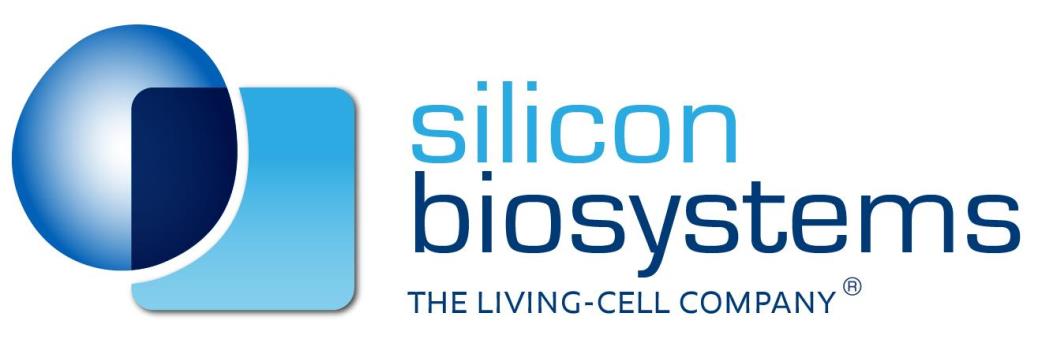
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**Combining NGS Sequencing with DEPArray™ "Digitalized Samples” to Resolve Heterogeneity   
on FFPE Tumours and Circulating Tumour Cells**

Fredag 8. mai kl 13-14  
  
Laboratoriebygget 7 etg.  
Møterom 7 Helse Bergen

Heterogeneity is a big challenge which has limited the effectiveness of molecular analysis of solid tumours. The introduction of Digital analytical methods, e.g. NGS and dPCR, has helped to manage heterogeneity through a higher resolution, in terms of minority populations detection offered by these technologies - but does not provide to the researcher the clarity of interpretation that only a homogeneous sample would offer.

DEP Array is a new technology capable of sorting and isolating pure single or pooled cells through a digitally controlled Dielectrophoretic field on a semiconductor chip. Single circulating tumour cells can be isolated from blood, as well as pools of 300 pure tumour and stromal cells from disaggregated FFPE tissue blocks. Pure single cells can undergo Whole Genome Amplification to obtain sufficient DNA for subsequent NGS analysis, while pools of 5 cells or more are readily usable for direct amplification with AmpliSeq™ panels.

We have tested both approaches to identify mutations via the use of AmpliSeq™ hot spot panels on Ion Torrent PGM with different kinds of tumour cells and tissues, including CTC and FFPE blocks.

Results show how interpretation of the underlying genetic alterations in tumour cells becomes far clearer on samples digitalized into collections of pure cells: somatic variants appear as germline; LoH is readily detectable; CNV is not hidden by dilution, etc. - all leading to a multidimensional understanding of tumour genetics and biology.

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