* Key words that are related with software use:
  + Data
  + Software
  + SCR
  + RRID
  + Analysis
  + Using can refer to:
    - Data
    - Software
    - Hardware tool ( apparatus )
      * Microscope, needle, Analyzer … etc.
    - A standard or guideline or procedure or a protocol
      * *DNA was extracted from blood using standard procedures*
    - A biological specimen, chemical solution, like:
      * Antibody
      * Cell Line
      * Plasmid … etc
* Key words that describe software usage purpose:
  + **Compared** - (compare experimental groups)
    - *experimental groups were compared using GraphPad Prism*
  + **Quantified** / Quantification
    - *Bands were quantified using the NIH ImageJ software*
    - *In all experiments, chemiluminescent signal was visualized using a Fuji LAS-4000 and quantified with Multigauge (RRID:SCR\_014299)*
    - *Quantification of cellular frequencies was performed using FlowJo software*
    - *StrataQuest software was also used to quantify cell-to-cell contact*
  + **Measurement** 
    - *Area measurements were obtained from … using ImageJ*
    - *The optical density of the protein band was measured with the use of the Image Lab (Bio-Rad) software*
  + **Analysis**
    - ***Analysis***
      * *All analysis and figure preparation was performed using ImageJ/FIJI (RRID:SCR\_002285; Schindelin et al., 2012****)***
      * *FCS files were analyzed, and B cell subsets were quantified using FlowJo software (version 10)*
      * *Pedigraph64, a software tool for graphing and analyzing large complex pedigrees*
      * *This hybrid descendant pedigree was further pruned using lineage pedigree visualization and analysis software6*
      * *The analysis was performed with the BD Accuri C6 Plus software (Becton Dickinson, San José, CA, USA, (RRID:SCR\_014422)*
      * *Raw data was statistically analyzed using t-tests in Excel (Microsoft Office 2010, v-0.14.0.7168.5000)*
    - **Statistical Analysis**
      * *Statistical analysis was performed using Prism Graph Pad*
      * *Graphpad Prism software (RRID: SCR\_002798) was used to analyze the data using one-way ANOVA*
      * *statistical analysis was also carried out using permutation-based non-parametric inference with 5,000 random permutations (FSL Randomise tool)*
      * *statistical analyses were conducted in the R statistical package (R Foundation, RRID:SCR\_001905)*
      * *The statistical analysis was made using Prism 5.0 (GraphPad, La Jolla, CA, USA, RRID:SCR\_002798) and Statistica 13.1 (StatSoft, Cracow, Poland, RRID:SCR\_014213)*
      * *Data was statistically analyzed using Graph Pad PRISM 7*
      * *statistical analyses were performed using SPSS statistical software*
      * *We conducted the statistics with the R functions*
    - **Data Analysis**
      * *Data analysis were performed using the Statistical Package for the Social Sciences*
      * *Data analyses were performed with R statistical software v.3.1.2 (RRID:SCR\_001905) and IBM SPSS statistics v. 20 (RRID:SCR\_002865)*
      * *All data analyses were performed using SPSS statistical software, version 25 (IBM SPSS, Chicago, IL, RRID: SCR\_002865)*
      * *the data were analyzed using CXP Software*
      * *Data analysis was performed with MaxQuant software*
      * *Data were analyzed for statistical significance using the GraphPad Prism Version 6.0 software*
      * *Data were analyzed using FlowJo software*
    - **Densitometric Analysis**
      * *densitometric analysis was performed using Quantity One V 4.2.1 software*
    - **voxel-based analyses**
      * *Voxel-based image analysis was performed with the SPM12 Statistical Parametric Mapping tool (RRID:SCR\_007037)*
    - **cross-sectional ROI analyses**
    - **Analysis of gene**
      * *The analysis of FNDC5 gene expression was done using the RQ Manager 1.2 software (Applied Biosystems)*
      * ***Gene Assembling*** 
        + *…, we assembled a high-quality genome using the combination of Platanus (version 1.2.1, RRID:SCR 015531)—[ software that can reconstruct genomic sequence]*
      * **Construct contigs**
        + *SOAPdenovo2 (version 2.04.4; RRID:SCR 014986) … was used to construct contigs*
      * **Fill Gaps**
        + *libraries were then used to fill gaps in scaffolds with the GapCloser (RRID:SCR 015026)*
      * **Generate Assembly**
        + *Platanus (version 1.2.1, RRID:SCR 015531) was used to generate a de novo assembly with a total of 1.0 Gb*
      * **Mapping**
        + *These reads were mapped onto the contigs using BWA-MEM (version 0.6.2, RRID:SCR 010910)*
      * **Correction of Mapping**
        + *Pilon (version 1.22, RRID:SCR 014731) [44] was also used to correct the assembly according to…*
      * **Generate Scaffolds**
        + *SSPACE (version 3.0, RRID:SCR 005056) was then used to generate scaffolds with the Illumina reads*
      * **Generate Trees** 
        + *…were subsequently used to generate neighbor-joining trees with fneighbor (PHYLIPNEW v3.69.650 within the package of EMBOSS v 6.6.0.0, RRID:SCR 006244)*
      * **Search sequences**
        + *RepeatMasker, RRID:SCR 012954) [49] was then used to search the repeat sequences*
      * **Map**
      * **Predict gene structure**
      * **Align** 
        + *The sequencing reads were aligned onto the genome assembly using HISAT2 version 0.1.6 (HISAT2, RRID:SCR 015530)*
        + *These cleaned RNA reads were aligned onto the reference genome (first version) using HISAT2 (version 0.1.6, RRID:SCR 015530)*
      * **Filter**
      * **evaluate**
      * **Calculate or determine**
        + *Expression values were calculated by Cufflink (version 2.2.1, RRID:SCR 014597) with defaulted parameters*
        + *the resolution limit was determined with TRIM\_DENZO*
      * **Draw heat map** 
        + *edgeR software (RRID:SCR 012802)*
      * **Validate**
        + *Scaffold v.4.8.4 (Proteome Software Inc., Portland, OR, RRID:SCR\_014345) was used to validate MS2 based peptide and protein identifications*
  + **Evaluate**
    - *… were evaluated blindly using the imaging program-Image J*
    - *Statistical significance was evaluated using the software GraphPad Prism statistics (v5, GraphPad Software, USA, RRID: SCR\_002798)*
    - *The BUSCO (RRID:SCR 015008) …was used to evaluate the completeness of our assembly*
  + **Data processing**
    - *DTI data processing was carried out using FMRIB’s Diffusion Toolkit (FDT)*
    - *The acquired raw MS2 data were processed by MaxQuant v.1.4.1.2 (RRID:SCR\_014485)*
  + **Annotation**
    - *Genomic repeat elements of the genome assembly were also identified and annotated using RepeatMasker*
    - *For repeat annotation, Repeat Modeler version 1.04 (Repeat Modeler, RRID:SCR 015027)*
    - *Then SnpEff (version 3.4, RRID:SCR 005191) [72] was used to annotate the genetic variants*
  + **Compute or calculate**
    - *MRI segmentations were computed with FreeSurfer (FS6 version 6.0; RRID:SCR\_001847*
    - *Intracranial volume (ICV) was calculated using FSL’s Brain Extraction Tool (Smith et al. 2002). FSL (RRID:SCR\_002823)*
  + **Fit or train a model**
    - *linear models (RStudio version 1.1.447; RRID:SCR\_00190540) were fit regressing each 18F-AV-45 ROI average*
    - *We used the polyfit function in MatlabTM (MATLAB and Statistics Toolbox, The MathWorks, Inc., Natick, MA) (RRID:SCR\_001622) to fit a regression slope for each participant, calculating slope average and goodness of fit*
  + **Pre- processing**
    - *preprocessing was performed using Statistical Parametric Mapping 8 (SPM8, RRID:SCR\_007037) and CONN Toolbox (RRID:SCR\_009550)*
  + **Draw / sketch** 
    - *The region of interests (ROI) was manually drawn around tumor and within muscle tissue using PMOD software (RRID:SCR\_016547)*
  + **Observation (Image acquisition and processing)**
    - *Example : Olympus cellSens Software -- image acquisition from a microscope , analysis and sharing of the image*
    - *NIS Elements software (Nikon) was used for image* ***acquisition and processing***
    - *We* ***captured and analyzed*** *images using a SPOT2e CCD camera (Diagnostic Instruments, Inc., Sterling Heights, MI) coupled to MetaMorph imaging software (Universal Imaging Corporation, Downingtown, PA)*
  + **Tracking and Analysis**
    - *Single particle tracking and analysis was carried out with custom software*
  + **Generate Data**
    - *Records of bead position over time were generated and analyzed using custom software*
  + **Optimize** 
    - *X-ray/stereochemistry weight and X-ray/ ADP weight were both optimized by phenix.refine in PHENIX (RRID:SCR\_014224)*
  + **Identify**
    - *A SalSite (RRID:SCR\_002850)30 EST contig (V4 contig436215) containing partial edn3 sequence was used to identify single nucleotide polymorphisms for a unique allele (edn3d)*
  + **Classify**
    - *BlastKOALA v.2.1 (Kanehisa et al., 2016, RRID:SCR\_012773) and eggNOG v.4.5.1 (Huerta-Cepas et al., 2016, RRID:SCR\_002456) were used to classify the proteins into functional categories*

Observations

* There are domain specific software
  + There are software that are used in Gene sequence Analysis.
  + For separate tasks there can be a dedicated software. Output from one software can be used as an input for another software in a pipe line.
* There are general purpose software
  + Some software are not domain specific and can be used in various fields. Example of such software are Data Analysis Tools like :
    - *Graphpad Prism software (RRID: SCR\_002798)*
    - *R statistical software v.3.1.2 (RRID:SCR\_001905)*
    - *IBM SPSS statistics v. 20 (RRID:SCR\_002865)*
    - *CXP Software*
    - *MaxQuant software*
    - *Data were analyzed for statistical significance using the GraphPad Prism Version 6.0 software*
    - *Data were analyzed using FlowJo software*
* Some software come with a hardware.
  + There are software that are used for acquisition of , for instance, an image from a microscope. This helps researchers to share their observation in the microscope with other scientists.
* A software can be custom made ( introduced as a novel software ) or it can be outsourced from previously done researches ( using existing software).
* A given software can be a general purpose (like R which can be used for statistical modelling, visualization, etc) or specialized ( only for specific tasks like gene mapping)
* A software can have different names
  + *Example: GraphPad and Prism refers to the same software*
* Purpose of software is often interrelated and it is possible to make generalization of software purpose. ( look at the graph below):
* For example: when a software includes all the functionalities , it can be said to be a general purpose