	9883790	0.07	0.8845
chr10	135534747	11864476	0.0875	0.9983
chr11	135006516	7757007	0.0575	0.6898
chr12	133851895	10403192	0.0777	0.7395
chr13	115169878	4861891	0.0422	0.5404
chr14	107349540	5391250	0.0502	0.5956
chr15	102531392	5911111	0.0577	0.6432
chr16	90354753	7089963	0.0785	0.9755
chr17	81195210	8229276	0.1014	0.9242
chr18	78077248	5237269	0.0671	0.9152
chr19	59128983	4742657	0.0802	1.2555
chr20	63025520	6729287	0.1068	0.925
chr21	48129895	3208139	0.0667	0.7061
chr22	51304566	1864447	0.0363	0.6117
chrMT	16571	32845	1.9821	3.9796
chrX	155270560	13787399	0.0888	0.8483
chrY	59373566	706677	0.0119	0.6784

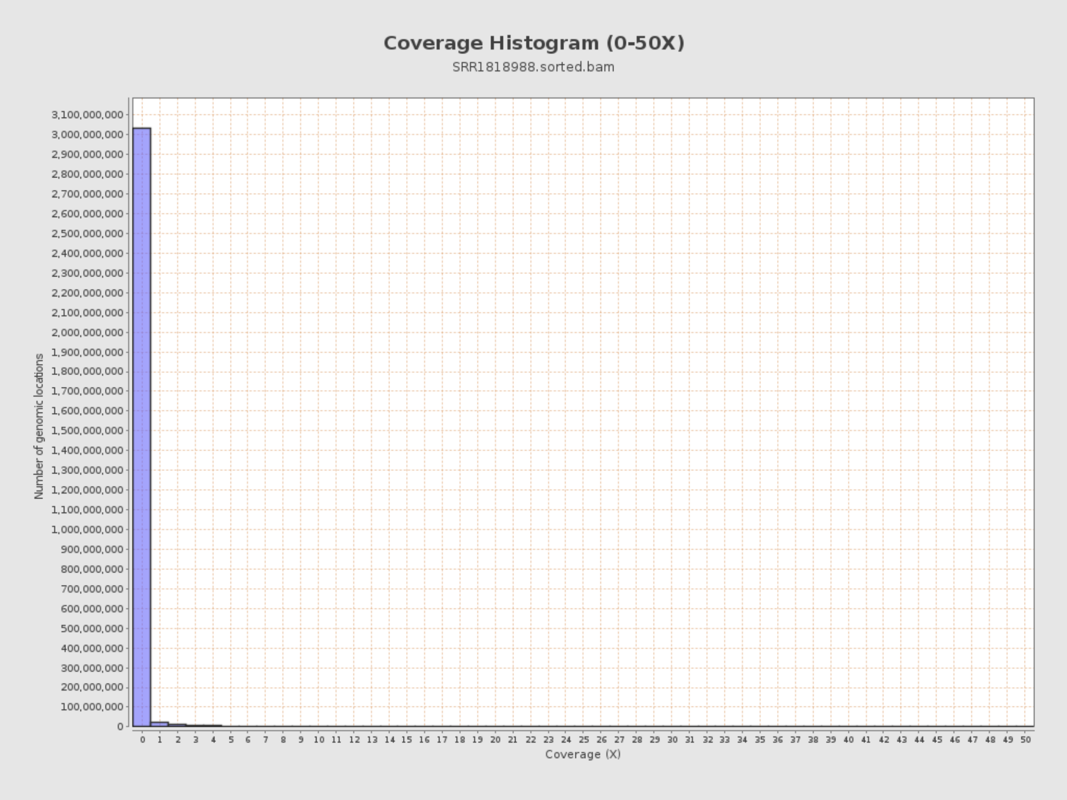
3. Results : Coverage across reference



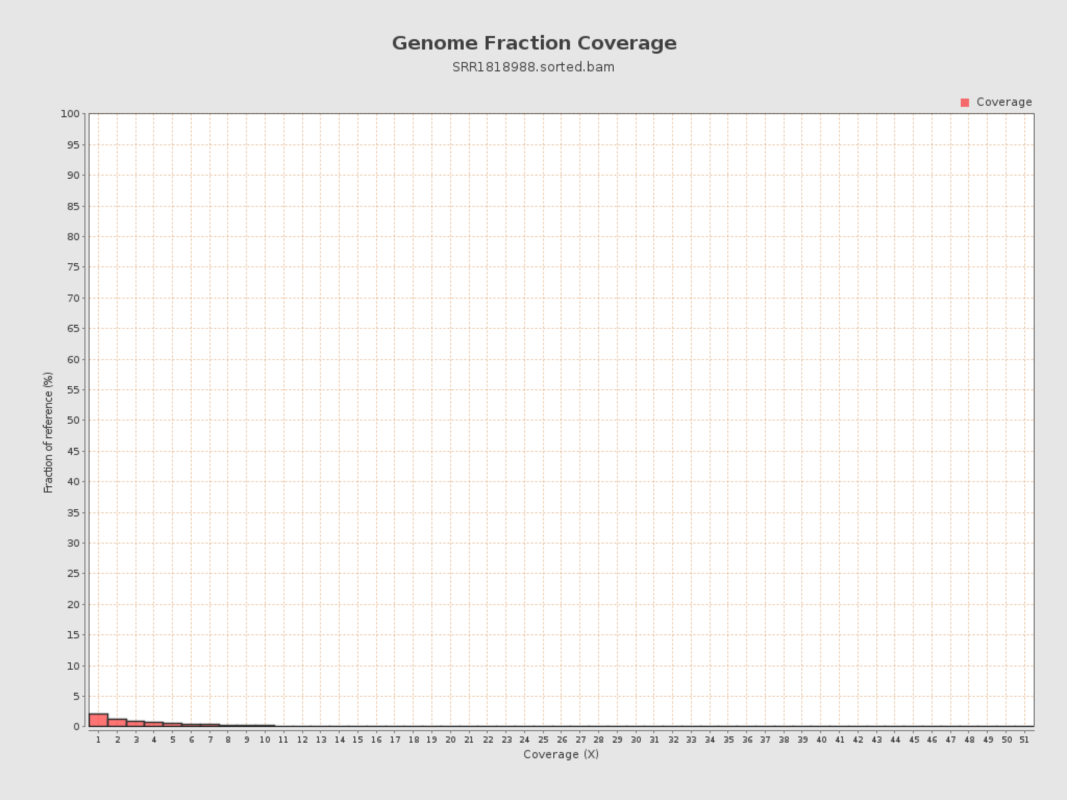
4. Results : Coverage Histogram



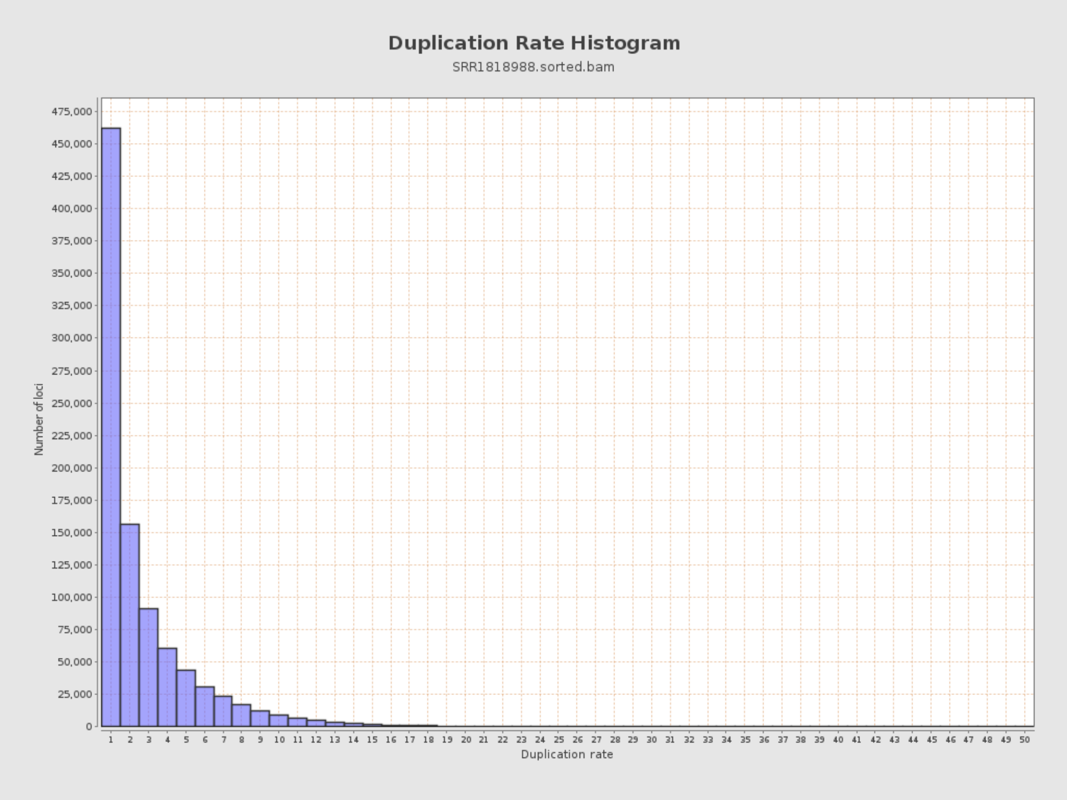
5. Results : Coverage Histogram (0-50X)



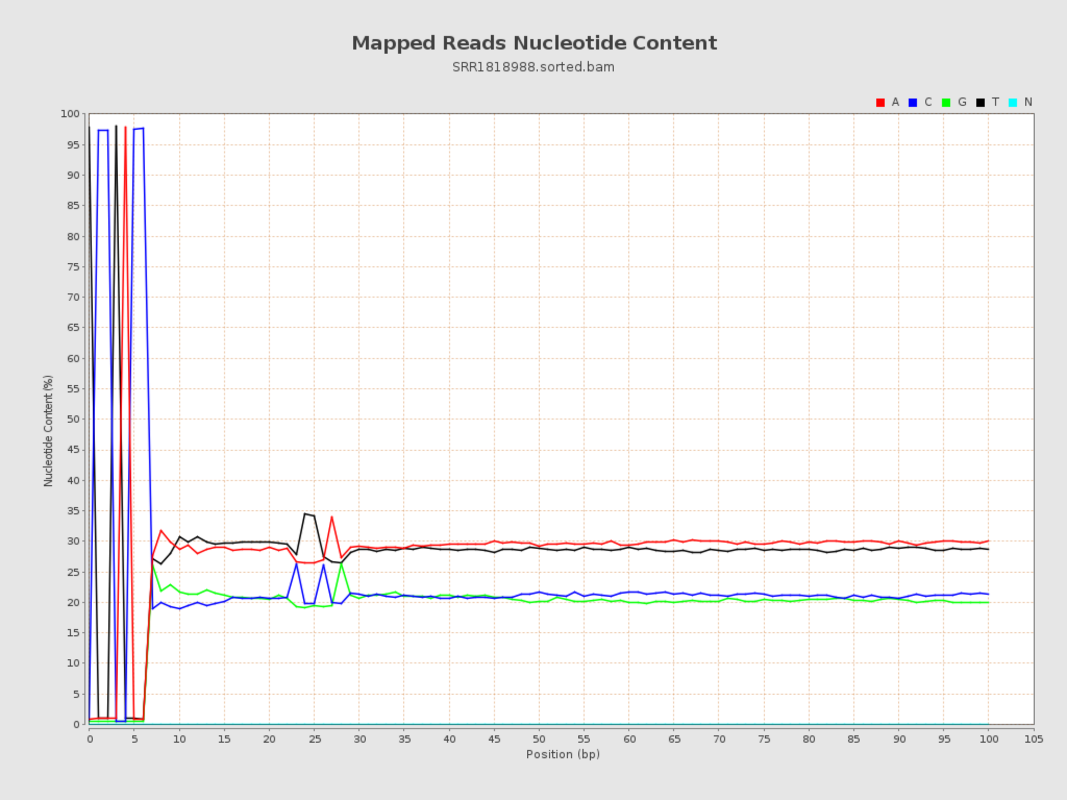
6. Results : Genome Fraction Coverage



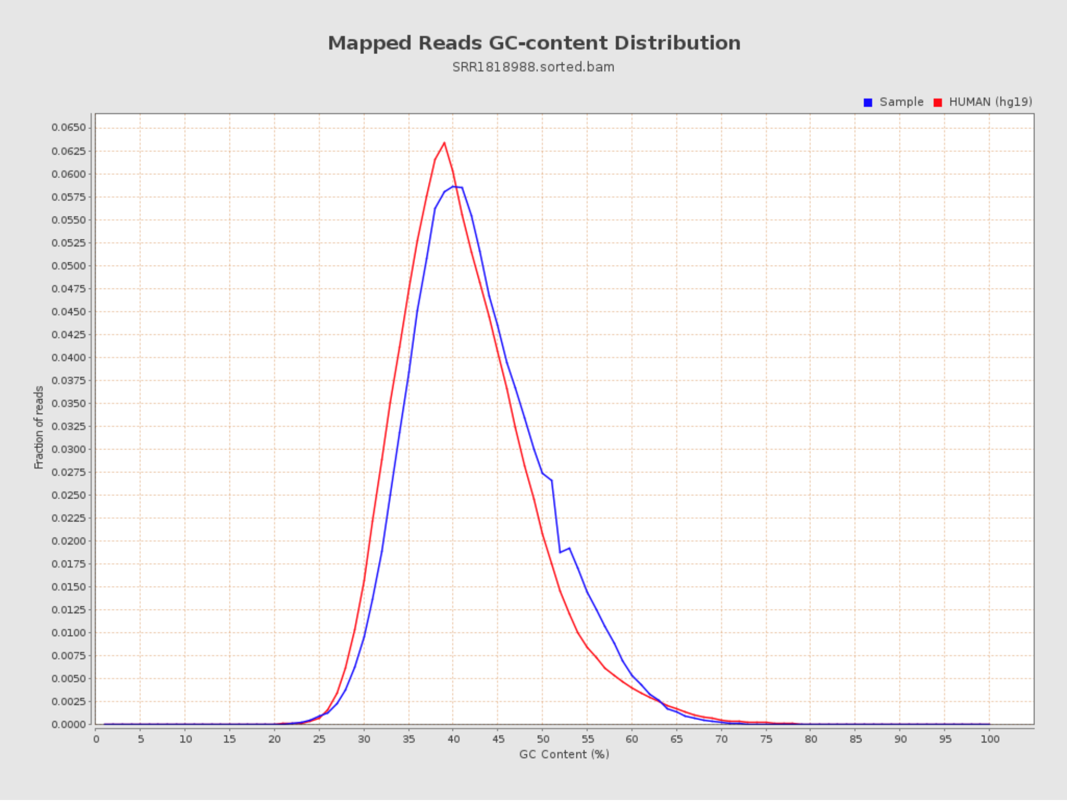
7. Results : Duplication Rate Histogram



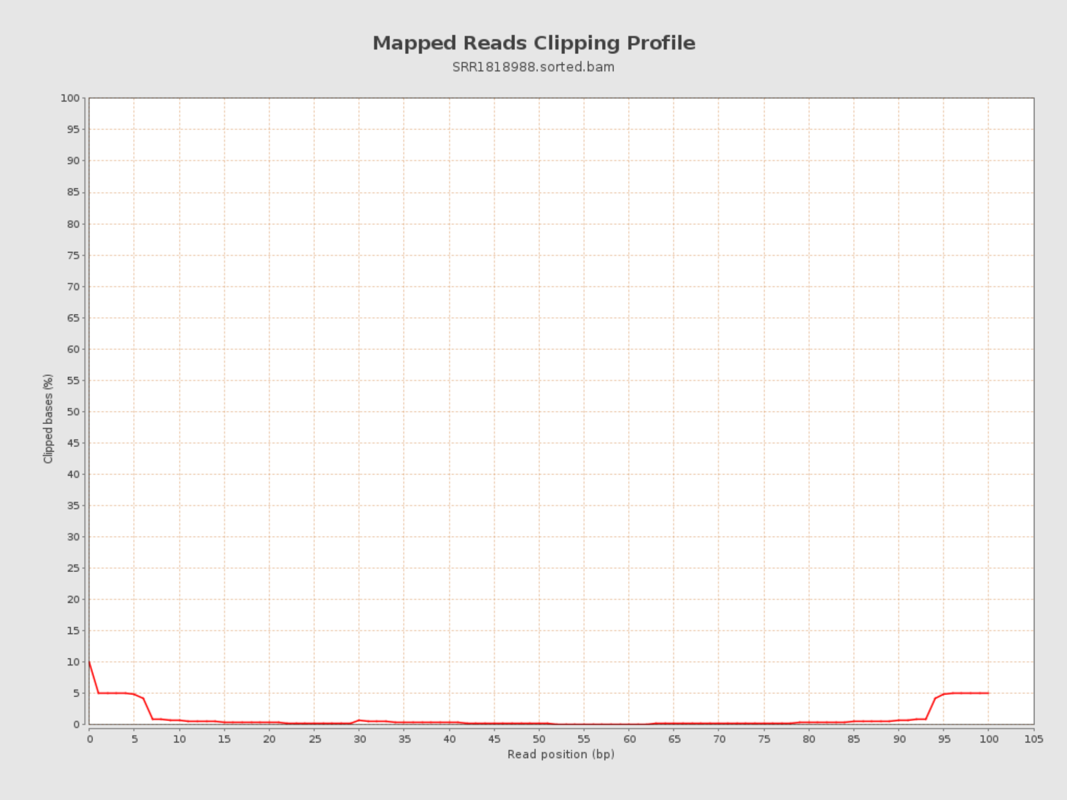
8. Results : Mapped Reads Nucleotide Content



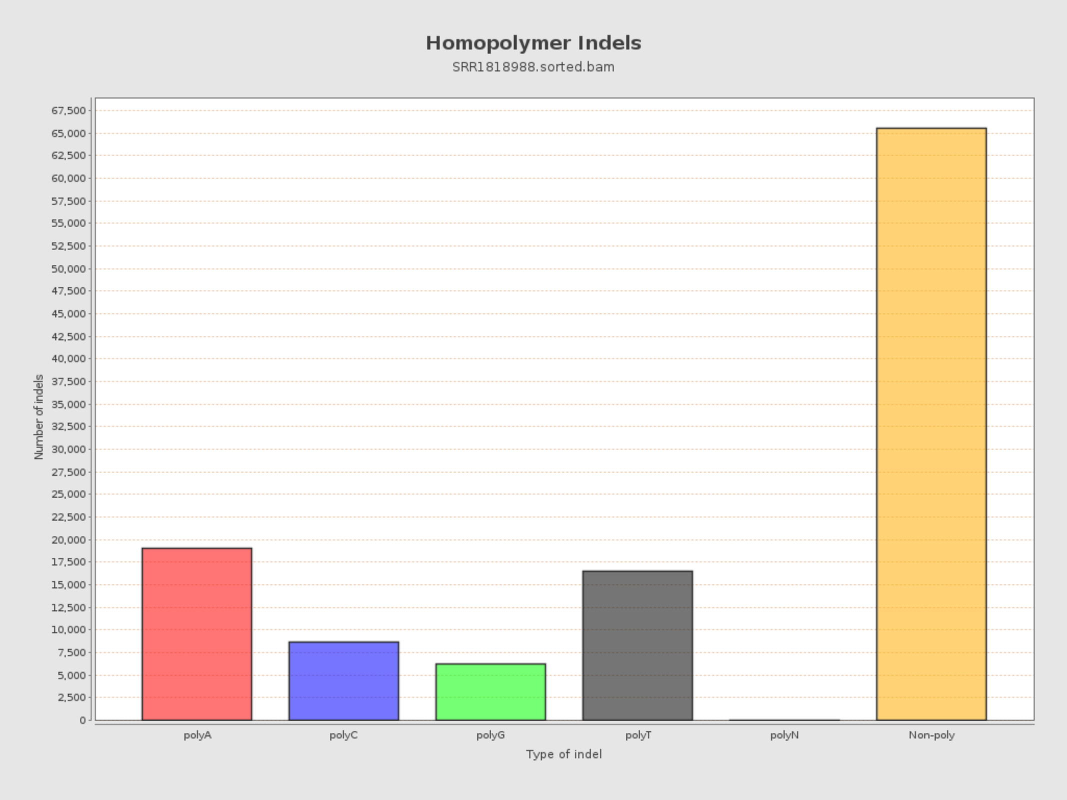
9. Results : Mapped Reads GC-content Distribution



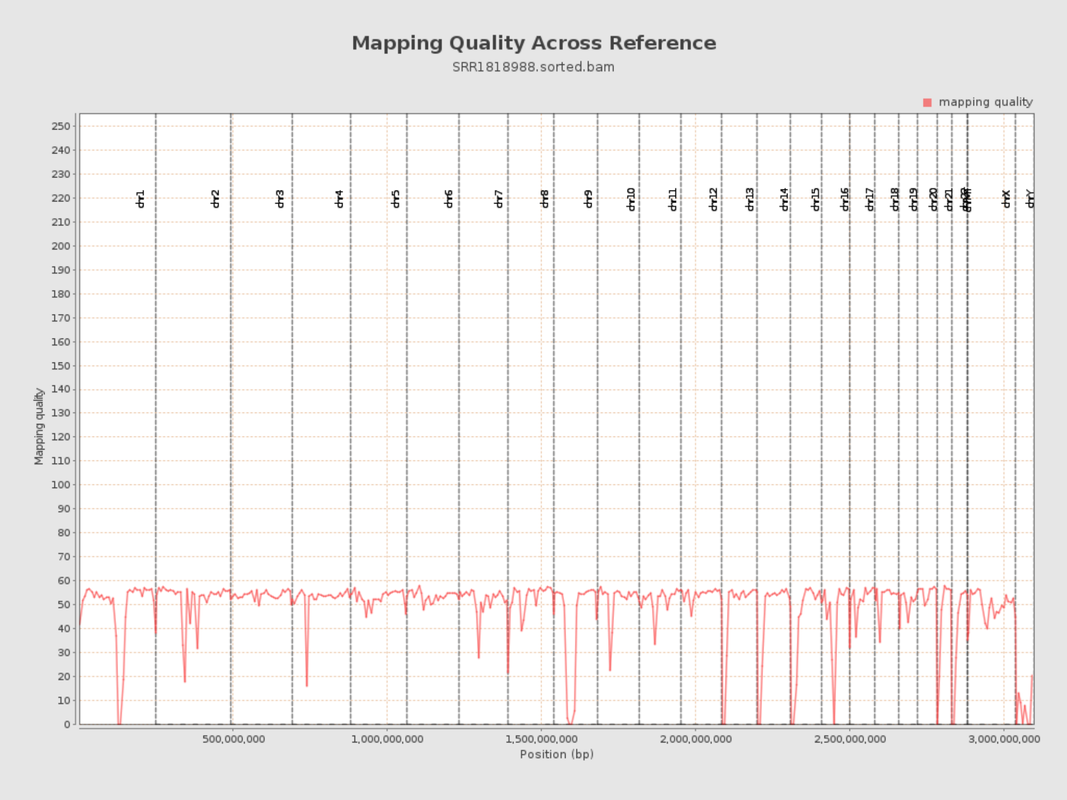
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram