

Supplementary Figure S1. Expression patterns and cut-off determination for AML Surfaceome. A: Expression of Surfaceome genes in hematopoietic stem cells in the bone marrow (HSCs - top panel), early hematopoietic progenitors in the bone marrow (HPC, middle panel) and CD14+ monocytes (bottom panel). Data derived from BloodSpot database (HemaExplorer). Cut-off used for filtering of Surfaceome candidates shown (calculated as the mean + SD). B: Expression of Surfaceome genes in non-hematopoietic tissue, displaying average non-heme tissue expression (top panel) or maximal non-heme tissue expression (from Genotype-Tissue Expression Project - GTEx). Cut-off used for filtering of Surfaceome candidates shown (calculated as the mean + SD).

50

10

log2 expression