Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 06:33:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090129.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_SRR090129 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090129.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 06:33:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090129.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,912,753
Mapped reads	16,810,627 / 80.38%
Unmapped reads	4,102,126 / 19.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	762 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,000,970 / 14.35%
Duplication rate	11.84%
Clipped reads	1,444,847 / 6.91%

2.2. ACGT Content

Number/percentage of A's	233,958,772 / 29.5%
Number/percentage of C's	160,789,367 / 20.27%
Number/percentage of T's	230,504,365 / 29.06%
Number/percentage of G's	167,708,495 / 21.15%
Number/percentage of N's	165,064 / 0.02%
GC Percentage	41.42%

2.3. Coverage

Mean	0.2563

Standard Deviation	1.3816

2.4. Mapping Quality

Mean Mapping Quality	44.35

2.5. Mismatches and indels

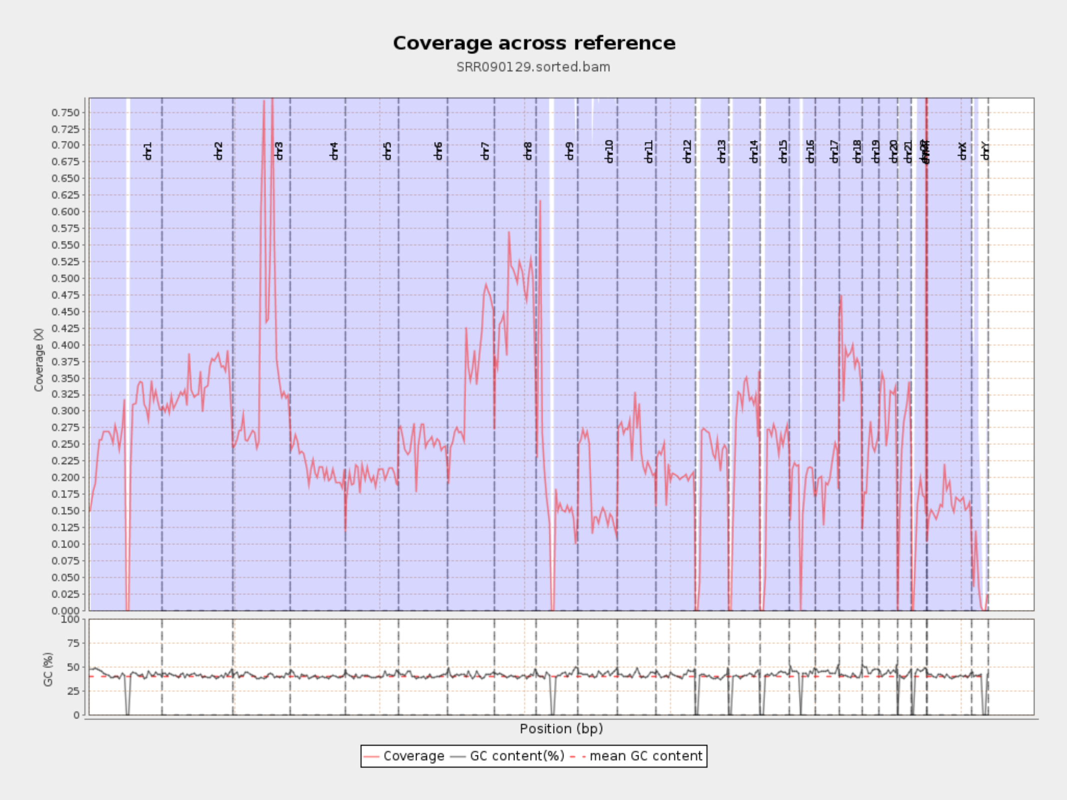
General error rate	0.62%
Mismatches	4,882,801
Insertions	31,028
Mapped reads with at least one insertion	0.18%
Deletions	96,933
Mapped reads with at least one deletion	0.58%
Homopolymer indels	45.92%

2.6. Chromosome stats

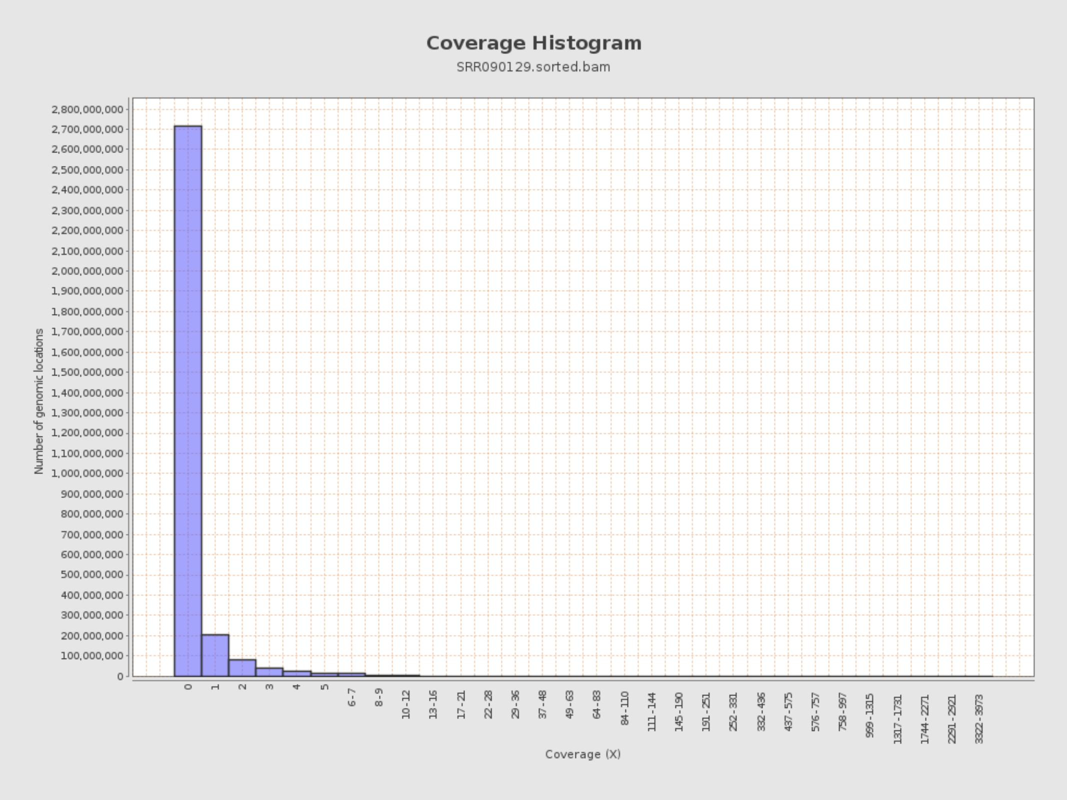
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	65061359	0.261	2.1691
chr2	243199373	82245957	0.3382	1.5541
chr3	198022430	73036660	0.3688	1.1473
chr4	191154276	41243600	0.2158	0.8608
chr5	180915260	36502285	0.2018	0.8169
chr6	171115067	43184200	0.2524	0.9785
chr7	159138663	56886772	0.3575	2.1729

chr8	146364022	68924540	0.4709	2.4911
chr9	141213431	25725349	0.1822	1.2174
chr10	135534747	24152668	0.1782	1.0909
chr11	135006516	33855285	0.2508	1.1315
chr12	133851895	27820539	0.2078	0.8501
chr13	115169878	23879335	0.2073	0.821
chr14	107349540	28332799	0.2639	0.9612
chr15	102531392	21621503	0.2109	0.8335
chr16	90354753	16495128	0.1826	0.817
chr17	81195210	16204426	0.1996	0.9345
chr18	78077248	30102973	0.3856	1.9832
chr19	59128983	13530438	0.2288	1.4747
chr20	63025520	19700084	0.3126	1.0932
chr21	48129895	11528466	0.2395	1.0191
chr22	51304566	6341948	0.1236	0.6322
chrMT	16571	52584	3.1733	3.2878
chrX	155270560	24836726	0.16	0.7985
chrY	59373566	2008256	0.0338	1.1526

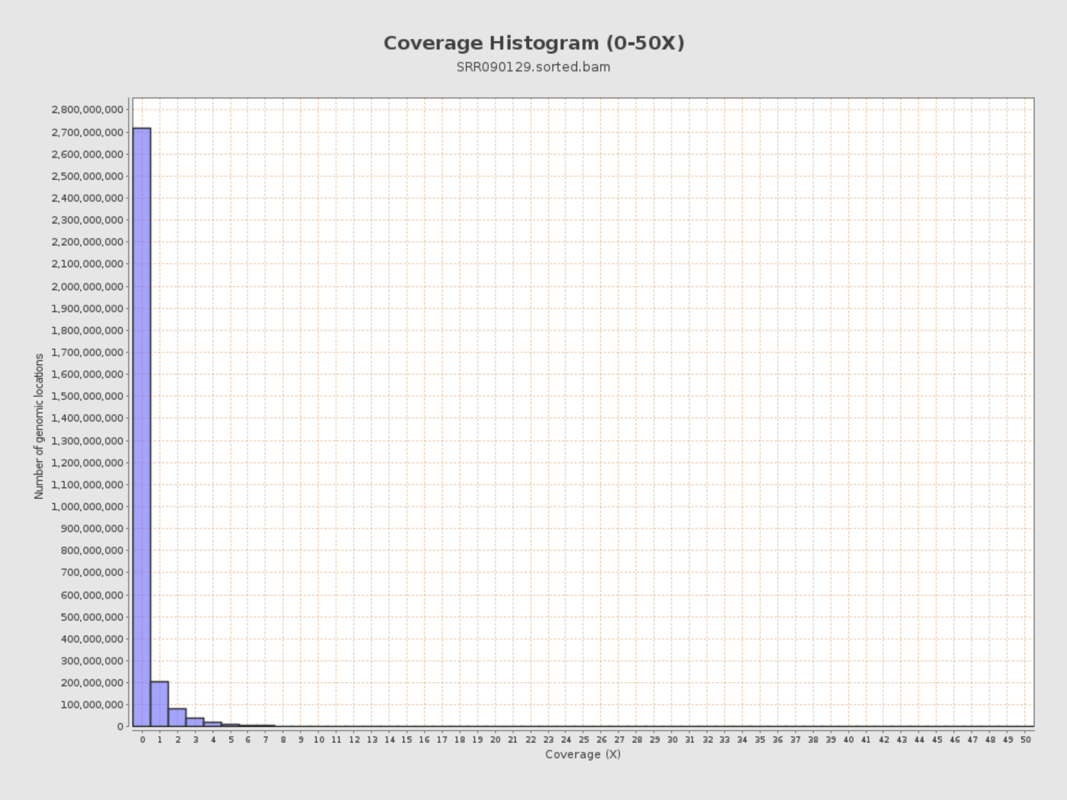
3. Results : Coverage across reference



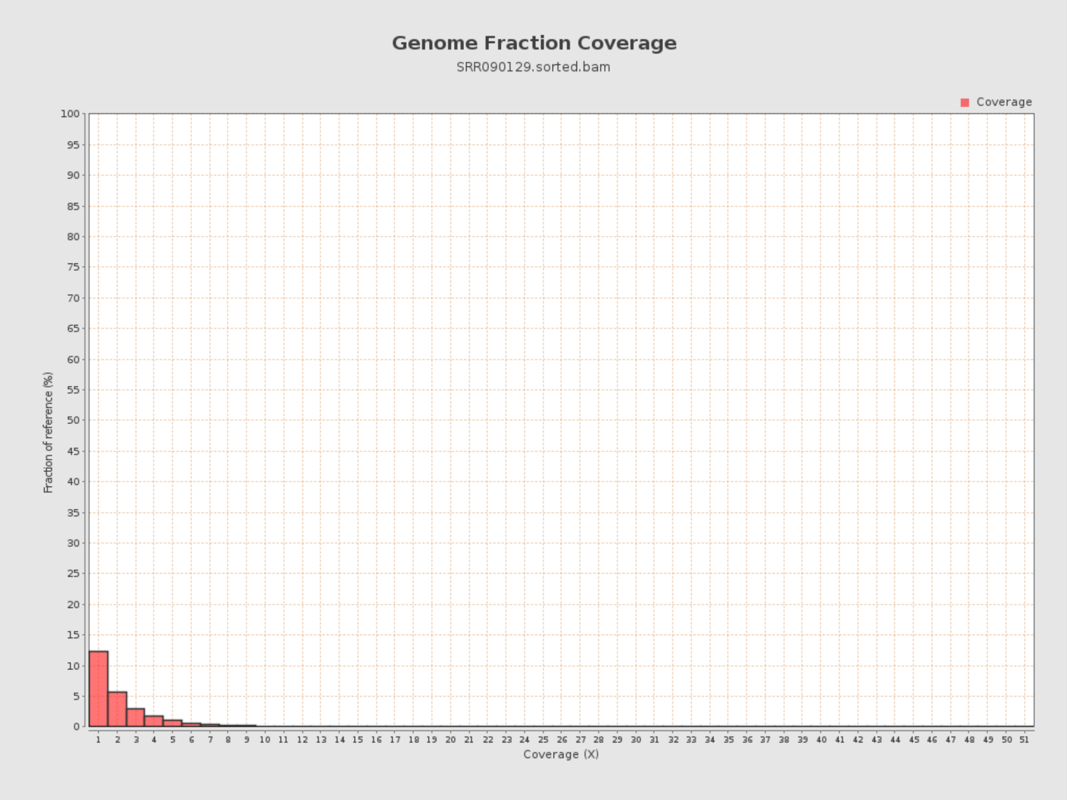
4. Results : Coverage Histogram



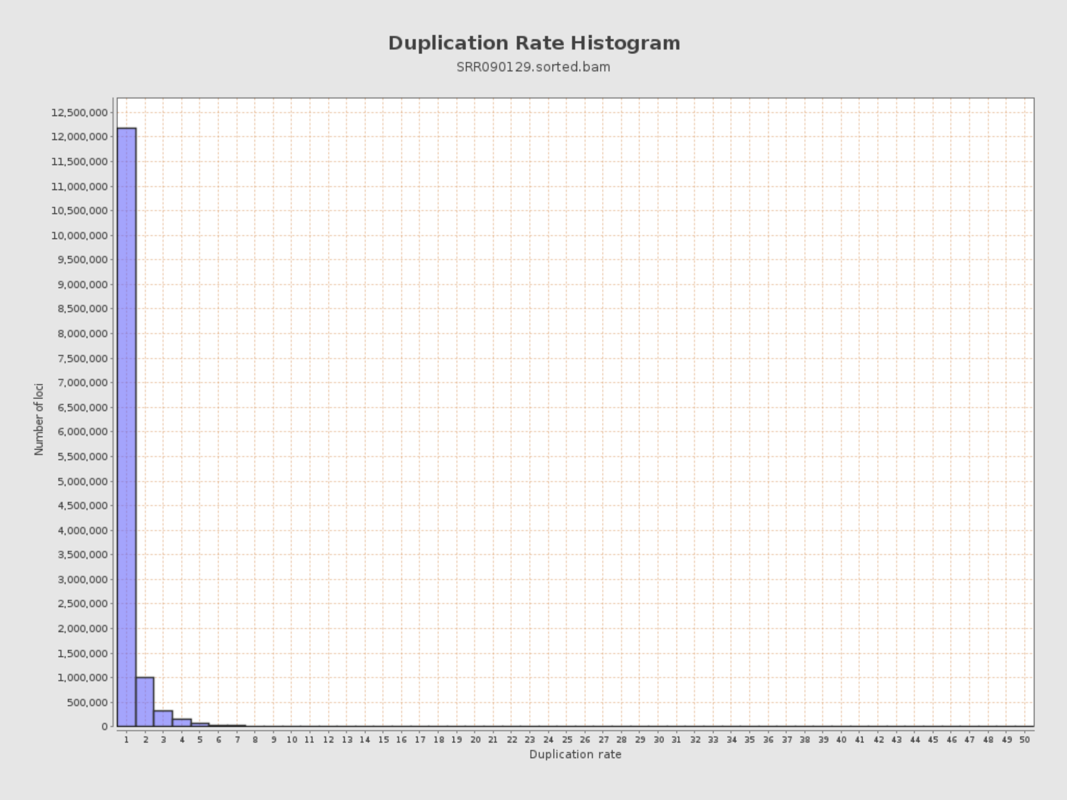
5. Results : Coverage Histogram (0-50X)



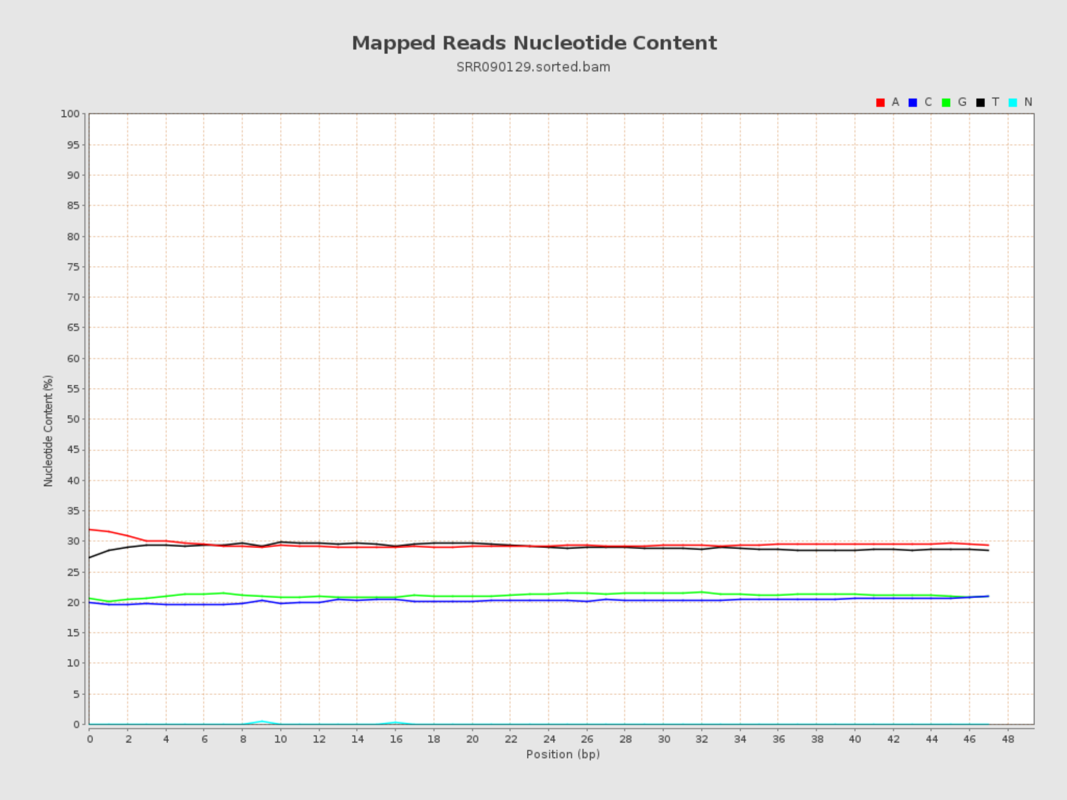
6. Results : Genome Fraction Coverage



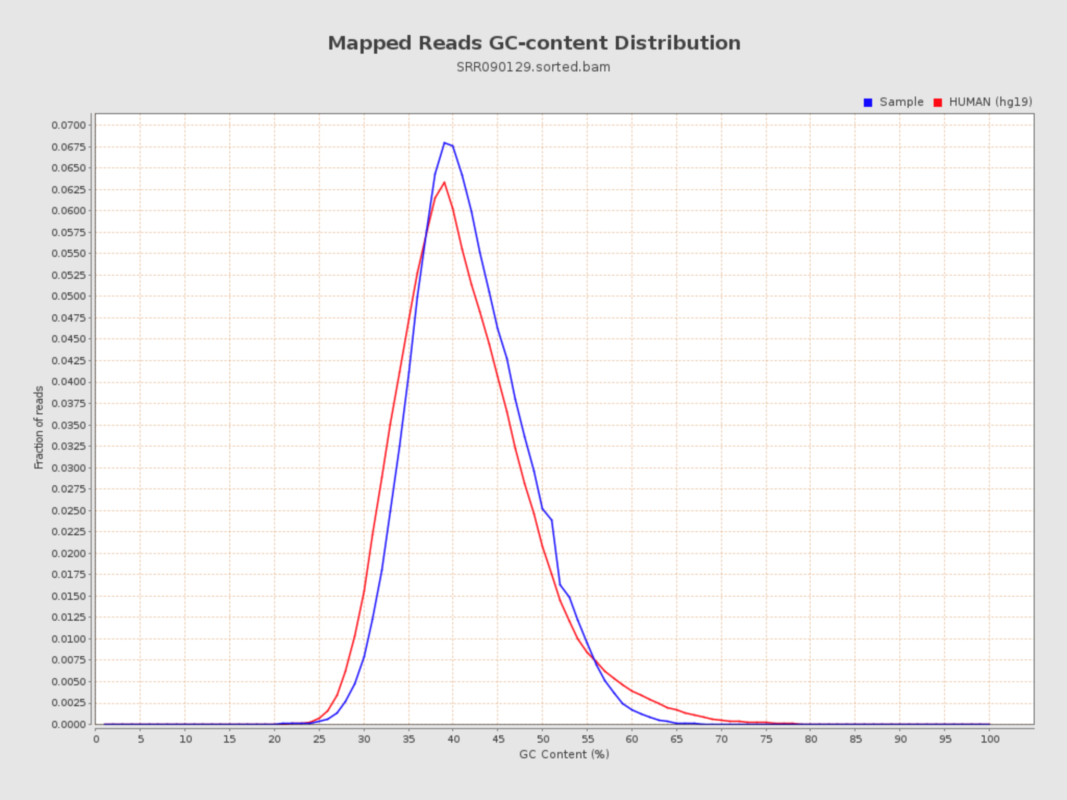
7. Results : Duplication Rate Histogram



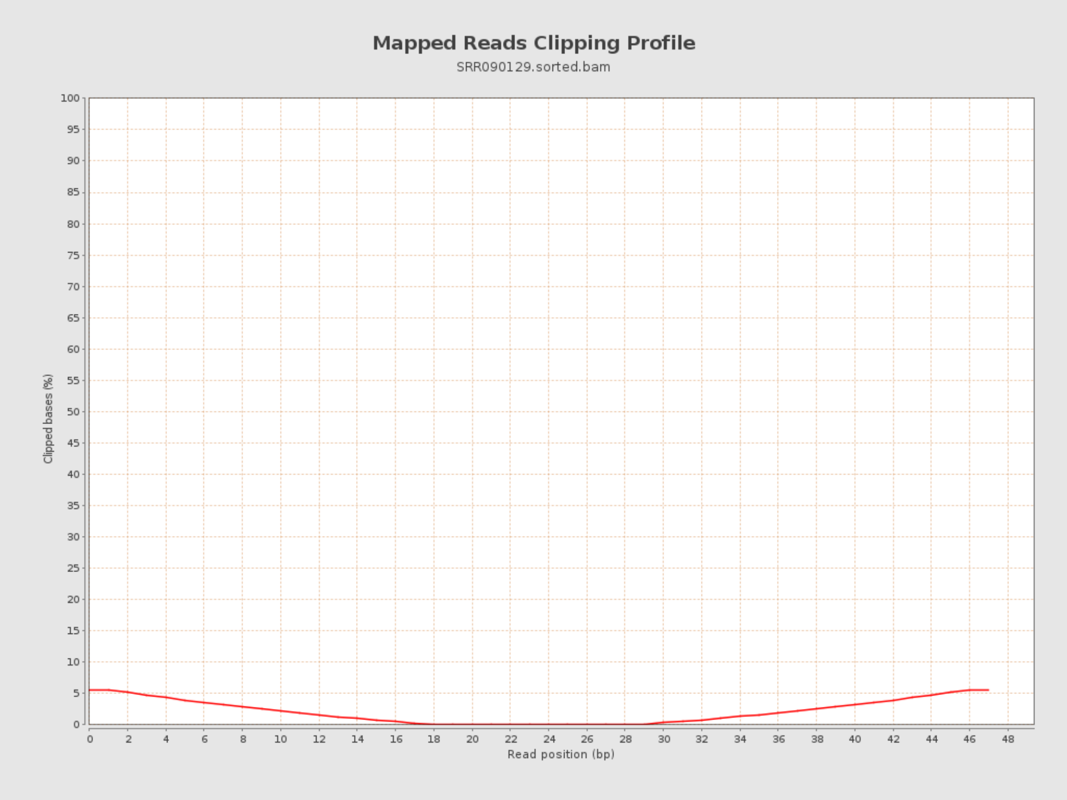
8. Results : Mapped Reads Nucleotide Content



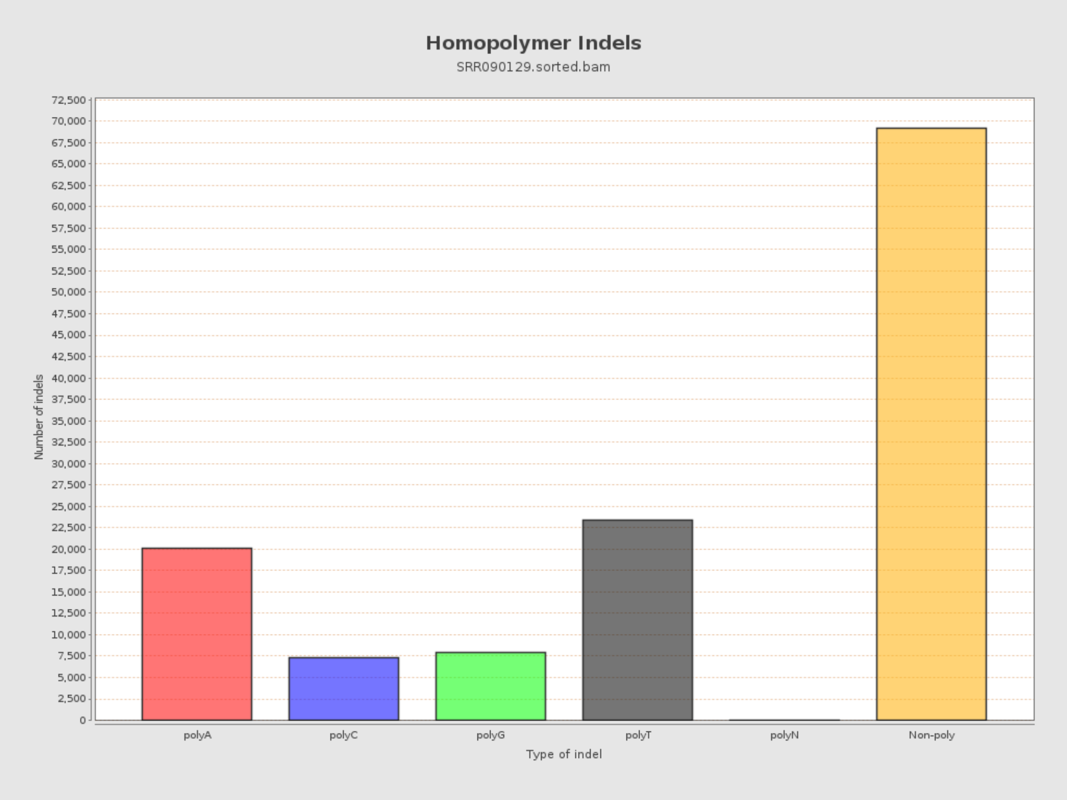
9. Results : Mapped Reads GC-content Distribution



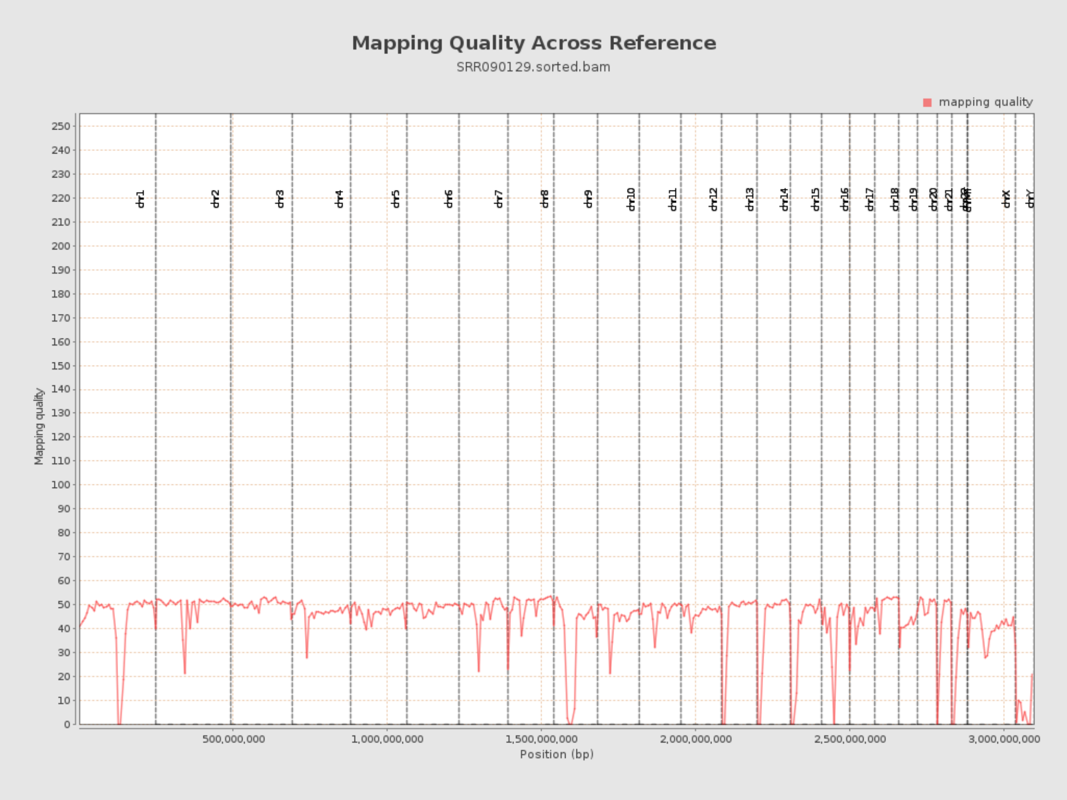
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram