Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:52:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524818.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_SRR10524818 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524818.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:52:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524818.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,612,118
Mapped reads	1,468,132 / 91.07%
Unmapped reads	143,986 / 8.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,759 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	57,027 / 3.54%
Duplication rate	2.99%
Clipped reads	1,469,255 / 91.14%

2.2. ACGT Content

Number/percentage of A's	20,032,892 / 23.89%
Number/percentage of C's	15,584,165 / 18.59%
Number/percentage of T's	27,041,417 / 32.25%
Number/percentage of G's	21,176,352 / 25.26%
Number/percentage of N's	9,999 / 0.01%
GC Percentage	43.84%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.2343

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

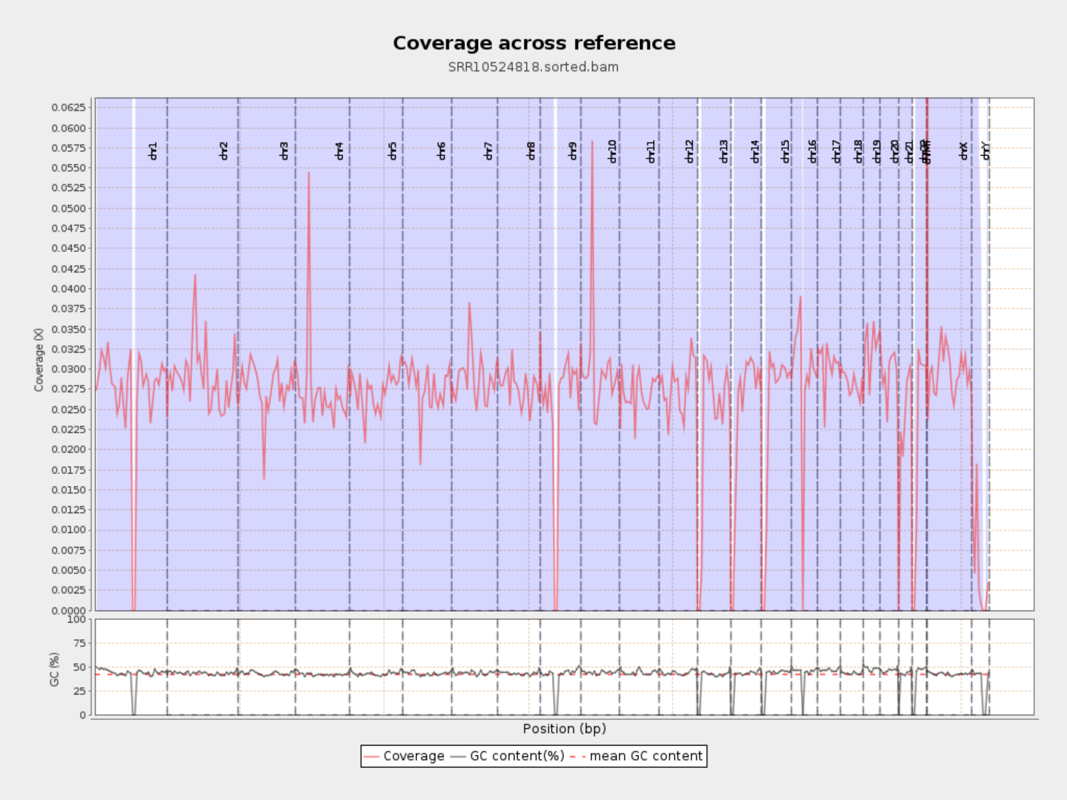
General error rate	0.51%
Mismatches	416,913
Insertions	6,515
Mapped reads with at least one insertion	0.44%
Deletions	16,067
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.18%

2.6. Chromosome stats

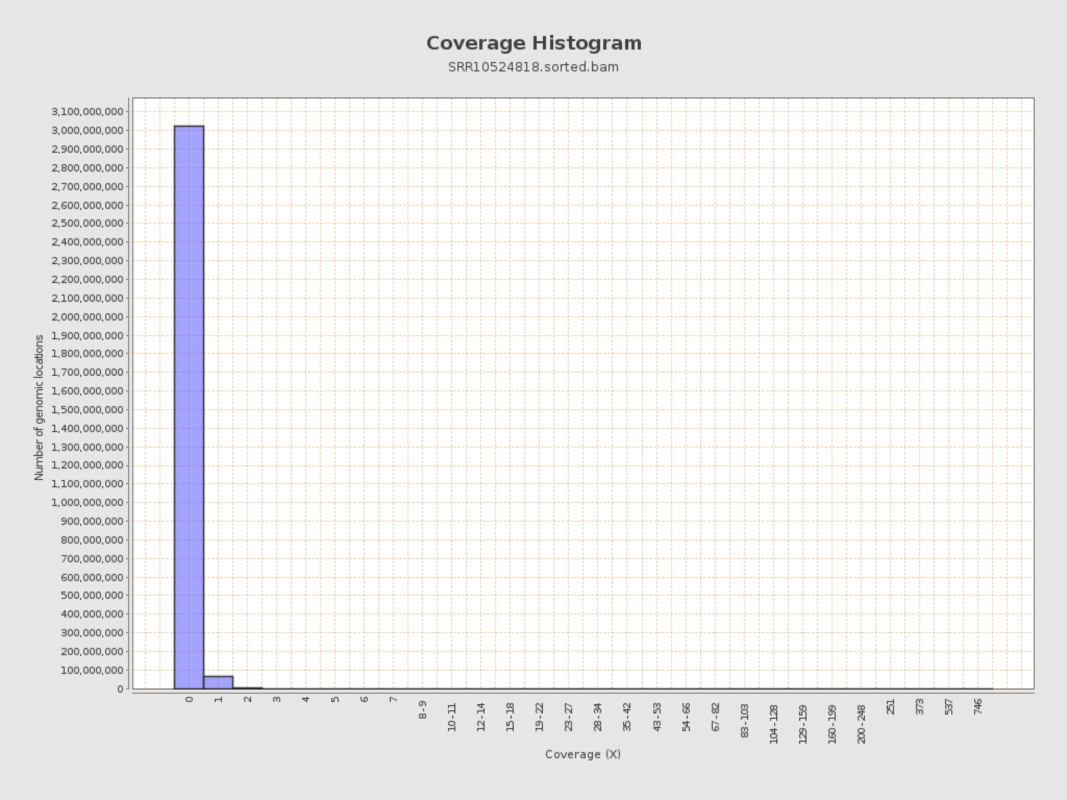
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6690834	0.0268	0.2677
chr2	243199373	7095260	0.0292	0.3785
chr3	198022430	5512596	0.0278	0.1871
chr4	191154276	5259535	0.0275	0.2184
chr5	180915260	4966363	0.0275	0.1839
chr6	171115067	4761049	0.0278	0.2028
chr7	159138663	4623684	0.0291	0.2763

chr8	146364022	4063239	0.0278	0.2065
chr9	141213431	3528490	0.025	0.205
chr10	135534747	4098205	0.0302	0.2936
chr11	135006516	3666053	0.0272	0.2119
chr12	133851895	3710644	0.0277	0.1853
chr13	115169878	2663658	0.0231	0.1686
chr14	107349540	2580672	0.024	0.1766
chr15	102531392	2466947	0.0241	0.1746
chr16	90354753	2594510	0.0287	0.2086
chr17	81195210	2488242	0.0306	0.2027
chr18	78077248	2200318	0.0282	0.2994
chr19	59128983	1931890	0.0327	0.2528
chr20	63025520	1846960	0.0293	0.2009
chr21	48129895	1100227	0.0229	0.1906
chr22	51304566	1086427	0.0212	0.1615
chrMT	16571	28951	1.7471	1.6859
chrX	155270560	4610907	0.0297	0.2044
chrY	59373566	295373	0.005	0.1519

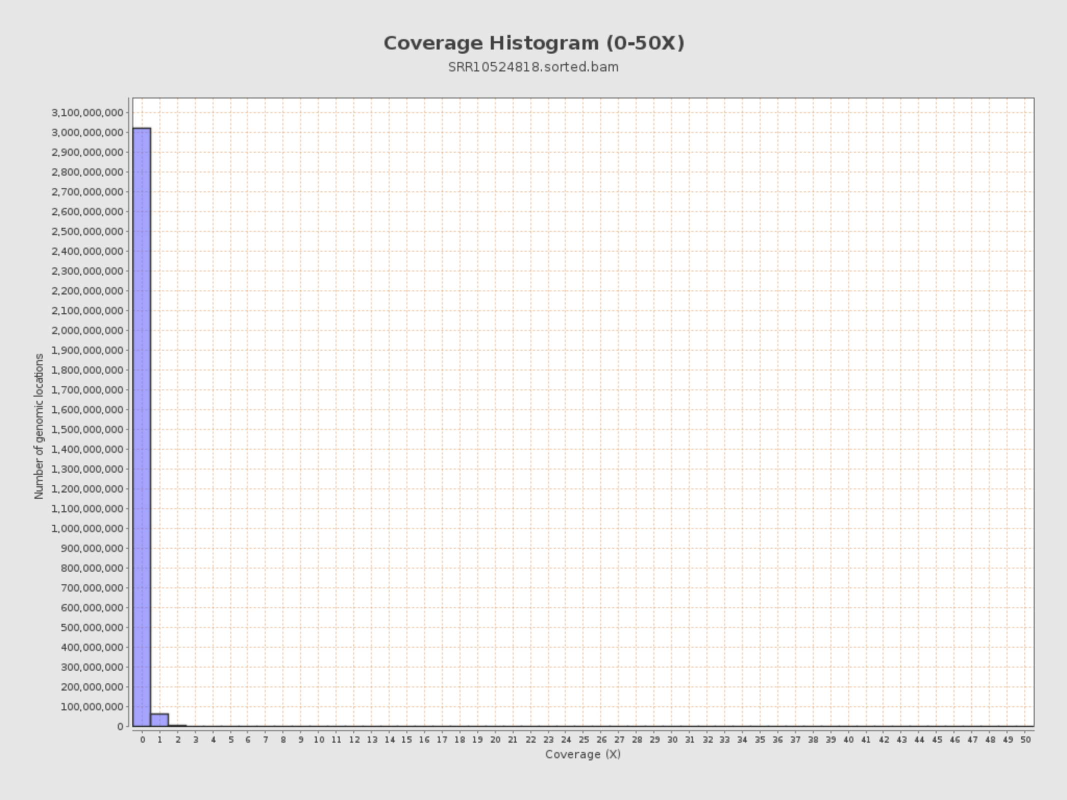
3. Results : Coverage across reference



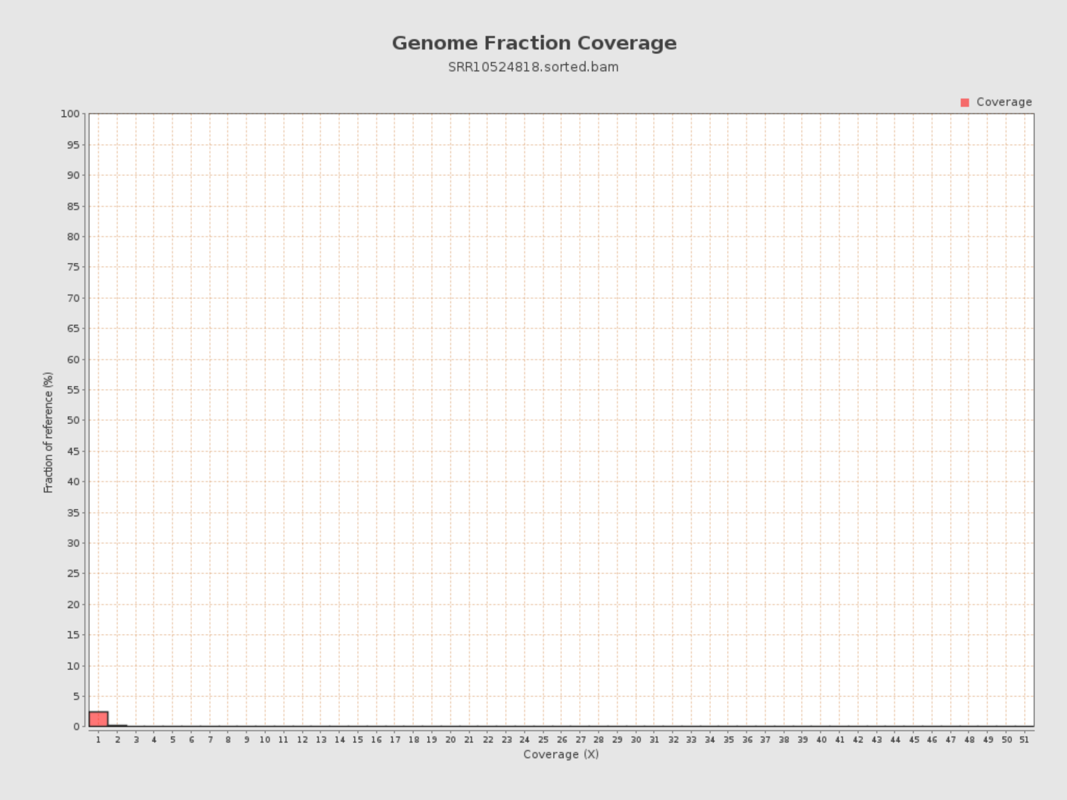
4. Results : Coverage Histogram



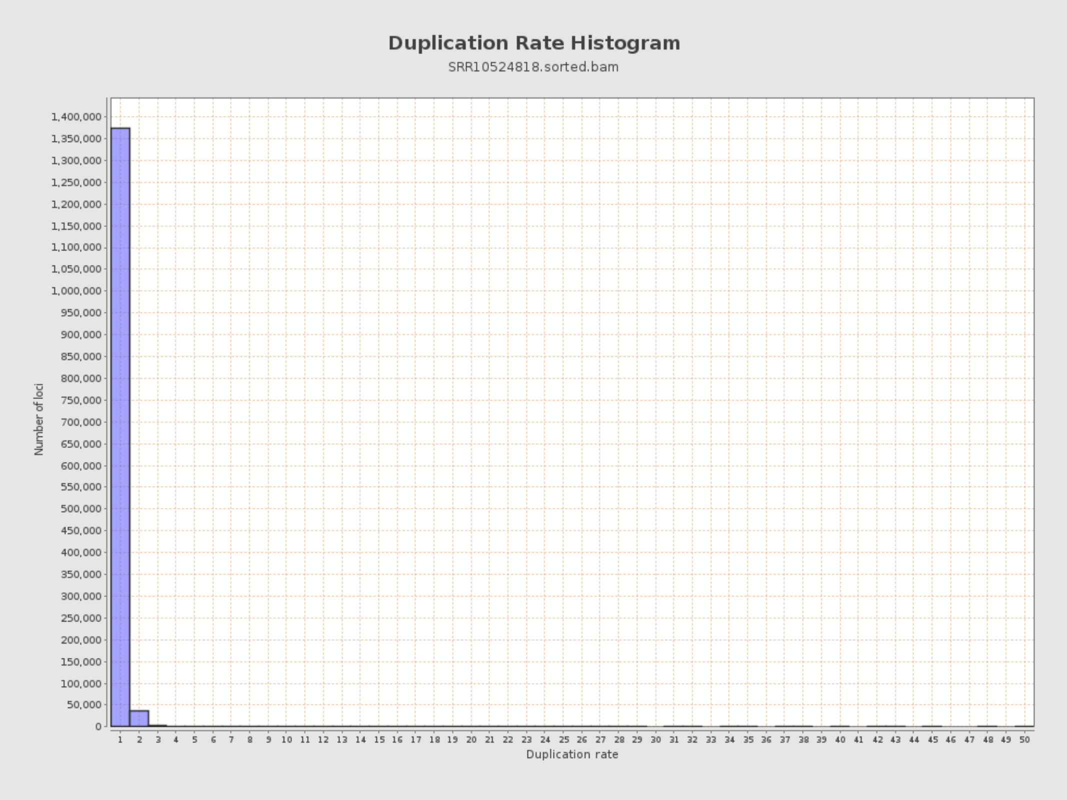
5. Results : Coverage Histogram (0-50X)



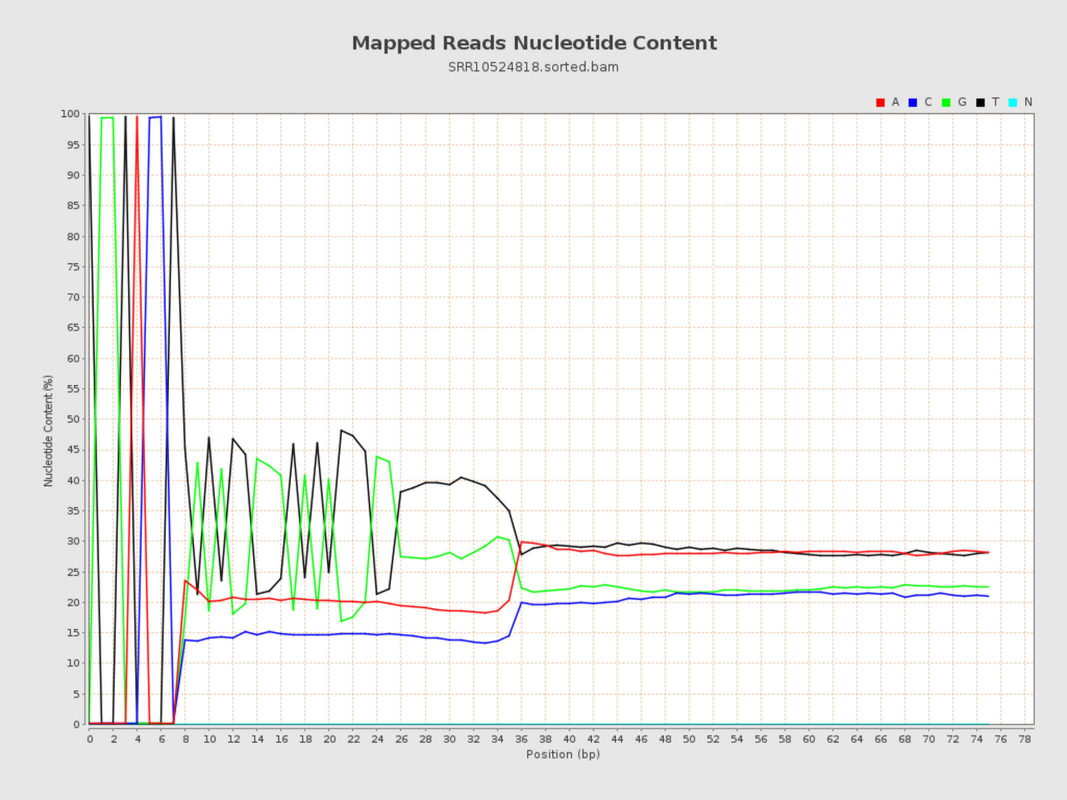
6. Results : Genome Fraction Coverage



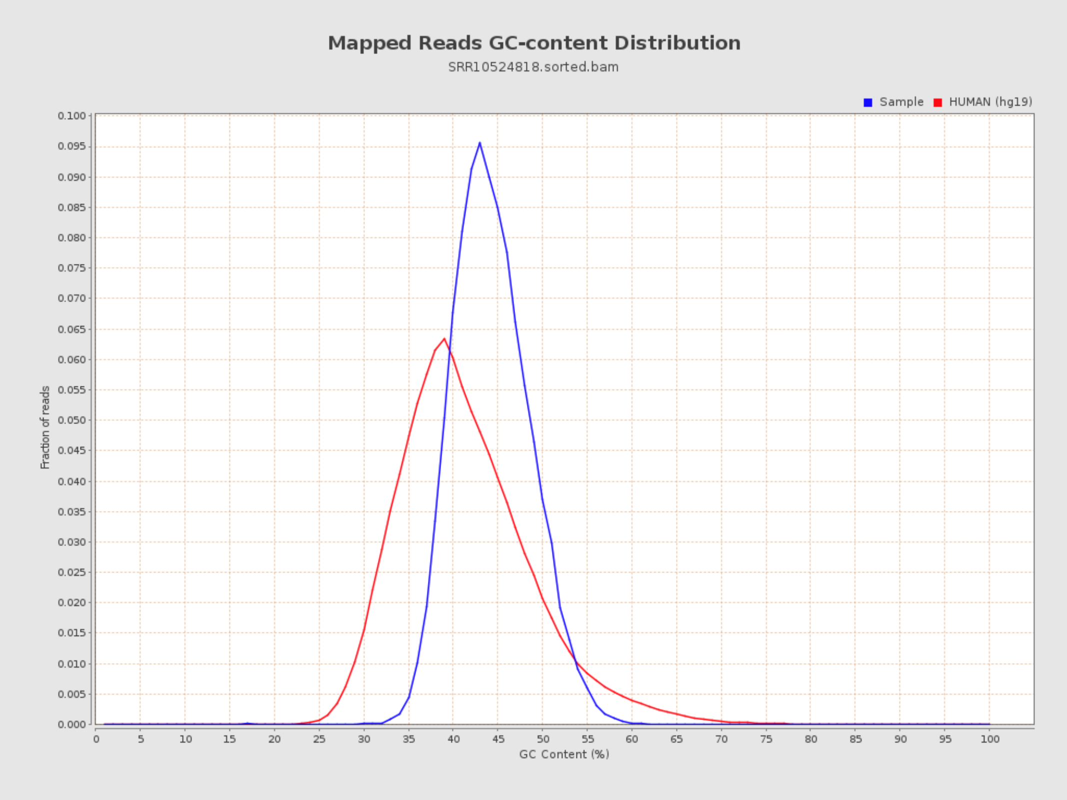
7. Results : Duplication Rate Histogram



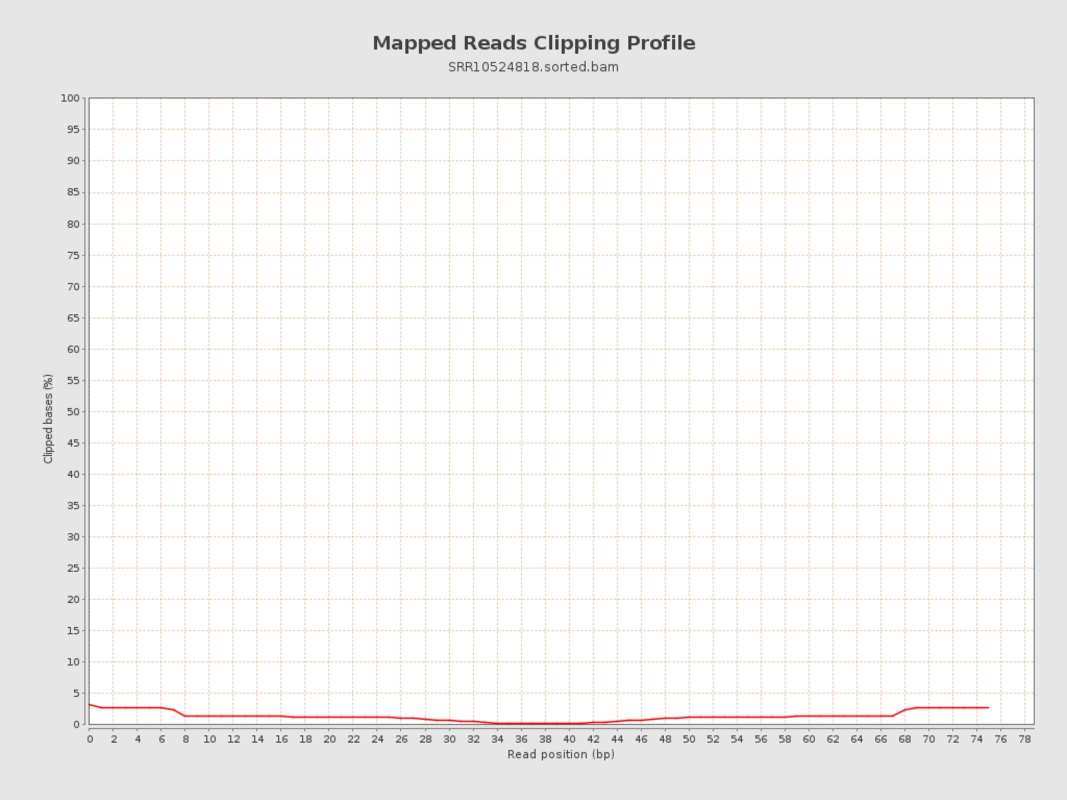
8. Results : Mapped Reads Nucleotide Content



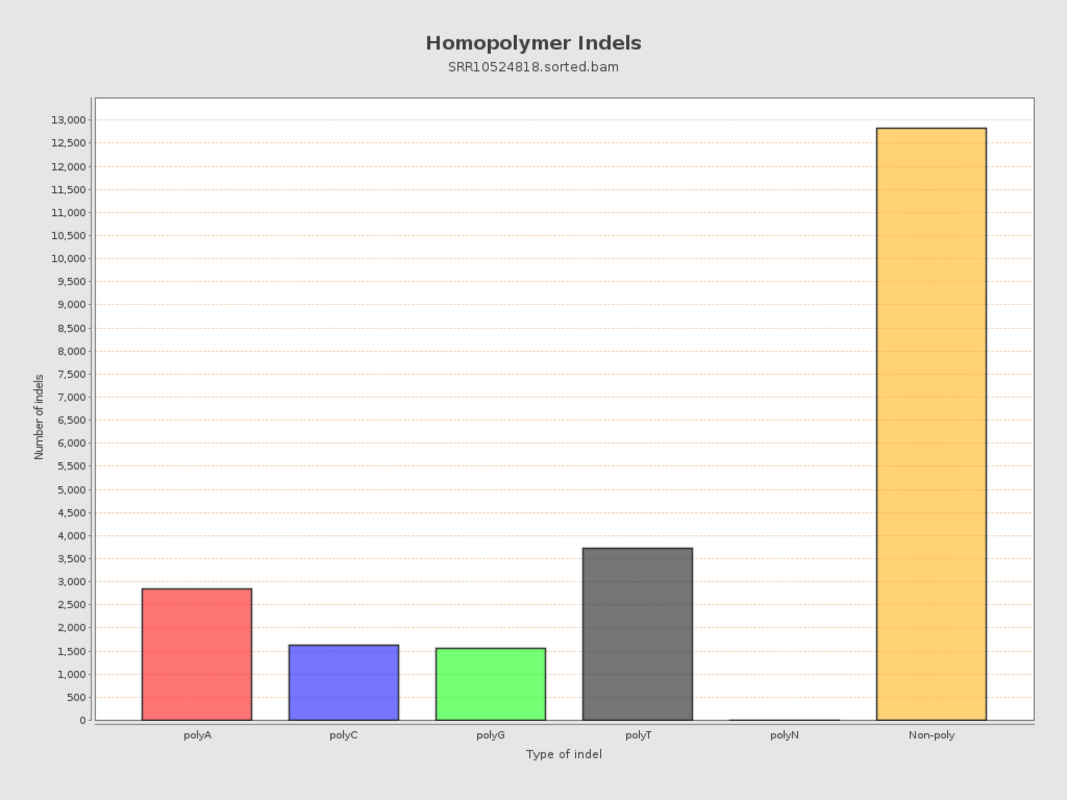
9. Results : Mapped Reads GC-content Distribution



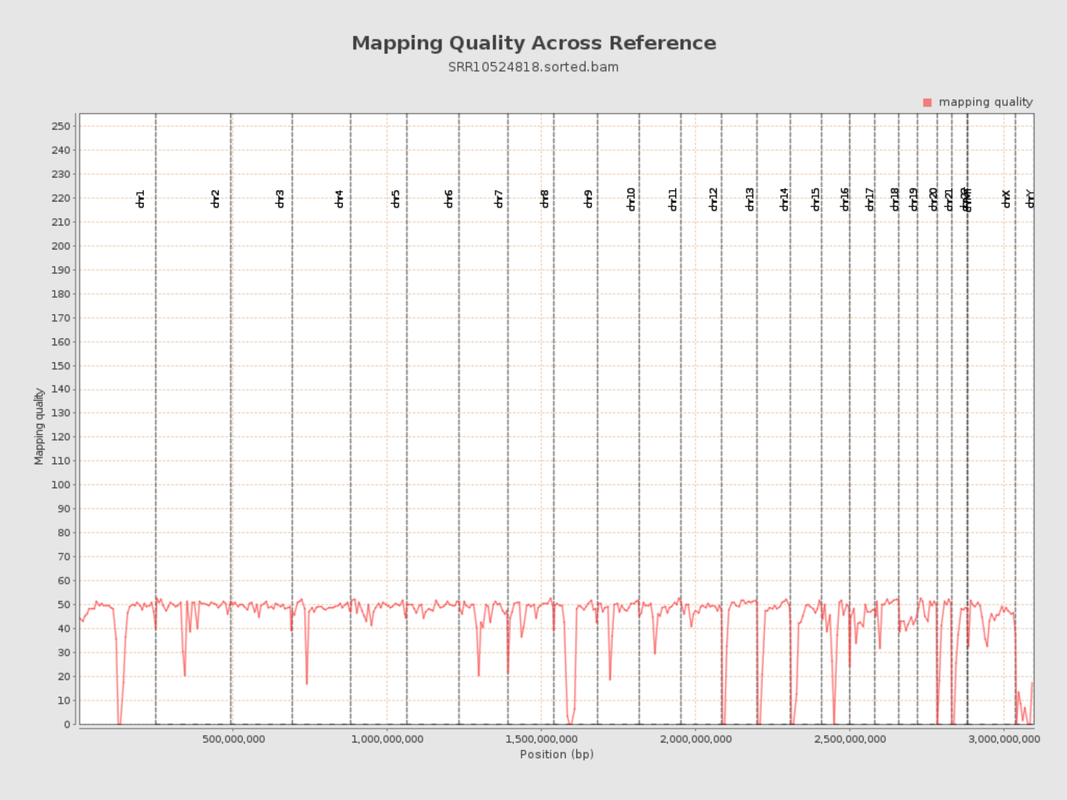
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram