

n=2088). Expression of Noggin was analysed using ANOVA and Kaplan-Meier analysis. Correlation between Noggin and angiogenic markers was evaluated using Spearman test. Impact on tumour growth was determined in a murine xenograft model by implant a triple negative breast cancer cell line (MDA-MB-231) with Noggin overexpression.

**Result:** Down-regulation of Noggin is revealed in both TCGA breast cancer cohort and the E-MTAB-6703. Reduced Noggin presents a correlation with poor relapse free survival. Moreover, patients with shorter overall survival exhibited higher expression of Noggin. Further analysis indicated that Noggin plays differential role in different subtypes of breast cancer. Lower expression of Noggin was seen in Her2 positive breast cancer compared with Luminal and Triple negative breast cancer (0.09(0.05–0.15) vs 0.13(0.06–0.24) vs 0.10(0.04–0.25)  $P < 0.001$ ). Noggin expression is positively correlated with BMP2, ACVR2A and ACVR1B and also fibroblast growth factor (FGF). Noggin reduced the in vivo tumour growth.

**Conclusion:** Noggin is reduced in breast cancer. Noggin expression has a subtype specific association with patients' survival in which the Noggin targeted BMP ligands and downstream receptors might be involved. Noggin inhibited in vivo tumour growth of MDA-MB-231 cells.

**Take-home Message:** Noggin is reduced in breast cancer. Noggin expression has a subtype specific association with patients' survival in which the Noggin targeted BMP ligands and downstream receptors might be involved.

### O30 Aberrant expression of noggin has a subtype specific association with survival of breast cancer patients

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**Introduction:** Noggin is an antagonist of bone morphogenetic proteins (BMP). High Noggin expression contributes formation of osteolytic bone lesions from breast cancer. However, the exact role of noggin in breast cancer is yet to be clarified.

**Method:** Expression of Noggin was analysed in both RNA sequencing data of breast cancer cohort (n = 1097) from The Cancer Genome Atlas (TCGA) and a gene array database of breast cancer (E-MTAB-6703,