Usage of High Throughput Sequencing in Virology
Belgian Society for Virology
Wednesday the 9th of September 2015
Université de Liège, Tour GIGA, Batiment B34
1 avenue de l'Hôpital, Sart-Tilman, Liège

9h00-9h20: Registration, Tour GIGA B34, 5th Floor, L. Frédéricq auditorium

9h20-9h45: Principles of High Throughput Sequencing Technology - Wouter Coppieters (ULg, GIGA)

9h50-10h15: Retroviral insertion site mapping and clonal abundance - Gillet Nicolas (ULg-GIGA, ULg Gembloux Agro BioTech)

10h20-10h45: Deep sequencing reveals abundant noncanonical retroviral microRNAs in B-cell leukemia/lymphoma - Anne Van den Broeke (ULg-GIGA, Institut Bordet)

10h45-11h00 coffee break

11h00-11h40: to be determined

11h45-12h30: Challenges for the transition from research use towards diagnostic tool: the case of plant virus diagnostic - Sebastien Massart (ULg – Gembloux Agro BioTech)

12h30 – 14h00: sandwich lunch

14h00-16h00: Virus discovery from HTS data, practical training session (10 people max, a dedicated room with 10 computers will be available) – Sebastien Massart (ULg – Gembloux Agro BioTech)