Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:57:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525028.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_SRR10525028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525028.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:57:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,177,217
Mapped reads	1,077,831 / 91.56%
Unmapped reads	99,386 / 8.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,175 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	31,015 / 2.63%
Duplication rate	2.12%
Clipped reads	1,081,423 / 91.86%

2.2. ACGT Content

Number/percentage of A's	15,371,047 / 24.59%
Number/percentage of C's	12,224,525 / 19.56%
Number/percentage of T's	19,478,895 / 31.16%
Number/percentage of G's	15,438,078 / 24.7%
Number/percentage of N's	654 / 0%
GC Percentage	44.25%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.1978

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

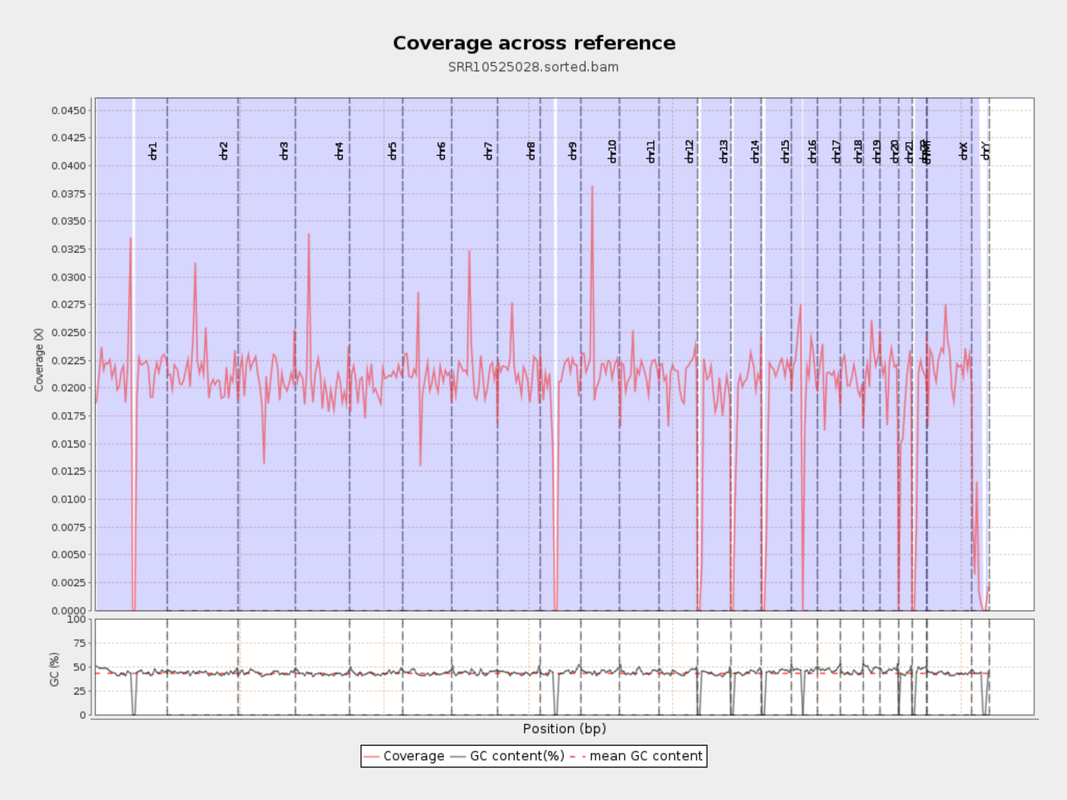
General error rate	0.5%
Mismatches	308,499
Insertions	3,501
Mapped reads with at least one insertion	0.32%
Deletions	12,161
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.39%

2.6. Chromosome stats

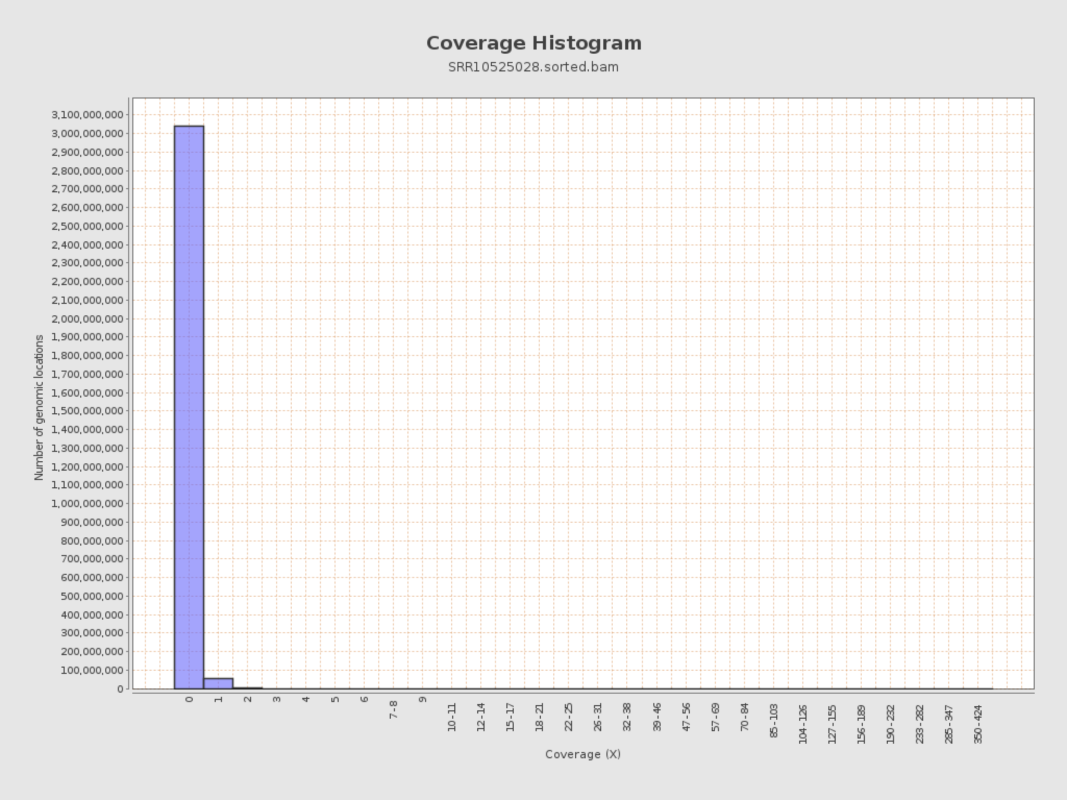
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5110313	0.0205	0.3327
chr2	243199373	5228527	0.0215	0.2281
chr3	198022430	4124901	0.0208	0.1541
chr4	191154276	3977513	0.0208	0.1695
chr5	180915260	3740982	0.0207	0.1528
chr6	171115067	3611771	0.0211	0.1778
chr7	159138663	3443309	0.0216	0.2229

chr8	146364022	3161365	0.0216	0.2103
chr9	141213431	2624122	0.0186	0.1712
chr10	135534747	3069497	0.0226	0.2122
chr11	135006516	2899441	0.0215	0.1878
chr12	133851895	2830817	0.0211	0.1556
chr13	115169878	1939516	0.0168	0.1375
chr14	107349540	1892121	0.0176	0.1439
chr15	102531392	1806357	0.0176	0.1437
chr16	90354753	1837863	0.0203	0.158
chr17	81195210	1697045	0.0209	0.166
chr18	78077248	1638310	0.021	0.2636
chr19	59128983	1322658	0.0224	0.2401
chr20	63025520	1340752	0.0213	0.1569
chr21	48129895	824530	0.0171	0.1532
chr22	51304566	765645	0.0149	0.1296
chrMT	16571	409	0.0247	0.1552
chrX	155270560	3452114	0.0222	0.1688
chrY	59373566	193513	0.0033	0.1021

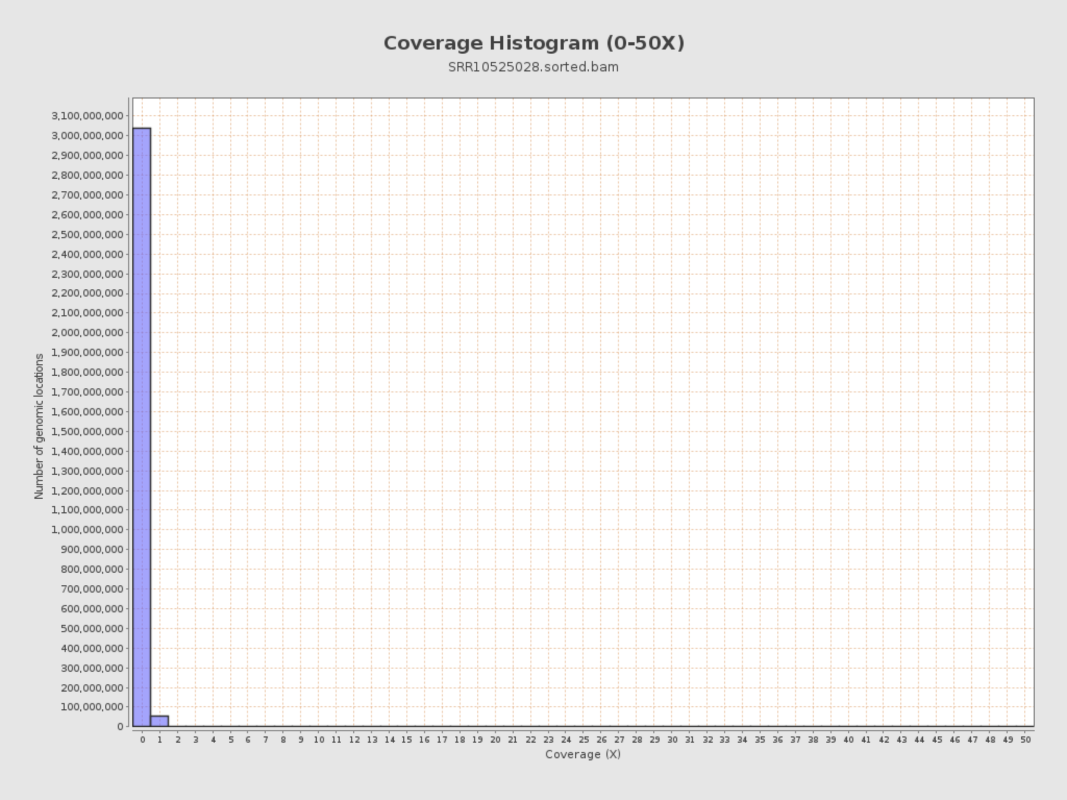
3. Results : Coverage across reference



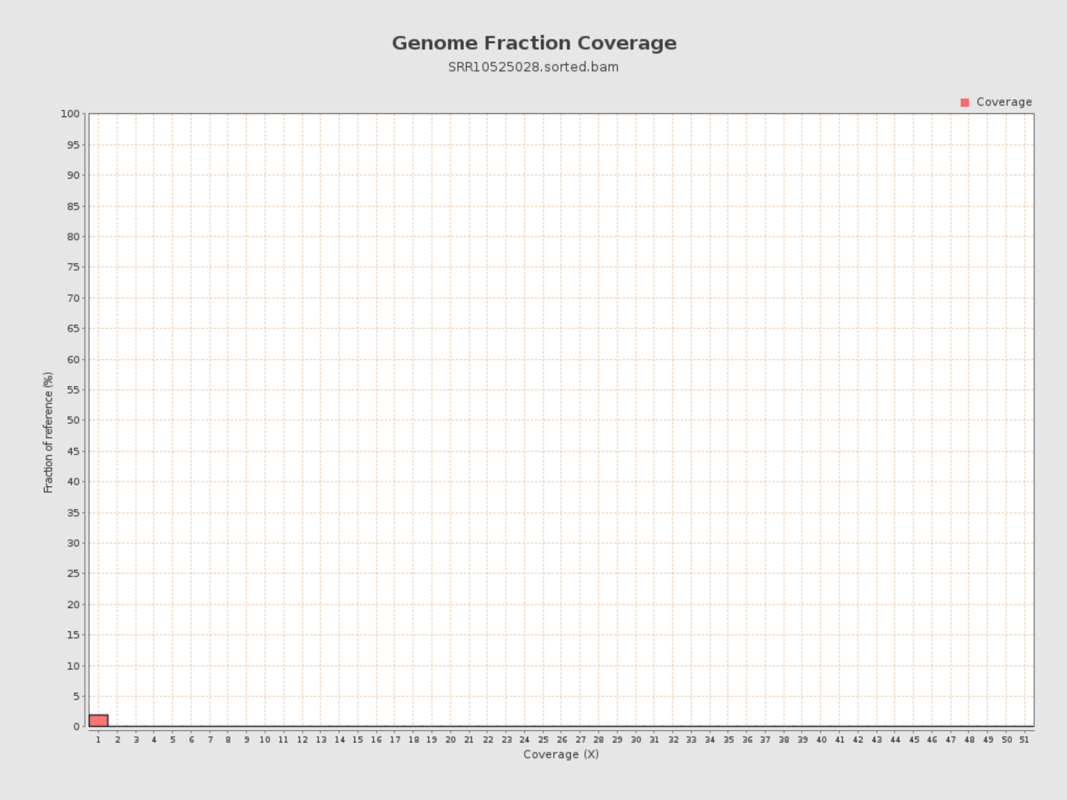
4. Results : Coverage Histogram



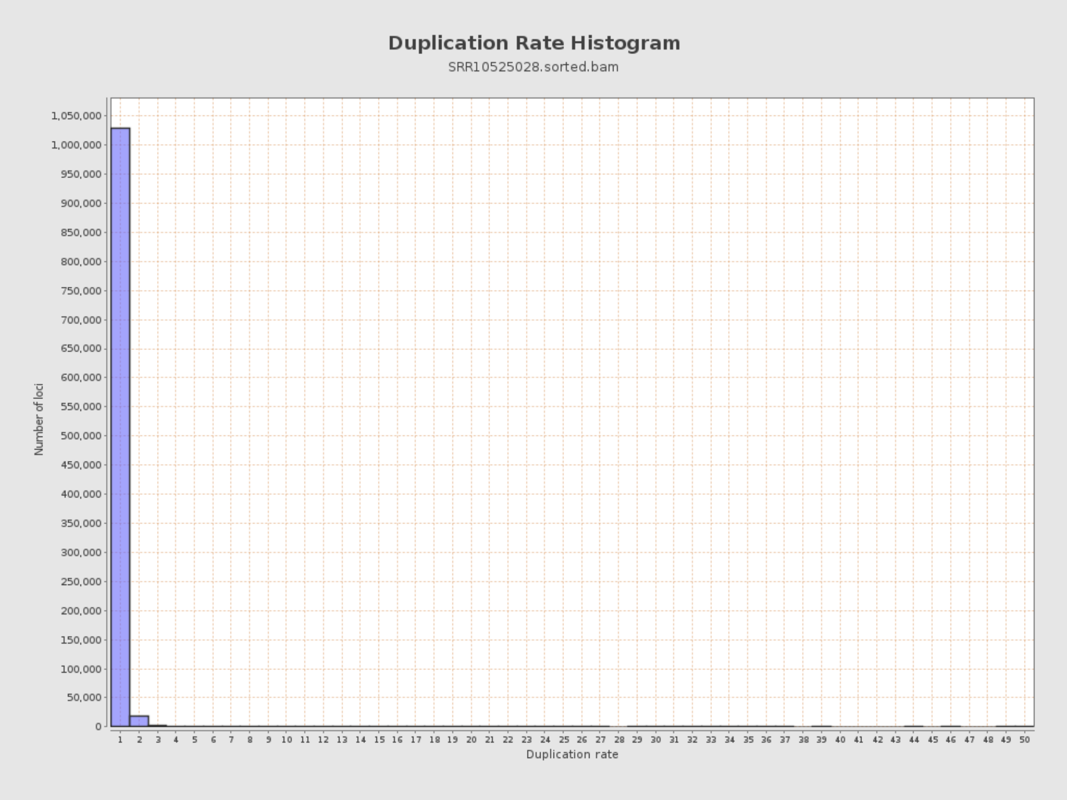
5. Results : Coverage Histogram (0-50X)



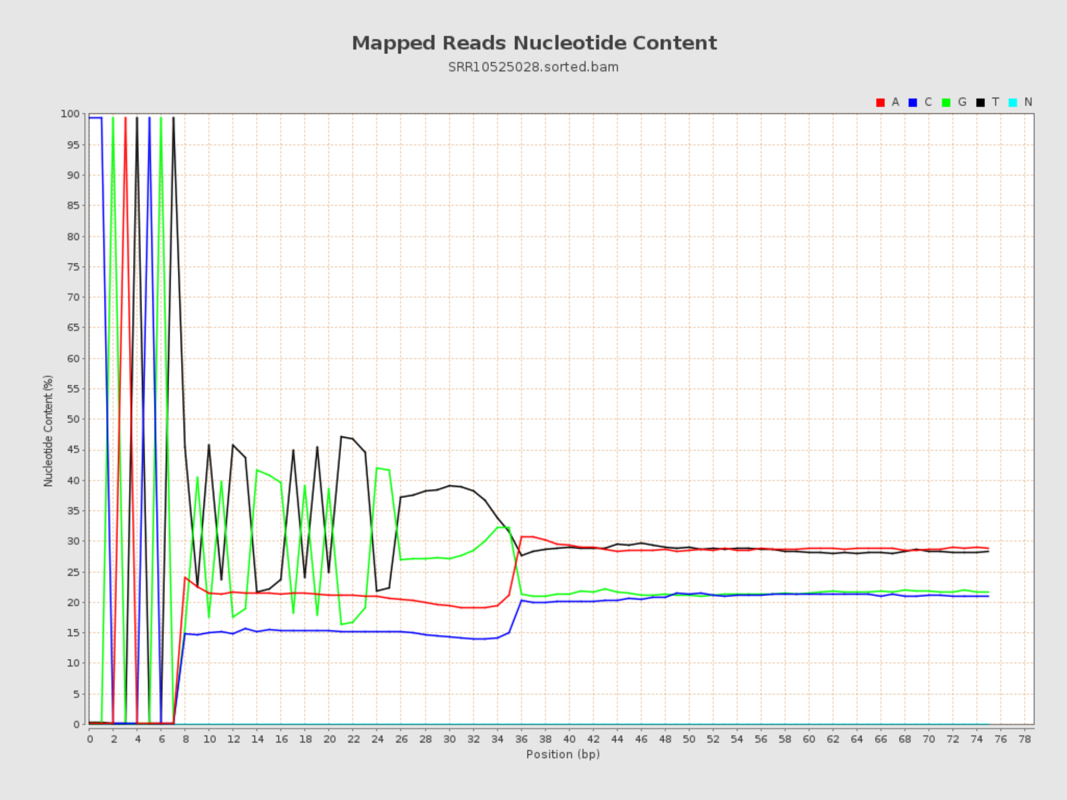
6. Results : Genome Fraction Coverage



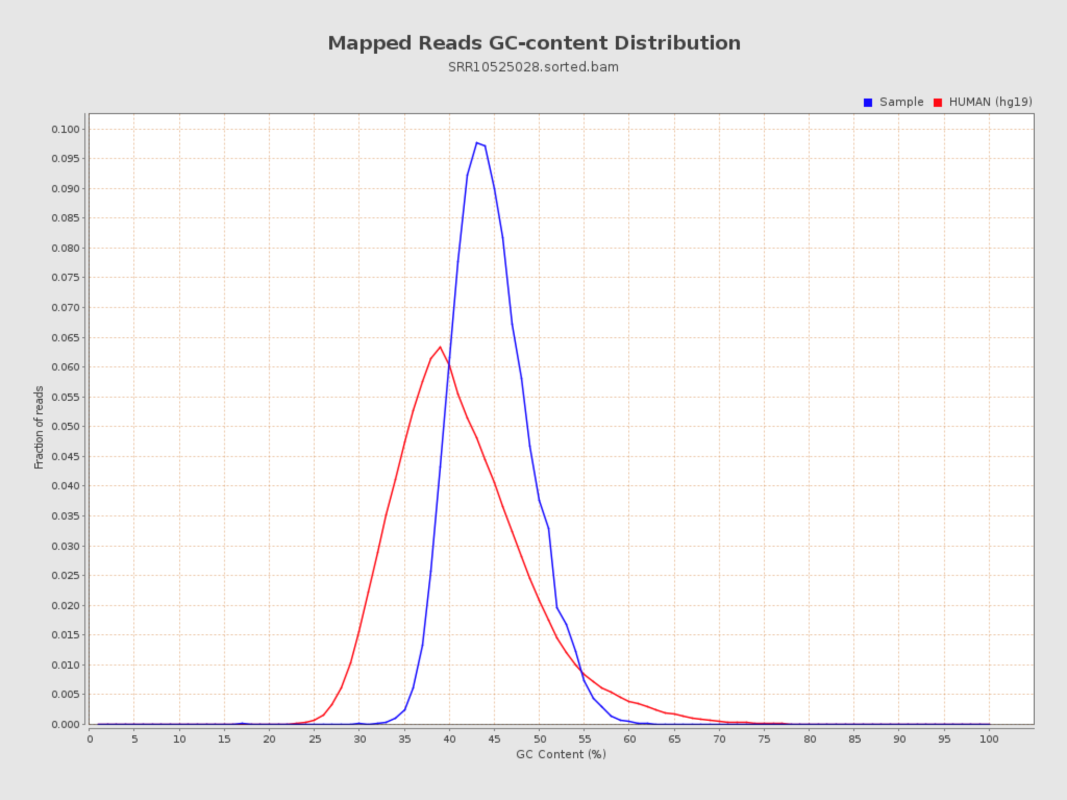
7. Results : Duplication Rate Histogram



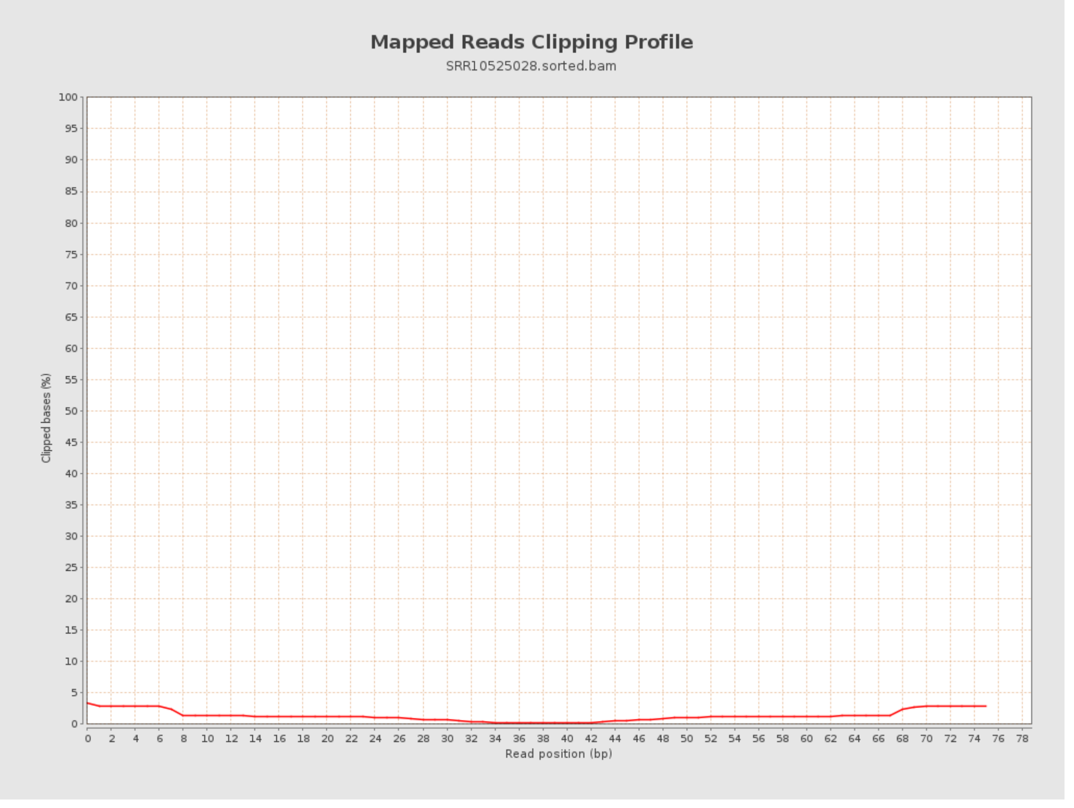
8. Results : Mapped Reads Nucleotide Content



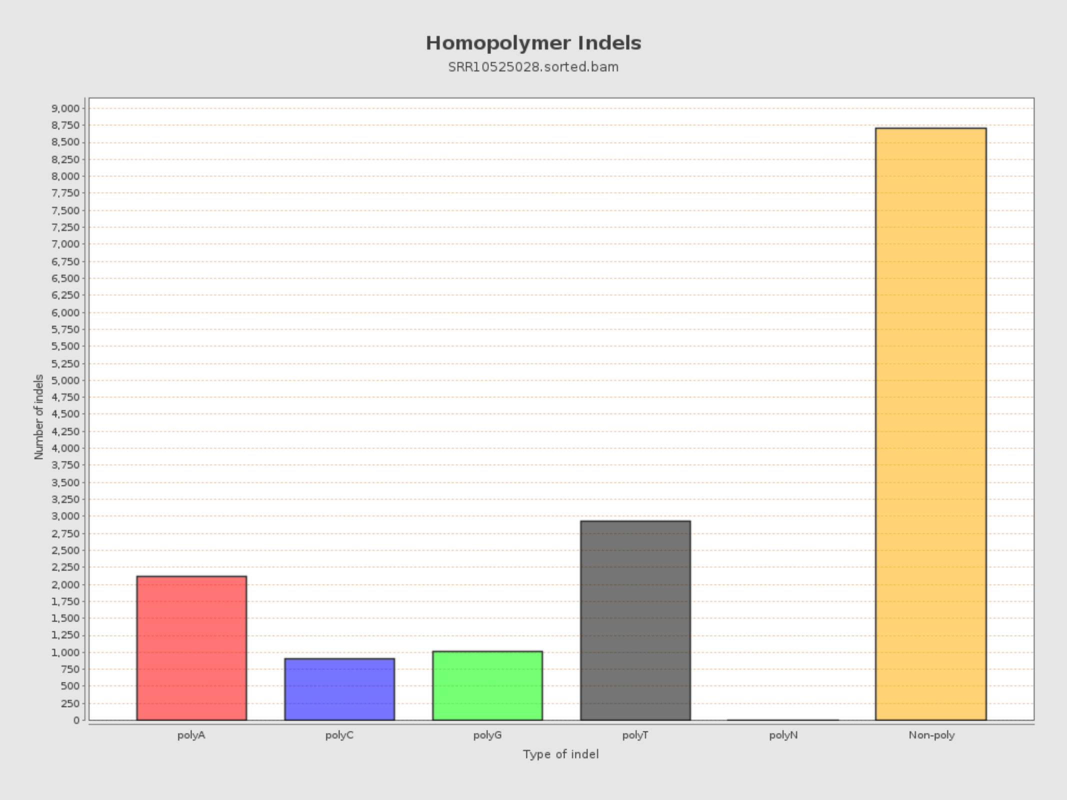
9. Results : Mapped Reads GC-content Distribution



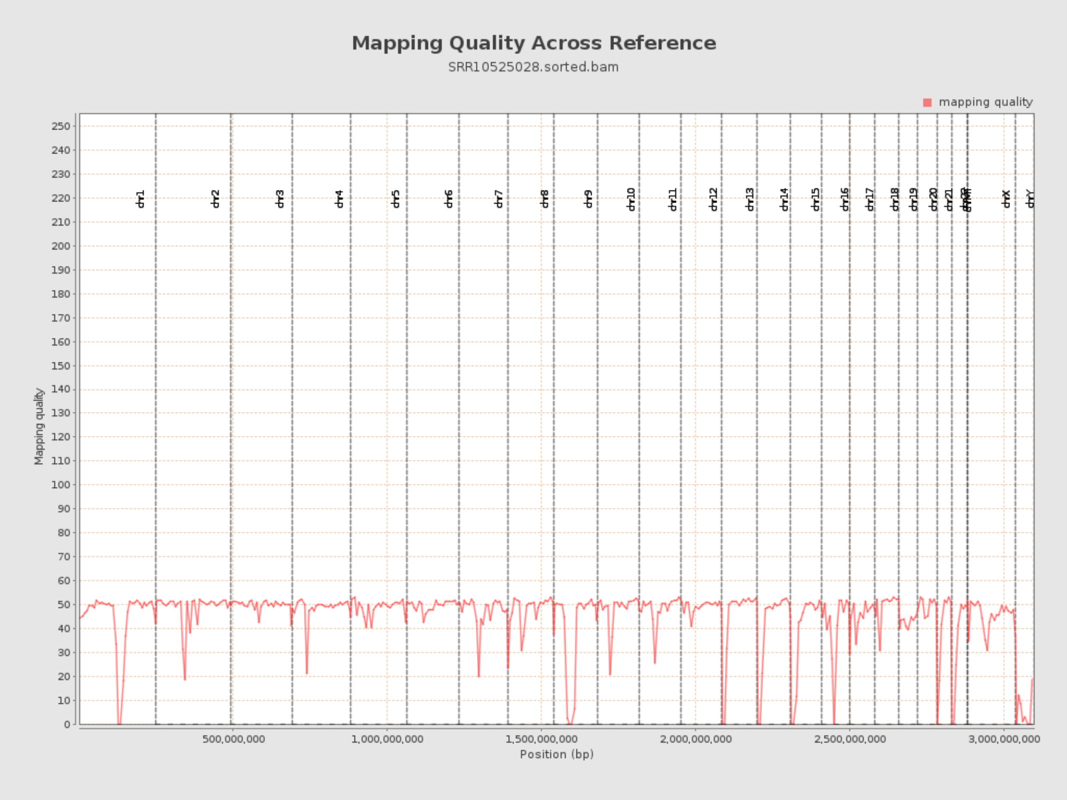
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram