Supplemental figure 1

Candidate target genes predicted *in silico*: qRT PCR validation using an independent sample set as described in materials and methods, but including only 11 AML samples: (A) HOXB6 (HOXB6_Fwd: AAGTGCTCCACTCCGGTCTA, HOXB6_probe: 6FAM-GACATACACACGTTACCAGACGCTG-TAMRA, HOXB6_Rev: GCTGAGCAGTTTGCTCTCCT), (B) OSBPL5 (OSBPL5_Fwd CACAGCCAAGTCCAGGTTTT, OSBPL5_probe 6FAM-AGCCGAGGATTACACCCTTACCAT-TAMRA, OSBPL5_R CGAAGAAGGGCTTGAGTTTG), (C) WT1 (WT1.2_Fwd: TACAGCACGGTCACCTTCG, WT1.2_probe: 6FAM-CTCATTCAAGCATGAGGATCCCAT-TAMRA, WT1.2_rev: GCGTCCTCAGCAGCAAAG), (D) BAHCC1 (BAHCC1.2_Fwd ACCGGCAGAGGATCTACTCA, BAHCC1.2_probe 6FAM-AGAAGTCTCGATGTCTGTACCCGG-TAMRA, BAHCC1.2_rev TCCAGGTCCTCATCTTCGTC), (E) WDR49: several splice variants have been described, and shown is the data from primer/probe set 3 quantifying ensemble variants 001, 002, 003, 201, 202 (WDR49.3_Fwd GGGCATTCATGCTTTTGATT, WDR49.3_probe 6FAM-GCCAGTGTAATAGCCGTCCAATTC-TAMRA, WDR49.3_rev GATGGACAGCTGGTGTTGAA). Primer/probe set 2 specific for variants 001, 003, 004, 202 and both lengths of exon 6 (WDR49.2_fwd GAGACTCGGCTTTTGACTGG, WDR49.2_probe.2 6FAM-ctaaatgttgggcaagatggagct-TAMRA, WDR49.2_rev GAAGTTTTGGGGTCGAAACA) shows comparable results (data not shown). (F) SMYD3 (SMYD3_Fwd CCATGGAGCCATACAGGATT, SMYD3_probe 6FAM-GTGATGAAAGTTGGCAAACTGCAG-TAMRA, SMYD3_Rev GCTGTGTTCTCTGCCATGTG).

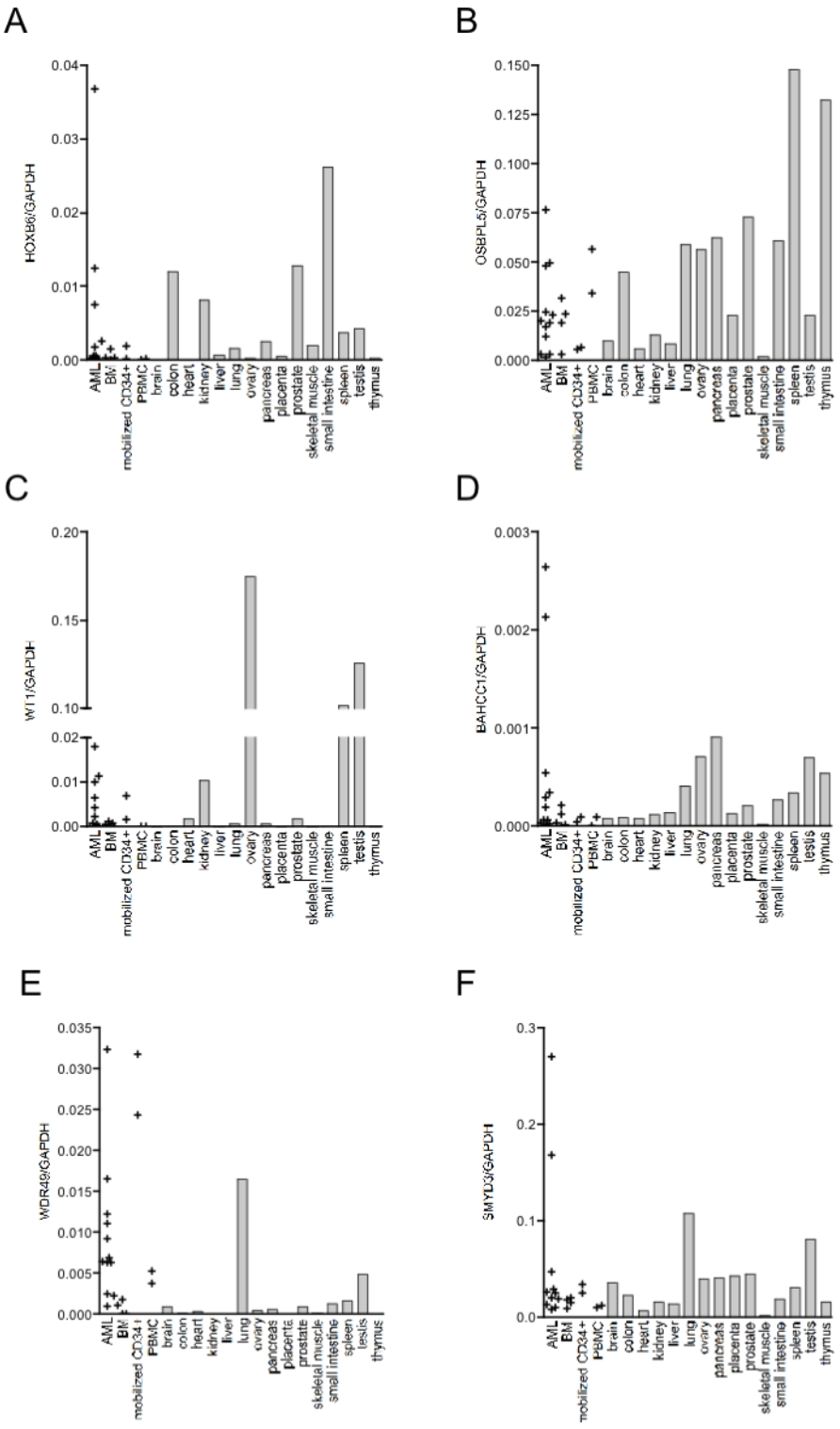
Supplemental figure 2:

Comparison of absolute expression of cyclin-A1 with WT1 based on qRT PCR. Shown are the copy numbers per copies of GAPDH quantified in the same unselected sample set. Horizontal lines represent medians, * $p<0.001$ (Wilcoxon signed rank test).

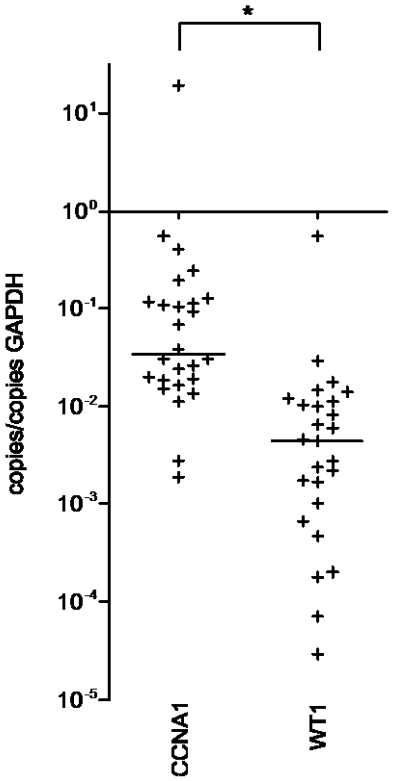
Supplemental figure 3:

Testing for HLA class I-restriction of immunogenic peptides in T-cell lines by IFNγ ICS: (A) Epitopes were first screened for HLA A*0201-restriction by testing the respective T-cell line for IFNγ production after stimulation by K562, K562 transfected with A*0201 and autoLCLs pulsed with the respective 15-mer. Two representative examples are shown: epitope 218-226 (15-mer 217-231), which is restricted to A*0201 and epitope 120-131 (15-mer 117-131), which is not restricted to A*0201. No unspecific IFNγ production was observed after stimulation with unpulsed LCLs (not shown). Plots are gated on $CD8^+$ cells, (B) in case of a HLA restriction other than to A*0201, the HLA-restrictions were determined using ICS for IFNγ production with 721.221 stimulator cells transfected with a single HLA allele or allogeneic LCLs sharing one or two HLA class I allele with the respective donor. For a representative example, IFNγ ICS plots gated on $CD8^+$ are shown for clone 2196.F10 specific for epitope 120-131. All stimulator cells were pulsed with the respective peptide. Untransfected 721.221s were used as negative control, autologous LCL were used as positive control. Allogeneic LBF LCL shared with donor 2196 only the C*0602 class I allele, LCL PF97387 shared alleles B*4403 and C*1601, and LCL WJR076 shared alleles A*0201 and B*5701. With only the latter being able to stimulate clone 2196.F10, epitope 120-131 is restricted to B*5701.

Supplemental figure 1:



Supplemental figure 2:



Supplemental figure 3: