

**Table 5c - Representative qualitative evidence supporting three models of DBF: IGA & IGA-Tech**

<b>(C) COMMERCE</b>	<b>IGA-Institute of Applied Genomics</b>	<b>IGA Technology Services</b>
<i>(i) Founder(s) with entrepreneurial track record</i>	<p><b>C1</b> - «BS-Seq. We have a proprietary software package for <b>WGBS-seq, RRBS-seq</b> and <b>Targeted BS-seq</b> data analysis. Quality control; Post-sequencing estimation of conversion rate using Lambda spike-in; Alignment to a reference; Methylation calling at single cytosine level; <b>Whole genome methylation statistics</b> (including distribution of methylation in the CG, ChG and Chh contexts in plants); Visualization of methylation distribution across the genome using CIRCOS images; Identification of Differentially Methylated Regions (DmRs) between samples. Our team is always available to consult with you on study design to ensure correct sequencing and bioinformatics strategies are used to meet your goals» (source: IGA website).</p>	
<i>(ii) Early hiring of senior exec from health care or pharma</i>	<p>«<b>C2(a)</b> - IGA iniziava a pensare e vedere in modo diverso il ruolo del bioinformatico perché i dati adesso non possono più essere osservati, ma serve l'elaborazione del bioinformatico per i dati più complessi. Molte aziende creano strumenti per sostituire il bioinformatico, ma questi strumenti non funzionano perché i problemi da affrontare sono troppo difficili, le macchine risolvono un unico problema, questo può andar bene per la diagnostica ... ma per una sola malattia!» (Cristian, interview_#04a, Alessandro, interview_#04b )</p>	<p>«<b>C2(b)</b> - Project D.NAMICA foresees to study the methodologies for the implementation of a computing platform for the integration of clinical and genetic indicators with the purpose to support research for the personalization of medicine. D.NAMICA is cofunded by ERDF - European Regional Development Fund - Friuli Venezia Giulia Region Operational Programme 2007 - 2013. It fosters the cooperation between research organizations, universities, technology transfer centres and enterprises. Project D.NAMICA will implement three pilot projects to help research activities to better understand the genetic characteristics of patients and their answers to personalized treatment in the following sectors: cardiology (DCM - dilatative cardiomyopathy), oncology (HCC - Hepatocellular carcinoma) and neurodegenerative diseases (SMA - Spinal muscular atrophy). (source: IGA-Tech website )</p>
<i>(iii) Initial emphasis on non-therapeutic applications</i>	<p><b>C4</b> - «<b>BISULFITE SEQUENCING (BS-SEQ). DNA methylation has been shown to play an important role in a wide variety of biological processes, including silencing of transposable elements, stem cell differentiation, embryonic development, genomic imprinting and inflammation.</b> Alteration of methylation patterns has been identified in many diseases, including cancer, diabetes, cardiovascular disease, inflammation and neurological disorders. By combining bisulfite treatment of genomic DNA with NextGen Sequencing, it is possible to sensitively measure cytosine methylation on a genome-wide scale within specific sequence contexts. By using restriction enzymes and bisulfite sequencing, it is possible to enrich for the areas of the genome that have a high CpG content. This approach, termed RRBS-seq (Reduced Representation Bisulfite Sequencing), reduces the amount of nucleotides needed to be sequenced to 1% of the genome size, allowing for a cost-effective single-base-pair resolution of methylated cytosines. The third alternative is targeted bisulfite sequencing, which is able to specifically capture selected genomic regions of interest associated with a disease or phenotype» (source: ... ).</p>	