

## **LIH: copy number alteration - Agilent aCGH, microarray**

### **Molecular Methods Description:**

Array-CGHs were performed as previously described <sup>1</sup> with the following exceptions. DNA was fragmented (200-500bp) using enzymatic digestion with RSA1 and Alu1 (Agilent Technologies) and labelled with the BioPrime aCGH Genomic labeling Kit (Life Technologies) and Cy3 and Cy5 dyes (GE Healthcare) following standard protocols for Agilent array-CGH (CGH enzymatic protocol v6.2; Ref # G4410-90010). Female or Male gDNA pool (Promega) was used as a reference. All labelling reactions were assessed using a Nanodrop 1000 (Thermo Fisher Scientific) before mixing and hybridized to either a 1x1M, 2x400K, 4x180K or 8x60K SurePrint G3 human CGH microarrays (Agilent Technologies) according to manufacturer's instructions (CGH enzymatic protocol v6.2; Ref # G4410-90010). Microarray slides were scanned using an Agilent 2565C DNA scanner and images were analyzed with Agilent Feature Extraction version 12.5, using default settings.

1. Stieber D, Golebiewska A, Evers L, et al. Glioblastomas are composed of genetically divergent clones with distinct tumourigenic potential and variable stem cell-associated phenotypes. *Acta neuropathologica* 2014; 127(2): 203-19.

### **Analysis Description:**

Data was assessed with a series of quality control metrics and analyzed using an aberration detection algorithm (ADM2) implemented in the CytoGenomics software versions 4.2 and 5.0.2.5 (Agilent Technologies). Aberrations were called using the ADM2 algorithm with a threshold setting of 6 and an aberration filter with a minimal number of probes=3 and a minimal AvgAbsLogRatio=0.25. Chromosomes X and Y were removed and supposedly non-coding areas with annotation 'unknown' were excluded from PDX finder submission.