Breast Invasive Carcinoma (TCGA, Provisional; 959 samples)

Genetic Alteration
- Amplification
- Deep Deletion
- mRNA Downregulation
- mRNA Upregulation
- Missense Mutation
- Truncating Mutation

A.

B. BCL9, mRNA Expression z-scores (microarray)

C. BCL9, Putative copy-number alterations from GISTIC

D. Exact 95% CI for BCL9 Amplification

E. BCL9 mRNA Expression z-scores (microarray)

Cancer type
- Mutation data
- CNA data
- All Tumors
- Basal
- Luminal A
- Luminal B
- HER2 enriched

No. Cases | Basal | Luminal A | Luminal B | HER2 enriched
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All tumors | 825 | 81 | 235 | 133 | 58
No. Amplified | 37 | 15 | 5 | 3 | 3
% Amplified | 4.5% | 18.5% | 2.1% | 2.3% | 5.2%
95% CI | 3.2%, 6.1% | 10.8%, 28.7% | 0.7%, 4.9% | 0.5%, 6.5% | 1.1%, 14.4%