Prognostic implications of mutations and expression of the Wilms tumor 1 (*WT1*) gene in adult acute T-lymphoblastic leukemia

Sandra Heesch,[1] Nicola Goekbuget,[2] Andrea Stroux,[3] Jutta Ortiz Tanchez,[1] Cornelia Schlee,[1] Thomas Burmeister,[1] Stefan Schwartz,[1] Olga Blau,[1] Ulrich Keilholz,[1] Antonia Busse,[1] Dieter Hoelzer,[2] Eckhard Thiel,[1] Wolf-Karsten Hofmann,[4] and Claudia D. Baldus[1]

[1]Charité, University Hospital Berlin, Campus Benjamin Franklin, Department of Hematology and Oncology, Berlin, Germany; [2]University Frankfurt am Main, Department of Hematology and Oncology, Frankfurt/Main, Germany; [3]Charité, University Hospital Berlin, Campus Benjamin Franklin, Department of Biostatistics and Clinical Epidemiology, Berlin, Germany, and [4]University Mannheim, Department of Hematology and Oncology, Mannheim, Germany

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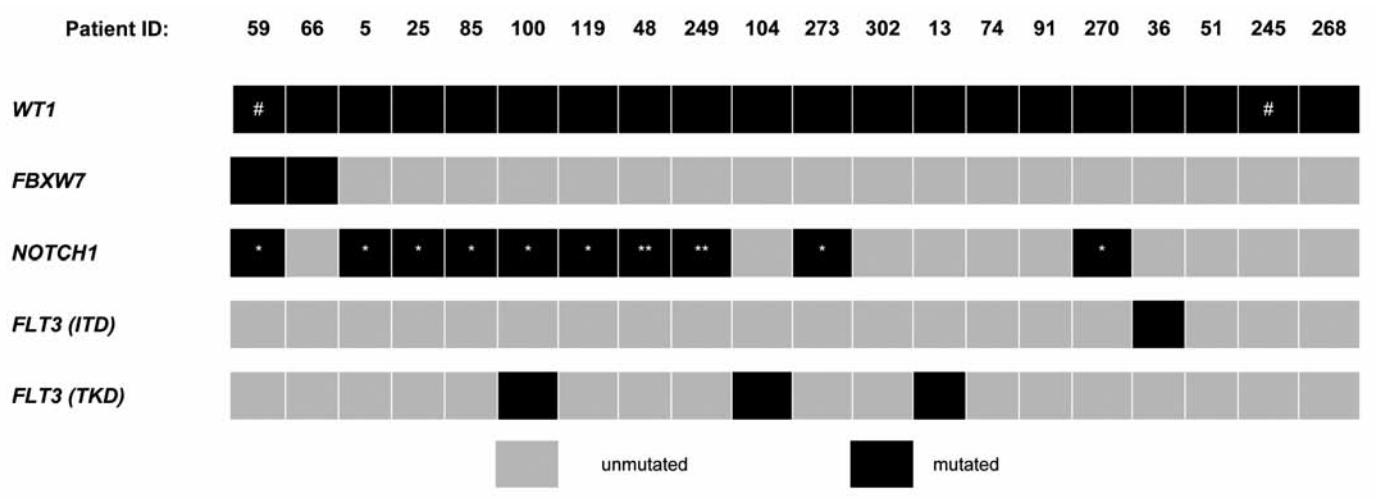

Online Supplementary Figure S1. Coexistence of *WT1* mutations with mutations in the *FBXW7*, *NOTCH1*, and *FLT3* genes. T-ALL patients with *WT1* mutations (n=20) are listed and coexistence of mutation in the *FBXW7*, *NOTCH1*, and *FLT3* genes are indicated by black boxes. # *WT1* mutations in exons 7 and 9; * *NOTCH1* mutations in the HD domain; ** *NOTCH1* mutations in the PEST domain; ITD: internal tandem duplication; TKD: D835 mutation in the tyrosine kinase domain.

Online Supplementary Table S1. T-ALL patients with *WT1* mutations.

Patient ID	Age	Sex	DNA change[#,†]	Clones[×]		Protein change[†,‡]	Outcome	T-ALL subtype
WT1^{mut7}								
36	20	M	clone a: 1305_1306insTTGAAAT clone b: [1304_1305insT; 1305_1306insACGATAC]	[5/10] [5/10]		Val371X Arg370LeufsX8	no clinical data available	early T-ALL
48	27	M	1334_1338dupCGGTC	[5/10]		Ala382Glyfs§	no clinical data available	mature T-ALL
51	22	F	[1300_1301insA; 1302dupG]	homozygote		Arg369ThrfsX7	failure/death	early T-ALL
249	18	M	1337_1340delinsAGATGAAGCACCGATACTT	[11/11]		Ser381ArgfsX2	relapse/death	thymic T-ALL
268	63	F	[1295-5_1309del20; 1312T>C; 1315_1316delAG]	[8/9]		[Asp367_Val371;Val347SerfsX10]	CCR/alive	early T-ALL
270	28	M	1305delinsCCC	[8/10]		Arg370ProfsX6	failure/death	mature T-ALL
273	30	F	clone a:1334delinsAA clone b: 1333_1334insG	[3/6] [3/6]		Arg380AlafsX5 Ser381ValfsX4	relapse/death	thymic T-ALL
302	31	F	1319_1320insCC	[6/6]		Thr377Argfs§	failure/death	mature T-ALL
5	24	M	1334delinsTA	[5/10]		Arg380X	CCR/alive	thymic T-ALL
13	32	M	clone a: [1304_1305insT; 1305_1306insACGATAC] clone b: 1305_1306insTTGAAAT	[4/10] [5/10]		Arg370LeufsX8 Val371X	SCT/alive	early T-ALL
25	21	F	clone a: 1305_1306insTAGCGCGGGGGCGGATTCAAGGGCGGCC clone b: 1305delinsCCCCC	[4/10] [5/10]		Val371SerfsX23 Arg370ProfsX16	relapse/alive	thymic T-ALL
66	40	M	1333dupA	[11/14]		Arg380ThrfsX5	death in CR	thymic T-ALL
74	32	F	1333dupA	[14/14]		Arg380ThrfsX5	relapse/death	thymic T-ALL
85	15	M	1305_1306insGTAACCCG	[5/5]		Val371X	SCT/alive	early T-ALL
91	26	M	1333_1334insCGGAGGGA	[4/5]		Ser381Argfs§	SCT/alive	mature T-ALL
100	40	M	1334delinsAA	[7/11]		Arg380LysfsX5	SCT/alive	early T-ALL
104	40	M	1301delinsGG	[5/5]		Arg369GlyfsX16	SCT/death	early T-ALL
119	23	F	1337_1338insGGGGTTTGGCATTGGGTAGGACGGT	[11/12]		Arg380TrpfsX12	SCT/alive	early T-ALL
WT1^{mut7} and *WT1*^{mut9}				Exon 7	Exon 9			
245	23	M	[1422_1423insGCGGGCC(+) =, 1581G>C*]	[4/6]	[homozygote]	[Met410Glnfs§ (+) Arg462Pro]	SCT/death	early T-ALL
59	36	F	[1334delinsGGG(+) =, 1581G>C*]	[5/10]	[12/13]	[Arg380Glyfs§ (+) Arg462Pro]	death in CR	thymic T-ALL

[§] *The stop codons created by these WT1mut7 do not occur until the 3' part of exon 7.* [#] *Nucleotide sequence variations numbering is according to Genbank accession number NM_024426.* [†] *The sequence variations are designated according to the current recommendations of the Human Genome Variation Society (http://www.hgvs.org/mutnomen/).* [‡] *The protein changes are theoretically deduced.* **1581G>C mutation previously reported in AML (see ref. 5 in main text).* [×] *Number of mutated clones/total number of analyzed clones. CCR: continuous complete remission; CR: complete remission; SCT: stem cell transplantation in first CR.*