

**Supplementary Table 1.** SWI/SNF-related gene probes on the Affymetrix U133 expression array and current assessment of gene expression in acute lymphoblastic leukemia ALL cells\*

Gene symbol	Gene name	Probe set ID	Public ID	Expression
ARID1A	AT-rich interactive domain 1A (SWI-like), BAF250	210649_s_at	AF231056	Yes
ARID1A	AT-rich interactive domain 1A (SWI-like), BAF250	218917_s_at	NM_018450	Yes
ARID1A	AT-rich interactive domain 1A (SWI-like), BAF250	212152_x_at	AI679080	Yes
SMARCA1	SWI/SNF, subfamily a, member 1, SNF2L1	215294_s_at	AK026426	No
SMARCA1	SWI/SNF, subfamily a, member 1, SNF2L1	203875_at	NM_003069	No
SMARCA1	SWI/SNF, subfamily a, member 1, SNF2L1	203873_at	M88163	No
SMARCA1	SWI/SNF, subfamily a, member 1, SNF2L1	203874_s_at	NM_003069	No
SMARCA2	SWI/SNF, subfamily a, member 2, BRM, core	212258_s_at	X72889	No
SMARCA2	SWI/SNF, subfamily a, member 2, BRM, core	206543_at	NM_003070	No
SMARCA2	SWI/SNF, subfamily a, member 2, BRM, core	206544_x_at	NM_003070	No
SMARCA2	SWI/SNF, subfamily a, member 2, BRM, core	212257_s_at	AW131754	No
SMARCA2	SWI/SNF, subfamily a, member 2, BRM, core	206542_s_at	AV725365	No
SMARCA2	SWI/SNF, subfamily a, member 2, BRM, core	217707_x_at	AI535683	No
HLTF	helicase-like transcription factor, SMARCA3	202983_at	AI760760	Yes
SMARCA4	SWI/SNF, subfamily a, member 4, BRG1, ATPase, core	208793_x_at	AI744900	Yes
SMARCA4	SWI/SNF, subfamily a, member 4, BRG1, ATPase, core	212520_s_at	AI684141	Yes
SMARCA4	SWI/SNF, subfamily a, member 4, BRG1, ATPase, core	208794_s_at	D26156	Yes
SMARCA4	SWI/SNF, subfamily a, member 4, BRG1, ATPase, core	214728_x_at	AK026573	Yes
SMARCA4	SWI/SNF, subfamily a, member 4, BRG1, ATPase, core	215714_s_at	AF254822	No
SMARCA4	SWI/SNF, subfamily a, member 4, BRG1, ATPase, core	213720_s_at	AI744900	No
SMARCA5	SWI/SNF, subfamily a, member 5, SNF2F	213251_at	AV712064	Yes
SMARCA5	SWI/SNF, subfamily a, member 5, SNF2F	213859_x_at	AI652586	No
SMARCA5	SWI/SNF, subfamily a, member 5, SNF2F	202303_x_at	NM_003601	No
SMARCAL1	SWI/SNF, subfamily a-like 1	218452_at	NM_014140	No
SMARCB1	SWI/SNF, subfamily b, member 1, SNF5, INI1, BAF47, core	212167_s_at	AK021419	Yes
SMARCC1	SWI/SNF, subfamily c, member 1, BAF155, core	201072_s_at	AW152160	Yes
SMARCC1	SWI/SNF, subfamily c, member 1, BAF155, core	201075_s_at	NM_003074	Yes
SMARCC1	SWI/SNF, subfamily c, member 1, BAF155, core	201073_s_at	AL040633	Yes
SMARCC1	SWI/SNF, subfamily c, member 1, BAF155, core	201074_at	AA593983	Yes
SMARCC2	SWI/SNF, subfamily c, member 2, BAF170, core	201320_at	BF663402	No
SMARCC2	SWI/SNF, subfamily c, member 2, BAF170, core	201321_s_at	NM_003075	Yes
SMARCD1	SWI/SNF, subfamily d, member 1, BAF60a	203183_s_at	NM_003076	Yes
SMARCD1	SWI/SNF, subfamily d, member 1, BAF60a	209518_at	AI869240	Yes
SMARCD2	SWI/SNF, subfamily d, member 2, BAF60b	201827_at	AF113019	Yes
SMARCD3	SWI/SNF, subfamily d, member 3, BAF60c	204099_at	NM_003078	No
SMARCE1	SWI/SNF, subfamily e, member 1, BAF57	211989_at	NM_003079	Yes
SMARCE1	SWI/SNF, subfamily e, member 1, BAF57	211988_at	BG289800	Yes
ACTL6A	actin-like 6A, BAF53a	202666_s_at	NM_004301	No
ACTL6B	actin-like 6B, BAF53b	206013_s_at	NM_016188	No
ACTL6B	actin-like 6B, BAF53b	206014_at	NM_016188	No
PB1	polybromo 1, BAF180	220355_s_at	NM_018165	Yes

\* ALL = acute lymphoblastic leukemia; ID = identifier

**Supplementary Table 2.** Gene probes associated with prednisolone sensitivity in primary acute lymphoblastic leukemia cells: the German Cooperative Study Group for Childhood Acute Lymphoblastic Leukemia COALL-92/97 and the ALL-IX Dutch Childhood Oncology Group discovery cohort\*

Gene symbol	Probe set ID	<i>P</i> †	Rho†	R/S ratio‡
ARID1A	212152_x_at	.022	-0.17	0.77 (.002)
ARID1A	218917_s_at	.007	-0.20	0.85 (.007)
ARID1A	210649_s_at	.005	-0.21	0.64 (.002)
ARID1A§		.002	-0.23	0.34 (.0007)
SMARCA4	208793_x_at	<.001	-0.26	0.65 (.001)
SMARCA4	208794_s_at	<.001	-0.27	0.58 (.0003)
SMARCA4	214728_x_at	.002	-0.24	0.64 (.001)
SMARCA4	212520_s_at	.001	-0.24	0.74 (.003)
SMARCA4§		<.001	-0.28	0.25 (.0004)
SMARCC2	201321_s_at	.002	-0.18	0.87 (.38)
SMARCB1	212167_s_at	<.001	-0.28	0.82 (.003)

\*LC<sub>50</sub> = concentration lethal to 50% of cells; ID = identification number; R/S = resistant versus sensitive ratio.

†*P* value and correlation coefficient value (Rho) were from a Spearman rank correlation test with concentration of prednisolone that is lethal to 50% of cells. All statistical tests were two-sided.

‡R/S ratios and their *P* value (Wilcoxon rank sum test) compared the median gene expression of resistant group with the median gene expression of sensitive group. For prednisolone, resistance = LC<sub>50</sub> ≥ 150 µg/mL; sensitivity = LC<sub>50</sub> ≤ 0.100 µg/mL. For dexamethasone, resistance = LC<sub>50</sub> ≥ 5.8 µg/mL; sensitivity = LC<sub>50</sub> ≤ 0.02 µg/mL.

§Representative *P* value and correlation coefficient value that are based on principal component analysis.

**Supplementary Table 3.** Genes contributing to variation in prednisolone sensitivity as measured by its concentration lethal to 50% of cells: the German Cooperative Study Group for Childhood Acute Lymphoblastic Leukemia COALL-92/97 and the ALL-IX Dutch Childhood Oncology Group discovery cohort\*

Gene	Five-gene model		Three-gene model	
	Estimate <sup>†</sup>	<i>P</i> value	Estimate <sup>†</sup>	<i>P</i> value
NR3C1	-0.72 (-1.21 to -0.23)	<.001	-0.61(-1.02 to -0.2)	<.001
ARID1A	-0.70 (-1.07 to -0.33)	.005	-0.90 (-1.38 to -0.42)	<.001
SMARCB1	-1.74 (-3.22 to -0.26)	.031	-2.38 (-4.41 to -0.35)	.001
SMARCA4	-0.29 (-0.79 to 0.21)	.19	—	—
SMARCC2	-0.86 (-2.07 to 0.35)	.16	—	—

\*Multiple linear regression model for prednisolone as measured by its concentration lethal to 50% of cells with five genes (multiple  $r^2 = 21.6\%$ ,  $P < .001$ ), and three genes (multiple  $r^2 = 19.8\%$ ,  $P < .001$ ).

— = gene excluded;  $LC_{50}$  = concentration lethal to 50% of cells. All statistical tests were two-sided.

<sup>†</sup>Estimate and 95% confidence interval from multiple linear regression analysis. Estimate represents the change in  $\log_2(LC_{50})$  with one-fold increase in the expression value.

**Supplementary Table 4.** Prediction accuracy, sensitivity, and specificity from the five-gene or the three-gene models\*

Drug and cohort	Five-gene model		Three-gene model	
	Value (95% CI)	<i>P</i> value	Value (95% CI)	<i>P</i> value
<b>Prednisolone in the COALL-DCOG discovery cohort</b>				
Prediction accuracy, %	76 (65 to 85)	<.001	77 (66 to 85)	<.001
Sensitivity, %	72 (54 to 87)		73 (57 to 89)	
Specificity, %	87 (75 to 94)		89 (75 to 96)	
<b>Prednisolone in the St. Jude validation cohort</b>				
Prediction accuracy, %	71 (58 to 81)	.016	64 (51 to 76)	.055
Sensitivity, %	67 (50 to 83)		57 (38 to 74)	
Specificity, %	76 (58 to 91)		72 (54 to 88)	
<b>Dexamethasone in the St. Jude validation cohort</b>				
Prediction accuracy, %	77 (63 to 91)	.005	71 (57 to 86)	.011
Sensitivity, %	67 (39 to 89)		67 (40 to 89)	
Specificity, %	91 (72 to 100)		73 (63 to 96)	

\* CI = confidence interval; COALL-DCOG = German Cooperative Study Group for Childhood Acute Lymphoblastic Leukemia COALL-92/97 and the ALL-IX Dutch Childhood Oncology Group.