

Suppl. Fig.3. EGFR and TGFB1 bubble plots

The ALS-affected twin's aligned RRBS reads are labeled ALS (2013) from the 2013 and ALS (2014) track from the 2014 sample. The unaffected twin's aligned RRBS reads are labeled NonALS (2013) from the 2013 sample, and NonALS (2014) from the 2014 sample. Filled black circles indicate methylated cytosines and unfilled circles indicate unmethylated cytosines. A) Visualization of the aligned RRBS reads to the fragment chr7:55,072,908-55,073,297 that is upstream of the EGFR transcription start site. Within the fragment, the NonALS (2013), NonALS (2014), ALS (2013), and ALS (2014) samples have 71.29%, 71.31%, 43.30%, and 40.19% of the aligned CpGs methylated respectively. B) Visualization of the aligned RRBS reads to the fragment chr19:41831930_41832049 that is downstream of the TGFB1 gene. The ALS-affected twin's aligned RRBS reads are labeled ALS.1 from the 2013 and ALS.2 track from the 2014 sample. Within the fragment, the NonALS (2013), NonALS (2014), ALS (2013), and ALS (2014) samples have 22.22%, 40.00%, 45.21%, and 54.55% of the aligned CpGs methylated respectively.

