Figure S1. Venn diagrams of differentially expressed genes in TKI resistance. Number of genes shown comparing the biological replicates of lowIM, highIM and nilotinib resistance to native cells. lowIM, 0.5 μM imatinib resistant; highIM, 2 μM imatinib resistant; N, 0.1 μM nilotinib; R1, resistant subline 1; R2, resistant subline 2; TKI, tyrosine kinase inhibitor.

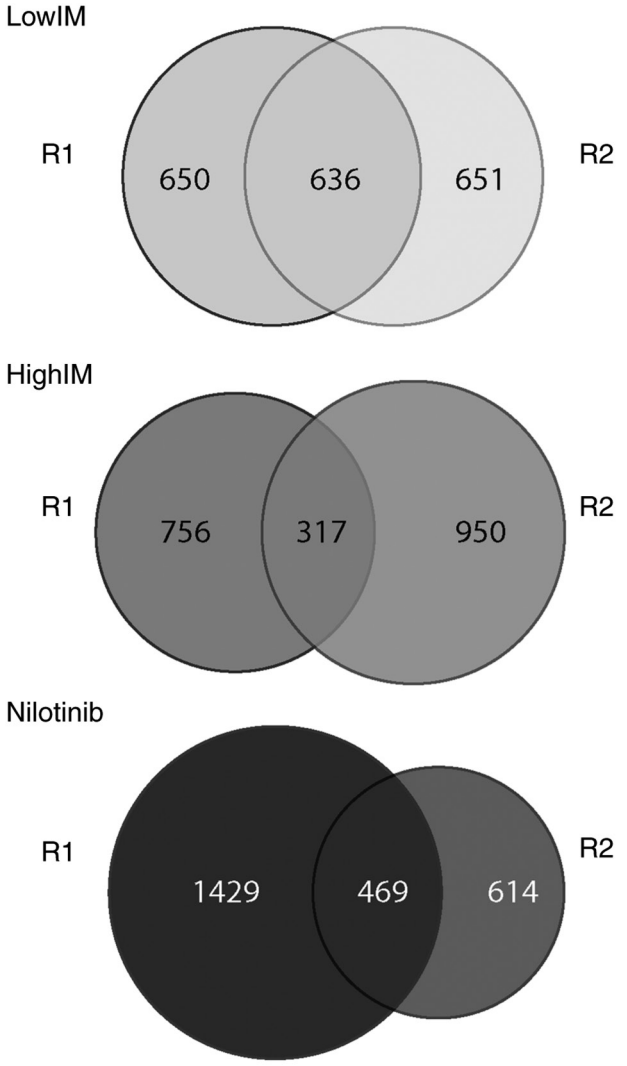

Figure S2. Comparison of gene expression profiles of imatinib and nilotinib resistance. (A) Venn diagram of differentially expressed genes in imatinib and nilotinib resistance. Number of differentially expressed genes shown for the comparison of lowIM, highIM and nilotinib resistance to native cells. lowIM: 0.5 μM imatinib; highIM: 2 μM imatinib; N, 0.1 μM nilotinib. (B) STRING analysis of genes being unidirectional differentially expressed genes in imatinib and nilotinib resistance. Turquoise: from curated databases; pink: experimentally determined; blue: gene co-occurrence; yellow: textmining; black: co-expression; purple: protein homology.

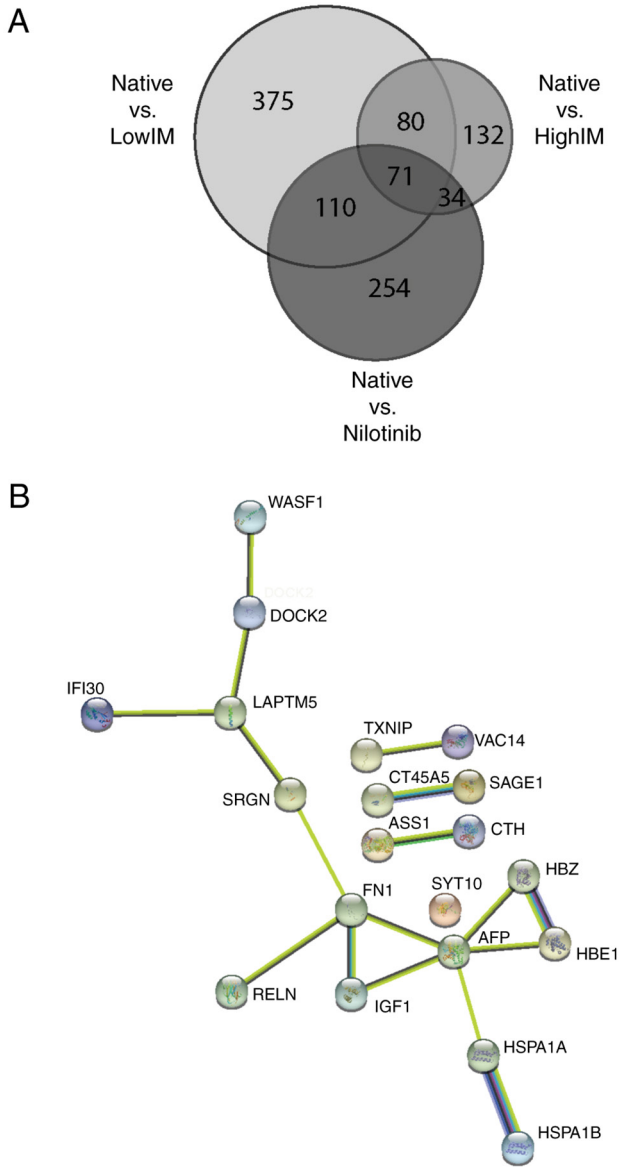

Figure S3. mRNA-expression of candidate genes in imatinib resistant sublines. Reverse transcription-quantitative PCR of (A) *BCL-2*, (B) *DNASE2*, (C) *IFI30*, (D) *NMU* and (E) *PDE4DIP* normalized to *TBP* and *GAPDH* and native cells. The genes were chosen due to their differential expression in the gene expression profile, as well as their association with differential methylated CpGs in the genome-wide methylation analysis. *P<0.05, **P<0.01 and ***P<0.001. Av, average/mean expression of both replicates; R1, replicate 1; R2, replicate 2; lowIM, 0.5 μM imatinib; highIM, 2 μM imatinib.