Supplementary information, Figure S5

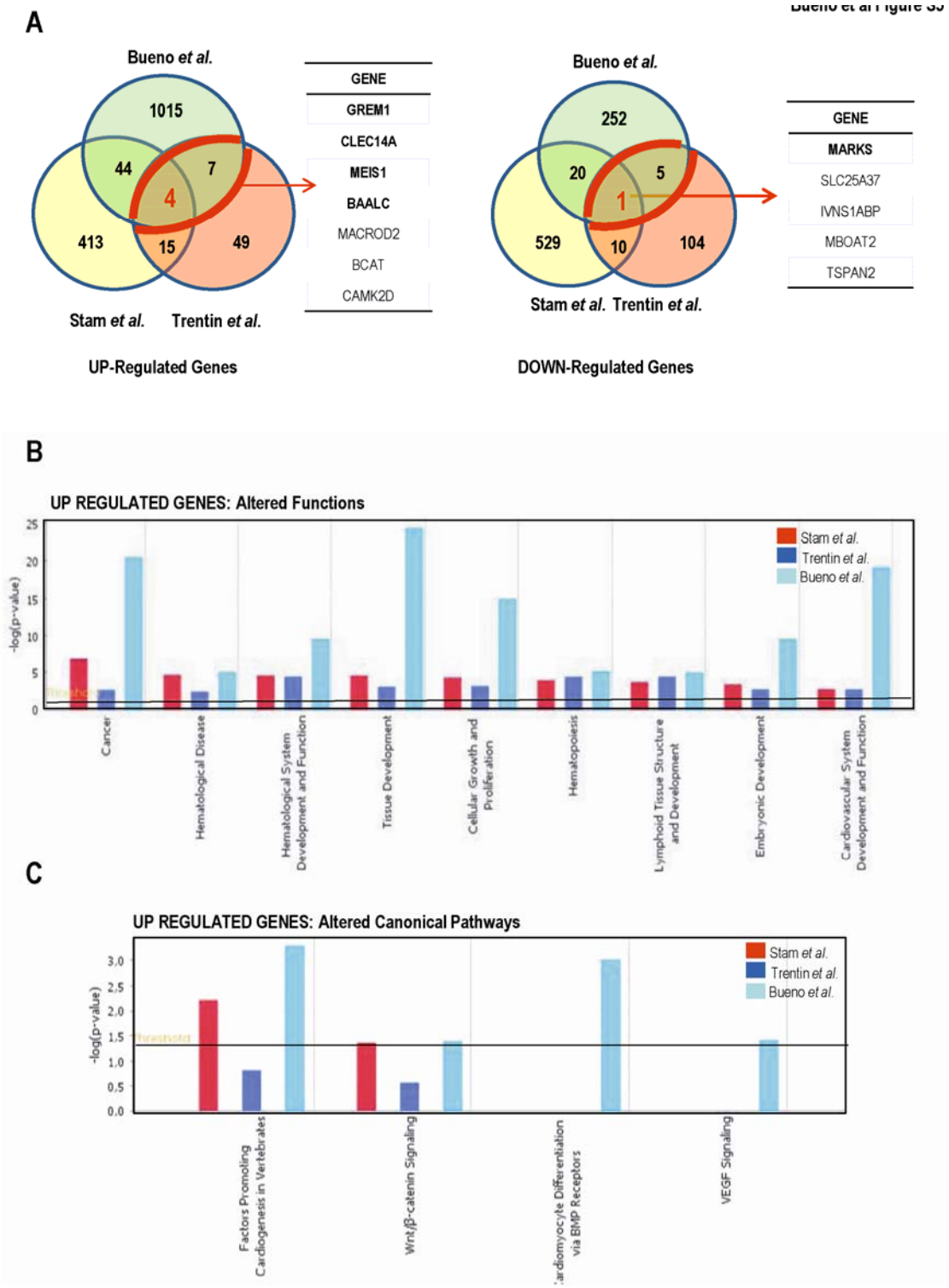

Figure S5 Comparative analysis of our gene expression profiling (GEP) with the GEP reported by Trentin *et al*. (2009) and Stam *et al*. (2010). **(A)** Venn diagram representing the number of genes commonly upregulated (left) and downregulated (right) between

MLL-AF4+ hESCs (relative to NEO hESCs), MLL-AF4+ infant B-ALL (relative to normal BM [Trentin, L. et al Eur J Hematol 2009]) and MLL-AF4+ infant B-ALL (relative to other MLL germline ALL [Stam, R.W. et al Blood 2010]). Those genes commonly regulated between the three GEP studies or between Bueno et al and Trentin et al (both studies used non-leukemic cells -hESCs or healthy BM CD34- as control) are identified. After GEP analysis, the groups of genes differentially upregulated in the three studies were compared and lists of biological functions and canonical pathways significantly altered were generated using the Ingenuity Pathways Analysis (IPA) 8 software. IPA software-based data mining generated a list of significantly upregulated gene functions **(B)** and canonical pathways **(C)** between MLL-AF4+ hESC/infant B-ALL and NEO hESCs/normal BM. As it can be observed, genes differentially upregulated in both MLL-AF4+ hESCs and MLL-AF4+ infant B-ALL were classified by the IPA software as involved in hematopoiesis, tissue development, VEFG signaling and cardiovascular/vasculo-endothelial system development and function.