Software Release Note

EmbryoMap-v1.2 Reference Database

This communication details the release of EmbryoMap-v1.2 reference database in eMap.

Background

The uneven distribution of GC content across the genome poses a well-recognised challenge for the analysis of chromosome copy number variation (CNV), particularly in regions rich in GC content such as the telomeres.

EmbryoMap-v1.2

The EmbryoMap-v1.2 reference database improves the stability of CNV analysis in GC-rich regions by more accurately capturing the sequencing read distribution and avoiding less reliable regions.

Updating your reference database:

Select the new reference database EmbryoMap-v1.2 from the reference database drop down menu to incorporate it into your analysis.

Note – The eMap analysis algorithm v1.42.8 is not changed.

If you have any questions, contact: support.genomics@vitrolife.com