Supplement for Bartram *et al.* 2014

<u>Content:</u>

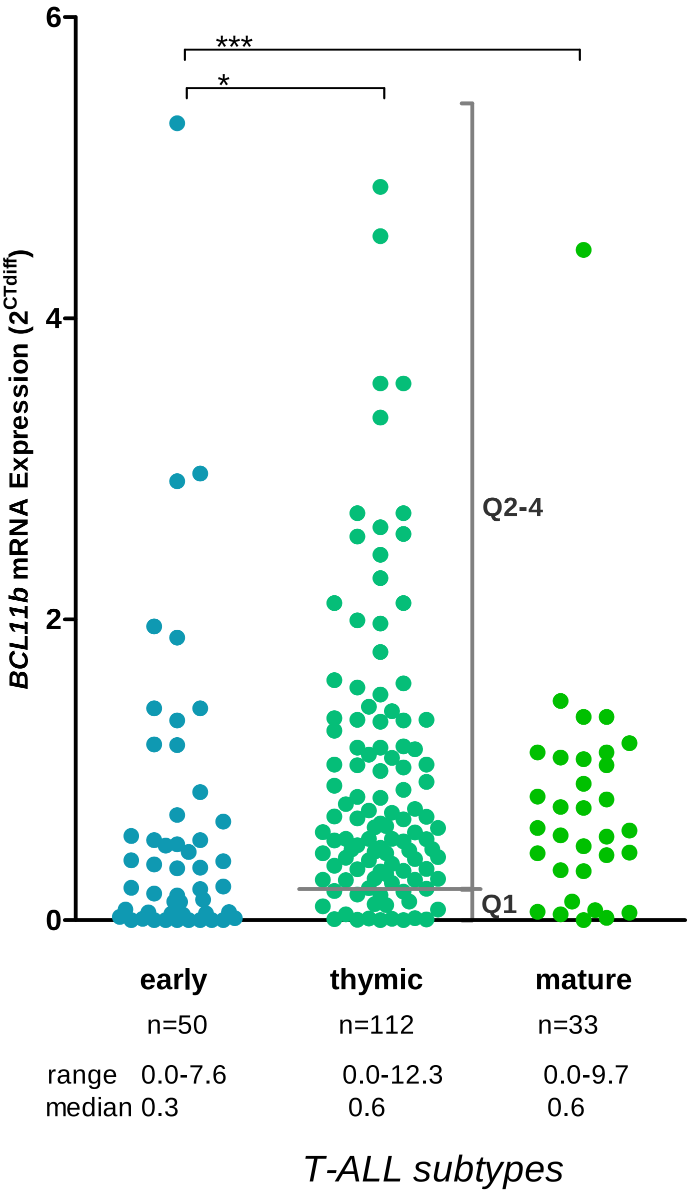

Figure S1: *BCL11b* mRNA expression in T-ALL immunophenotypic subtypes
Patients with early T-ALL immunophenotype showed a significantly lower expression than thymic or mature T-ALL patients. *BCL11b* expression quartiles were defined on the basis of the whole T-ALL cohort for further analysis. Patients with low or lacking expression were combined in Q1 and patients with high expression in Q2-4.
Outliers (n=4 thymic T-ALL patients, *BCL11b* expression values: 6.3, 7.6, 9.7, 12.3) were omitted from the diagram but included in the statistical analysis. BM = bone marrow; * P=0.03, *** P<0.01

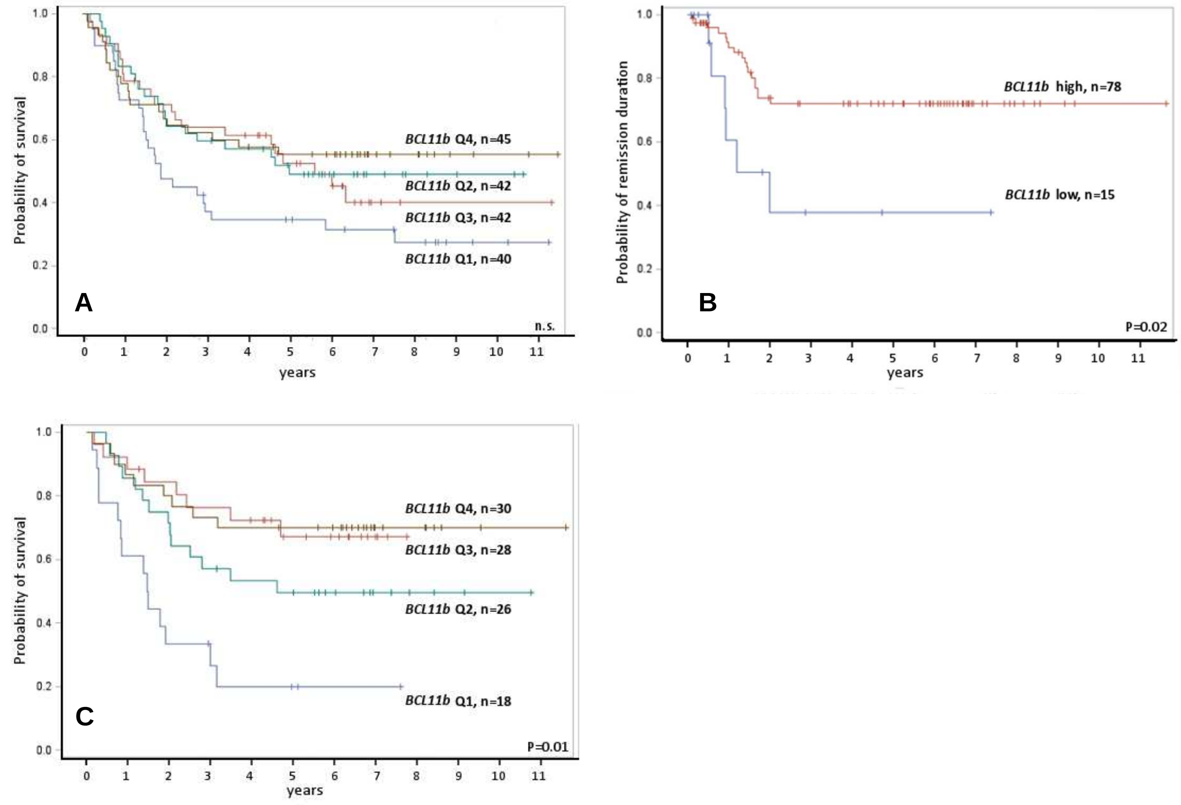

Figure S2: Kaplan-Meier analyses of overall survival (OS) in T-ALL with respect to *BCL11b* mRNA expression. **A**: OS of the overall T-ALL cohort according to *BCL11b* expression quartiles (Q1: n=40; 35% OS at 5 yrs; Q2: n=42; 52% OS at 5 yrs; Q3: n=42; 52% OS at 5 yrs; Q4: n=45; 55% OS at 5 yrs; n.s.) **B:** Thymic T-ALL patients with low *BCL11b* expression showed a significant shorter remission duration than thymic patients with high *BCL11b* expression (Q1: n=15, 38% CR at 5 yrs; Q2-4: n=78, 72% CR at 5 yrs; P=0.02). **C**: OS of thymic T-ALL patients according to *BCL11b* expression quartiles (Q1: n=18, 20% at 5 yrs; Q2 n=26, 67% at 5 yrs¸ Q3 n=18, 50% at 5 yrs; Q4 n=30, 70% at 5 yrs; P=0.01).

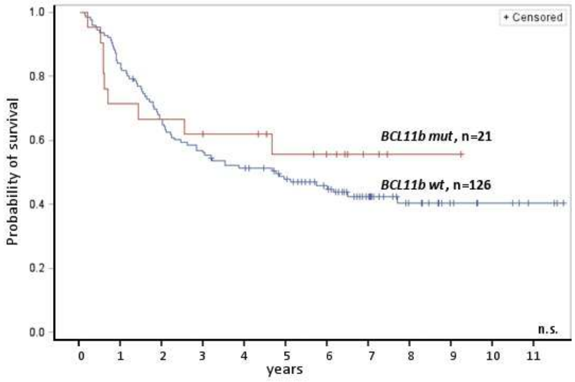

Figure S3: Kaplan-Meier analysis of overall survival (OS) with respect to the *BCL11b* mutation status. No significant difference in OS was observed in patients with mutated vs. wild type *BCL11b* (*BCL11b-wt*: n=126; 48% OS at 5 yrs; *BCL11b*-mut: n=21; 56% OS at 5 yrs; n.s.; log-rank test).

Table S1: Primer sets designed for human *BCL11b* exon 4 (NP_612808.1)		
Name	**Region**	**Sequence**
forward1	exon4_1	ACGCTGTCTCTGCCTTTCTG
reverse1	exon4_1	CTCCGAGTCCATGCTGAAG
forward2	exon4_2	GCTGCTACTGGAGAACGAGAG
reverse2 [1]	exon4_2	CTCGGGTTTCCATAGGACTTC
forward3	exon4_2	CCACCACGAGAGCGACC
reverse3	exon4_2	TTGACGTCGTTAGTCAGCAAG
forward4	exon4_2	GCCAAGCGCATCAAGGTG

Table S2: Probe sets two-fold up-regulated in the *BCL11b*-low group compared to *BCL11b*-high group of T-ALL patients (n=86); 229 probe sets, 181 genes

Probe Set	Ratio	P-value	Gene name
202625_at	3.70	1.43E-09	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
202626_s_at	3.51	2.58E-09	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
225659_at	2.61	2.01E-08	speckle-type POZ protein-like
227013_at	6.10	5.65E-08	LATS, large tumor suppressor, homolog 2 (Drosophila)
238669_at	2.36	1.73E-07	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
215706_x_at	2.36	2.95E-07	zyxin
204689_at	3.08	4.66E-07	hematopoietically expressed homeobox
208890_s_at	3.22	4.97E-07	plexin B2
203749_s_at	2.52	5.30E-07	retinoic acid receptor, alpha
217478_s_at	3.92	8.26E-07	major histocompatibility complex, class II, DM alpha
208767_s_at	2.54	8.79E-07	lysosomal protein transmembrane 4 beta
227195_at	10.12	9.36E-07	zinc finger protein 503
228188_at	8.53	1.35E-06	FOS-like antigen 2
235252_at	2.38	1.72E-06	kinase suppressor of ras 1
31845_at	2.59	1.83E-06	E74-like factor 4 (ets domain transcription factor)
225658_at	2.59	1.83E-06	speckle-type POZ protein-like
201566_x_at	2.56	1.83E-06	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
211302_s_at	3.73	1.94E-06	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)
203708_at	3.85	2.32E-06	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)
225955_at	2.41	2.46E-06	meteorin, glial cell differentiation regulator-like; similar to meteorin, glial cell differentiation regulator-like
212658_at	2.32	2.77E-06	lipoma HMGIC fusion partner-like 2
228170_at	7.81	2.94E-06	oligodendrocyte transcription factor 1
204490_s_at	2.40	3.49E-06	CD44 molecule (Indian blood group)
204908_s_at	2.36	4.15E-06	B-cell CLL/lymphoma 3
209307_at	4.04	4.39E-06	SWAP switching B-cell complex 70kDa subunit
225262_at	3.11	4.65E-06	FOS-like antigen 2
201163_s_at	3.18	6.89E-06	insulin-like growth factor binding protein 7
228964_at	2.10	9.06E-06	PR domain containing 1, with ZNF domain
209619_at	4.13	1.25E-05	CD74 molecule, major histocompatibility complex, class II invariant chain
210754_s_at	2.85	1.39E-05	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
201536_at	2.23	1.72E-05	dual specificity phosphatase 3
204204_at	2.78	1.91E-05	solute carrier family 31 (copper transporters), member 2
201162_at	3.63	2.01E-05	insulin-like growth factor binding protein 7
211991_s_at	5.09	2.23E-05	major histocompatibility complex, class II, DP alpha 1
226397_s_at	3.67	2.35E-05	-
228831_s_at	3.03	2.47E-05	guanine nucleotide binding protein (G protein), gamma 7
212975_at	2.32	2.73E-05	DENN/MADD domain containing 3
226459_at	3.07	3.18E-05	phosphoinositide-3-kinase adaptor protein 1
203820_s_at	2.03	3.34E-05	insulin-like growth factor 2 mRNA binding protein 3
204198_s_at	2.12	3.70E-05	runt-related transcription factor 3
218627_at	2.16	3.88E-05	DNA-damage regulated autophagy modulator 1
211990_at	3.51	4.29E-05	major histocompatibility complex, class II, DP alpha 1
214953_s_at	2.10	4.73E-05	amyloid beta (A4) precursor protein
204440_at	2.45	4.96E-05	CD83 molecule

Continuation I of Table S2

Probe Set	Ratio	P-value	Gene name
211654_x_at	3.07	5.21E-05	major histocompatibility complex, class II, DQ beta 1; similar to major histocompatibility complex, class II, DQ beta 1
201137_s_at	4.85	5.47E-05	major histocompatibility complex, class II, DP beta 1
200808_s_at	2.08	5.47E-05	zyxin
211597_s_at	3.46	5.74E-05	HOP homeobox
201170_s_at	2.70	5.74E-05	basic helix-loop-helix family, member e40
209312_x_at	2.62	6.03E-05	major histocompatibility complex, class II, DR beta 4; major histocompatibility complex, class II, DR beta 1
208092_s_at	2.63	6.32E-05	family with sequence similarity 49, member A
213537_at	4.64	6.63E-05	major histocompatibility complex, class II, DP alpha 1
215933_s_at	2.89	6.63E-05	hematopoietically expressed homeobox
200602_at	2.84	6.63E-05	amyloid beta (A4) precursor protein
212120_at	2.64	8.40E-05	ras homolog gene family, member Q; similar to small GTP binding protein TC10
227425_at	2.62	9.23E-05	RALBP1 associated Eps domain containing 2
222582_at	2.22	9.67E-05	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
230917_at	2.65	1.01E-04	RNA, 7SK small nuclear
204670_x_at	3.11	1.11E-04	major histocompatibility complex, class II, DR beta 4; major histocompatibility complex, class II, DR beta 1
209545_s_at	2.91	1.11E-04	receptor-interacting serine-threonine kinase 2
231779_at	3.11	1.16E-04	interleukin-1 receptor-associated kinase 2
215193_x_at	3.00	1.16E-04	major histocompatibility complex, class II, DR beta 3
224681_at	2.31	1.16E-04	guanine nucleotide binding protein (G protein) alpha 12
225344_at	2.80	1.27E-04	nuclear receptor coactivator 7
224800_at	2.25	1.27E-04	WD repeat and FYVE domain containing 1
214651_s_at	2.83	1.39E-04	homeobox A9
206028_s_at	2.26	1.39E-04	c-mer proto-oncogene tyrosine kinase
214039_s_at	4.06	1.53E-04	lysosomal protein transmembrane 4 beta
226438_at	2.35	1.53E-04	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)
210136_at	2.11	1.53E-04	myelin basic protein
218880_at	2.47	1.60E-04	FOS-like antigen 2
203603_s_at	2.35	1.67E-04	zinc finger E-box binding homeobox 2
208690_s_at	3.35	1.75E-04	PDZ and LIM domain 1
203332_s_at	2.02	1.82E-04	inositol polyphosphate-5-phosphatase, 145kDa
209239_at	2.51	1.99E-04	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
209835_x_at	2.38	2.18E-04	CD44 molecule (Indian blood group)
212014_x_at	2.29	2.27E-04	CD44 molecule (Indian blood group)
212611_at	2.29	2.27E-04	deltex homolog 4 (Drosophila)
210982_s_at	3.27	2.59E-04	major histocompatibility complex, class II, DR alpha
228461_at	2.01	2.59E-04	SH3 domain containing ring finger 3
213348_at	3.39	2.70E-04	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
209200_at	2.69	2.70E-04	myocyte enhancer factor 2C
227961_at	2.66	2.82E-04	cathepsin B
235072_s_at	3.09	2.94E-04	-
223380_s_at	2.77	3.07E-04	LATS, large tumor suppressor, homolog 2 (Drosophila)
204249_s_at	2.33	3.07E-04	LIM domain only 2 (rhombotin-like 1)
232231_at	2.23	3.07E-04	runt-related transcription factor 2
209606_at	2.34	3.34E-04	cytohesin 1 interacting protein
203320_at	2.13	3.34E-04	SH2B adaptor protein 3
222780_s_at	4.54	3.64E-04	brain and acute leukemia, cytoplasmic
204233_s_at	2.34	3.79E-04	choline kinase alpha
209199_s_at	3.03	4.12E-04	myocyte enhancer factor 2C
226550_at	2.64	4.12E-04	-
228181_at	2.02	4.48E-04	solute carrier family 30 (zinc transporter), member 1

Continuation II of Table S2

Probe Set	Ratio	P-value	Gene name
228153_at	4.46	4.67E-04	ring finger protein 144B
224909_s_at	2.28	4.67E-04	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1
229221_at	2.12	F204670_x_at	CD44 molecule (Indian blood group)
230348_at	2.76	4.86E-04	LATS, large tumor suppressor, homolog 2 (Drosophila)
207761_s_at	2.50	5.07E-04	methyltransferase like 7A
202284_s_at	2.43	5.72E-04	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
229114_at	2.22	5.72E-04	GRB2-associated binding protein 1
225524_at	2.50	5.96E-04	anthrax toxin receptor 2
208078_s_at	2.59	6.20E-04	salt-inducible kinase 1
216944_s_at	2.47	6.45E-04	inositol 1,4,5-triphosphate receptor, type 1
224391_s_at	2.06	6.45E-04	sialic acid acetylesterase
218346_s_at	2.25	6.72E-04	sestrin 1
218520_at	2.03	6.99E-04	TANK-binding kinase 1
204912_at	2.17	7.87E-04	interleukin 10 receptor, alpha
209191_at	4.19	8.85E-04	tubulin, beta 6
209457_at	2.52	9.94E-04	dual specificity phosphatase 5
200839_s_at	2.31	9.94E-04	cathepsin B
58780_s_at	2.11	9.94E-04	hypothetical protein FLJ10357
212907_at	2.46	1.03E-03	solute carrier family 30 (zinc transporter), member 1
225567_at	2.34	1.07E-03	
210665_at	2.99	1.16E-03	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
203932_at	2.35	1.20E-03	major histocompatibility complex, class II, DM beta
222603_at	2.54	1.25E-03	endoplasmic reticulum metallopeptidase 1
206674_at	2.34	1.35E-03	fms-related tyrosine kinase 3
239412_at	2.41	1.37E-03	interferon regulatory factor 5
209374_s_at	3.80	1.40E-03	immunoglobulin heavy constant gamma 1 (G1m marker); immunoglobulin heavy constant mu; immunoglobulin heavy variable 3-7; immunoglobulin heavy constant gamma 3 (G3m marker); immunoglobulin heavy variable 3-11 (gene/pseudogene); immunoglobulin heavy variabl
224571_at	2.01	1.40E-03	interferon regulatory factor 2 binding protein 2
36711_at	2.62	1.50E-03	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)
206478_at	2.55	1.50E-03	KIAA0125
208894_at	3.12	1.68E-03	major histocompatibility complex, class II, DR alpha
208306_x_at	2.76	1.74E-03	major histocompatibility complex, class II, DR beta 4; major histocompatibility complex, class II, DR beta 1
235670_at	2.25	1.74E-03	syntaxin 11
200953_s_at	2.41	1.87E-03	cyclin D2
215087_at	2.21	1.87E-03	chromosome 15 open reading frame 39
204882_at	2.14	2.01E-03	Rho GTPase activating protein 25
242931_at	2.71	2.09E-03	LON peptidase N-terminal domain and ring finger 3
228532_at	2.26	2.24E-03	chromosome 1 open reading frame 162
213844_at	2.94	2.68E-03	homeobox A5
204491_at	2.03	2.68E-03	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)
230866_at	2.03	2.68E-03	cysteinyl leukotriene receptor 1
238376_at	2.37	2.77E-03	C-type lectin domain family 16, member A
203037_s_at	2.12	2.77E-03	metastasis suppressor 1
203710_at	2.05	2.77E-03	inositol 1,4,5-triphosphate receptor, type 1
226657_at	2.03	2.77E-03	chromosome 17 open reading frame 103
221773_at	2.45	2.87E-03	ELK3, ETS-domain protein (SRF accessory protein 2)
212632_at	2.01	2.97E-03	syntaxin 7
221766_s_at	2.14	3.07E-03	family with sequence similarity 46, member A
210835_s_at	2.18	3.18E-03	C-terminal binding protein 2
212442_s_at	2.20	3.29E-03	LAG1 homolog, ceramide synthase 6

Continuation III of Table S2			
Probe Set	**Ratio**	**P-value**	**Gene name**
200742_s_at	2.11	3.29E-03	tripeptidyl peptidase I
225612_s_at	3.54	3.41E-03	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
203799_at	2.05	3.41E-03	CD302 molecule; lymphocyte antigen 75
241756_at	2.08	3.53E-03	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
212086_x_at	2.03	3.65E-03	lamin A/C
226267_at	2.42	3.77E-03	Jun dimerization protein 2
203504_s_at	2.11	3.77E-03	ATP-binding cassette, sub-family A (ABC1), member 1
223343_at	3.20	4.46E-03	membrane-spanning 4-domains, subfamily A, member 7
227345_at	2.46	4.46E-03	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain
213258_at	4.11	4.61E-03	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
223501_at	2.40	4.76E-03	tumor necrosis factor (ligand) superfamily, member 13b
225589_at	2.27	4.76E-03	SH3 domain containing ring finger 1
210664_s_at	2.67	4.92E-03	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
202724_s_at	2.25	4.92E-03	forkhead box O1
212827_at	3.87	5.25E-03	immunoglobulin heavy constant gamma 1 (G1m marker); immunoglobulin heavy constant mu; immunoglobulin heavy variable 3-7; immunoglobulin heavy constant gamma 3 (G3m marker); immunoglobulin heavy variable 3-11 (gene/pseudogene); immunoglobulin heavy variabl
205027_s_at	2.58	5.25E-03	mitogen-activated protein kinase kinase kinase 8
227200_at	2.09	5.43E-03	
212509_s_at	2.19	5.79E-03	matrix-remodelling associated 7
230233_at	2.27	5.98E-03	RasGEF domain family, member 1B
238509_at	2.23	6.17E-03	cullin 1
227020_at	2.10	6.17E-03	yippee-like 2 (Drosophila)
217707_x_at	2.04	6.58E-03	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
229560_at	2.23	6.79E-03	toll-like receptor 8
225372_at	2.15	7.23E-03	chromosome 10 open reading frame 54
206310_at	2.02	7.69E-03	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)
206631_at	2.09	7.94E-03	prostaglandin E receptor 2 (subtype EP2), 53kDa
209306_s_at	4.23	8.19E-03	SWAP switching B-cell complex 70kDa subunit
242064_at	2.03	8.19E-03	sidekick homolog 2 (chicken)
209676_at	2.76	8.44E-03	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
209543_s_at	2.48	8.71E-03	CD34 molecule
228314_at	2.21	9.25E-03	leucine rich repeat containing 8 family, member C
225033_at	2.19	9.25E-03	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
220603_s_at	2.24	9.83E-03	multiple C2 domains, transmembrane 2
242794_at	2.36	1.04E-02	mastermind-like 3 (Drosophila)
227983_at	2.41	1.08E-02	Rab interacting lysosomal protein-like 2
205609_at	3.27	1.14E-02	angiopoietin 1
200696_s_at	2.10	1.14E-02	gelsolin (amyloidosis, Finnish type)
226452_at	2.26	1.18E-02	pyruvate dehydrogenase kinase, isozyme 1
226844_at	2.11	1.21E-02	MOB1, Mps One Binder kinase activator-like 2B (yeast)
225337_at	2.11	1.21E-02	abhydrolase domain containing 2
239598_s_at	2.01	1.25E-02	lysophosphatidylcholine acyltransferase 2
212446_s_at	2.53	1.28E-02	LAG1 homolog, ceramide synthase 6
235463_s_at	2.13	1.28E-02	LAG1 homolog, ceramide synthase 6
229450_at	2.73	1.36E-02	interferon-induced protein with tetratricopeptide repeats 3
238732_at	2.25	1.36E-02	collagen, type XXIV, alpha 1
216268_s_at	2.21	1.44E-02	jagged 1 (Alagille syndrome)
218858_at	2.06	1.53E-02	DEP domain containing 6
213902_at	2.14	1.57E-02	N-acylsphingosine amidohydrolase (acid ceramidase) 1

Continuation IV of Table S2			
Probe Set	**Ratio**	**P-value**	**Gene name**
201204_s_at	2.19	1.62E-02	ribosome binding protein 1 homolog 180kDa (dog)
201200_at	2.14	1.62E-02	cellular repressor of E1A-stimulated genes 1
231972_at	2.04	1.62E-02	
226818_at	3.20	1.66E-02	macrophage expressed 1
206544_x_at	2.52	1.66E-02	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
211612_s_at	2.41	1.66E-02	interleukin 13 receptor, alpha 1
225673_at	2.07	1.66E-02	myeloid-associated differentiation marker
221523_s_at	2.14	1.76E-02	Ras-related GTP binding D
202768_at	2.28	1.86E-02	FBJ murine osteosarcoma viral oncogene homolog B
205098_at	2.42	2.08E-02	chemokine (C-C motif) receptor 1
214696_at	2.11	2.13E-02	chromosome 17 open reading frame 91
210797_s_at	2.18	2.44E-02	2'-5'-oligoadenylate synthetase-like
204203_at	2.02	2.44E-02	CCAAT/enhancer binding protein (C/EBP), gamma
203753_at	2.44	2.51E-02	transcription factor 4
215285_s_at	2.34	2.51E-02	putative homeodomain transcription factor 1
209774_x_at	2.46	2.57E-02	chemokine (C-X-C motif) ligand 2
201218_at	2.41	2.57E-02	C-terminal binding protein 2
224973_at	2.23	2.64E-02	family with sequence similarity 46, member A
202429_s_at	2.14	2.64E-02	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform
210999_s_at	2.98	2.71E-02	growth factor receptor-bound protein 10
228573_at	2.09	2.86E-02	anthrax toxin receptor 2
238002_at	3.86	2.93E-02	golgi integral membrane protein 4
212314_at	2.47	2.93E-02	KIAA0746 protein
222698_s_at	2.41	2.93E-02	Impact homolog (mouse)
239835_at	2.29	2.93E-02	kelch repeat and BTB (POZ) domain containing 8
218284_at	2.61	3.09E-02	SMAD family member 3
204614_at	2.12	3.51E-02	serpin peptidase inhibitor, clade B (ovalbumin), member 2
200838_at	2.44	3.60E-02	cathepsin B
205401_at	2.51	3.88E-02	alkylglycerone phosphate synthase
209301_at	2.17	4.07E-02	carbonic anhydrase II
212719_at	2.14	4.07E-02	PH domain and leucine rich repeat protein phosphatase 1
212592_at	3.13	4.28E-02	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
221491_x_at	2.76	4.28E-02	major histocompatibility complex, class II, DR beta 3
217997_at	2.21	4.38E-02	pleckstrin homology-like domain, family A, member 1
201887_at	4.13	4.49E-02	interleukin 13 receptor, alpha 1
205239_at	2.44	4.49E-02	amphiregulin; amphiregulin B
223502_s_at	2.16	4.49E-02	tumor necrosis factor (ligand) superfamily, member 13b
214449_s_at	2.25	4.60E-02	ras homolog gene family, member Q; similar to small GTP binding protein TC10

Table S3: Probe sets two-fold up-regulated in the *BCL11b*-high group compared to the *BCL11b*-high group of T-ALL patients (n=86); (200 probe sets, 162 genes)

Probe Set	Ratio	P-value	Gene name
219528_s_at	7.24	9.35E-14	B-cell CLL/lymphoma 11B (zinc finger protein)
206804_at	4.06	2.95E-10	CD3g molecule, gamma (CD3-TCR complex)
221558_s_at	3.59	9.95E-08	lymphoid enhancer-binding factor 1
202789_at	2.96	1.98E-07	phospholipase C, gamma 1
227766_at	3.45	3.60E-07	ligase IV, DNA, ATP-dependent
213623_at	3.41	4.97E-07	kinesin family member 3A
207434_s_at	7.18	1.27E-06	FXYD domain containing ion transport regulator 2
211005_at	3.65	1.35E-06	linker for activation of T cells
226864_at	5.60	1.83E-06	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
213539_at	2.41	2.19E-06	CD3d molecule, delta (CD3-TCR complex)
204890_s_at	3.41	2.32E-06	lymphocyte-specific protein tyrosine kinase
204777_s_at	6.19	3.11E-06	mal, T-cell differentiation protein
205674_x_at	6.71	3.49E-06	FXYD domain containing ion transport regulator 2
222803_at	3.41	4.65E-06	phosphoribosyl transferase domain containing 1
220429_at	2.72	4.92E-06	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3
243362_s_at	5.07	5.51E-06	hypothetical protein LOC641518
205255_x_at	2.61	7.28E-06	transcription factor 7 (T-cell specific, HMG-box)
214032_at	2.33	7.69E-06	zeta-chain (TCR) associated protein kinase 70kDa
222288_at	4.11	9.06E-06	unc-5 homolog B
205590_at	4.64	9.57E-06	RAS guanyl releasing protein 1 (calcium and DAG-regulated)
202850_at	2.13	1.01E-05	ATP-binding cassette, sub-family D (ALD), member 3
219812_at	2.94	1.25E-05	poliovirus receptor related immunoglobulin domain containing
235733_at	2.98	1.25E-05	glucoside xylosyltransferase 2
36545_s_at	2.03	1.32E-05	Sfi1 homolog, spindle assembly associated (yeast)
225591_at	2.13	1.81E-05	F-box protein 25
224719_s_at	2.18	1.81E-05	chromosome 12 open reading frame 57
241871_at	2.97	1.81E-05	calcium/calmodulin-dependent protein kinase IV
233198_at	2.14	2.01E-05	golgi autoantigen, golgin subfamily a, 2-like 1
219532_at	3.87	2.35E-05	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4
216705_s_at	2.41	2.35E-05	adenosine deaminase
205871_at	2.09	2.60E-05	plasminogen-like B2; plasminogen-like B1
227077_at	2.28	2.88E-05	zinc finger protein 286A
213060_s_at	2.97	3.18E-05	chitinase 3-like 2
201014_s_at	2.08	3.34E-05	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
202534_x_at	2.40	3.52E-05	dihydrofolate reductase
241074_at	3.48	4.73E-05	immunoglobulin heavy variable 3-33-2 pseudogene
228792_at	2.38	4.96E-05	solute carrier family 24, member 5
220865_s_at	3.16	5.21E-05	prenyl (decaprenyl) diphosphate synthase, subunit 1
213556_at	2.18	5.47E-05	similar to R28379_1
211535_s_at	2.62	5.47E-05	fibroblast growth factor receptor 1
206150_at	3.19	5.47E-05	CD27 molecule
210094_s_at	4.47	5.74E-05	par-3 partitioning defective 3 homolog (C. elegans)
232001_at	2.42	6.03E-05	hypothetical protein LOC439949
219156_at	2.17	6.32E-05	synaptojanin 2 binding protein
205456_at	2.15	6.63E-05	CD3e molecule, epsilon (CD3-TCR complex)

Continuation I of Table S3			
Probe Set	**Ratio**	**P-value**	**Gene name**
224926_at	3.36	7.65E-05	exocyst complex component 4
226925_at	2.60	8.40E-05	acid phosphatase-like 2
205673_s_at	2.11	8.81E-05	ankyrin repeat and SOCS box-containing 9
244033_at	4.07	9.23E-05	chromosome 14 open reading frame 145
241859_at	3.93	9.67E-05	phospholipase C-like 1
39248_at	5.67	9.67E-05	aquaporin 3 (Gill blood group)
229533_x_at	2.38	1.01E-04	zinc finger protein 680
229202_at	2.69	1.16E-04	pecanex-like 2 (Drosophila)
206460_at	4.07	1.22E-04	adherens junctions associated protein 1
217147_s_at	2.45	1.27E-04	T cell receptor associated transmembrane adaptor 1
235371_at	2.92	1.46E-04	glycosyltransferase 8 domain containing 4
213193_x_at	2.68	1.53E-04	T cell receptor beta variable 19; T cell receptor beta constant 1
238593_at	2.41	1.53E-04	chromosome 11 open reading frame 80
205005_s_at	2.32	1.75E-04	N-myristoyltransferase 2
218472_s_at	2.06	1.82E-04	pelota homolog (Drosophila)
211796_s_at	2.59	2.08E-04	T cell receptor beta constant 2; T cell receptor beta variable 5-4; T cell receptor beta variable 3-1; T cell receptor beta variable 7-2
228988_at	2.47	2.37E-04	zinc finger protein 711
221606_s_at	3.48	2.37E-04	nucleosomal binding protein 1
210487_at	2.65	2.59E-04	deoxynucleotidyltransferase, terminal
242292_at	2.21	2.70E-04	chromosome X open reading frame 50B; chromosome X open reading frame 50
205831_at	3.19	2.82E-04	CD2 molecule
228455_at	2.14	2.94E-04	RNA binding motif protein 15
201518_at	2.20	3.49E-04	chromobox homolog 1 (HP1 beta homolog Drosophila)
228280_at	2.52	3.79E-04	zinc finger CCCH-type, antiviral 1-like
205559_s_at	2.31	4.30E-04	proprotein convertase subtilisin/kexin type 5
241864_x_at	2.98	4.30E-04	-
218984_at	2.15	4.48E-04	pseudouridylate synthase 7 homolog (S. cerevisiae)
227350_at	2.49	4.67E-04	helicase, lymphoid-specific
208146_s_at	2.49	4.86E-04	carboxypeptidase, vitellogenic-like
228049_x_at	2.30	5.07E-04	small nucleolar RNA, C/D box 60
201194_at	2.07	5.07E-04	selenoprotein W, 1
213958_at	2.01	5.07E-04	CD6 molecule
206545_at	4.16	5.49E-04	CD28 molecule
228303_at	2.23	5.72E-04	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
243279_at	2.15	5.72E-04	-
211052_s_at	2.40	5.96E-04	tubulin folding cofactor D
229851_s_at	2.33	5.96E-04	chromosome 11 open reading frame 54
221521_s_at	2.09	6.20E-04	GINS complex subunit 2 (Psf2 homolog)
213939_s_at	2.54	6.72E-04	RUN and FYVE domain containing 3
235383_at	2.39	6.72E-04	myosin VIIB
223530_at	2.00	7.56E-04	tudor and KH domain containing
204849_at	2.03	7.56E-04	transcription factor-like 5 (basic helix-loop-helix)
201792_at	2.73	7.56E-04	AE binding protein 1
218477_at	2.09	8.18E-04	transmembrane protein 14A
227921_at	2.35	8.85E-04	ENSG00000212911
204142_at	2.50	1.03E-03	enolase superfamily member 1
227790_at	2.35	1.07E-03	ubiquitin-conjugating enzyme E2C binding protein
203362_s_at	2.05	1.07E-03	MAD2 mitotic arrest deficient-like 1 (yeast)
236846_at	2.29	1.07E-03	hypothetical protein LOC284757
48808_at	2.46	1.11E-03	dihydrofolate reductase

Continuation II of Table S3			
Probe Set	**Ratio**	**P-value**	**Gene name**
222771_s_at	2.14	1.16E-03	myelin expression factor 2
204159_at	2.45	1.20E-03	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
203238_s_at	3.11	1.25E-03	Notch homolog 3 (Drosophila)
236451_at	2.20	1.25E-03	-
204718_at	2.68	1.40E-03	EPH receptor B6
211709_s_at	2.13	1.40E-03	C-type lectin domain family 11, member A
213385_at	2.33	1.45E-03	chimerin (chimaerin) 2
225386_s_at	2.47	1.50E-03	heterogeneous nuclear ribonucleoprotein L-like
219109_at	2.05	1.62E-03	sperm associated antigen 16
228423_at	2.06	1.74E-03	microtubule-associated protein 9
221081_s_at	2.50	1.94E-03	DENN/MADD domain containing 2D
221286_s_at	2.15	2.01E-03	hypothetical protein MGC29506
212672_at	2.06	2.09E-03	similar to Serine-protein kinase ATM (Ataxia telangiectasia mutated) (A-T, mutated); ataxia telangiectasia mutated
238430_x_at	2.35	2.09E-03	schlafen family member 5
205758_at	3.01	2.16E-03	CD8a molecule
227266_s_at	2.32	2.32E-03	FYN binding protein (FYB-120/130)
214835_s_at	2.22	2.49E-03	similar to sucb; succinate-CoA ligase, GDP-forming, beta subunit
243996_at	2.07	2.58E-03	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)
212813_at	2.20	2.58E-03	junctional adhesion molecule 3
219148_at	2.31	2.68E-03	PDZ binding kinase
232238_at	2.54	2.68E-03	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
204759_at	3.35	2.77E-03	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2
241505_at	2.72	2.77E-03	-
242136_x_at	2.11	2.97E-03	C-terminal binding protein 2 pseudogene
226548_at	2.06	3.07E-03	SH3-binding domain kinase 1
63009_at	2.13	3.18E-03	SHQ1 homolog (S. cerevisiae)
232180_at	2.09	3.53E-03	UDP-glucose pyrophosphorylase 2
210676_x_at	2.36	3.53E-03	RANBP2-like and GRIP domain containing 5; RANBP2-like and GRIP domain containing 4; RANBP2-like and GRIP domain containing 3; RANBP2-like and GRIP domain containing 8; RANBP2-like and GRIP domain containing 7; RANBP2-like and GRIP domain containing 6
200897_s_at	2.55	3.53E-03	palladin, cytoskeletal associated protein
212372_at	2.27	3.53E-03	myosin, heavy chain 10, non-muscle
207445_s_at	2.51	4.03E-03	chemokine (C-C motif) receptor 9
232392_at	2.24	4.46E-03	splicing factor, arginine/serine-rich 3
203764_at	2.28	4.76E-03	discs, large (Drosophila) homolog-associated protein 5
225619_at	2.06	4.92E-03	SLAIN motif family, member 1
227552_at	2.05	4.92E-03	septin 1
205830_at	2.13	4.92E-03	calmegin
244043_at	2.41	5.08E-03	transcription factor Dp-2 (E2F dimerization partner 2)
203394_s_at	3.35	5.08E-03	hairy and enhancer of split 1, (Drosophila)
205267_at	2.29	5.43E-03	POU class 2 associating factor 1
239253_at	2.15	5.43E-03	-
225655_at	2.08	5.60E-03	ubiquitin-like with PHD and ring finger domains 1
209569_x_at	2.03	5.79E-03	DNA segment on chromosome 4 (unique) 234 expressed sequence
209754_s_at	2.00	6.58E-03	thymopoietin
226610_at	2.27	6.79E-03	centromere protein V
243016_at	2.36	7.01E-03	thymidylate synthetase
226365_at	2.07	8.19E-03	-
202431_s_at	2.11	8.71E-03	v-myc myelocytomatosis viral oncogene homolog (avian)
240458_at	2.42	8.71E-03	inositol 1,4,5-triphosphate receptor, type 2

Continuation III of Table S3			
Probe Set	**Ratio**	**P-value**	**Gene name**
222344_at	3.04	8.98E-03	chromosome 5 open reading frame 13
218437_s_at	2.00	1.04E-02	leucine zipper transcription factor-like 1
226587_at	2.05	1.11E-02	small nuclear ribonucleoprotein polypeptide N; SNRPN upstream reading frame
227663_at	2.03	1.11E-02	-
239930_at	2.10	1.21E-02	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)
202412_s_at	2.06	1.21E-02	ubiquitin specific peptidase 1
226685_at	2.04	1.21E-02	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)
216620_s_at	2.71	1.28E-02	Rho guanine nucleotide exchange factor (GEF) 10
213093_at	2.80	1.28E-02	protein kinase C, alpha
236140_at	2.04	1.28E-02	glutamate-cysteine ligase, modifier subunit
205449_at	2.20	1.36E-02	SAC3 domain containing 1
226085_at	2.23	1.36E-02	chromobox homolog 5 (HP1 alpha homolog, Drosophila)
203404_at	2.05	1.53E-02	armadillo repeat containing, X-linked 2
204825_at	2.02	1.76E-02	maternal embryonic leucine zipper kinase
209884_s_at	2.04	1.81E-02	solute carrier family 4, sodium bicarbonate cotransporter, member 7
204146_at	2.02	1.81E-02	RAD51 associated protein 1
224496_s_at	2.26	1.96E-02	transmembrane protein 107
230493_at	2.46	2.02E-02	shisa homolog 2 (Xenopus laevis)
200862_at	2.19	2.08E-02	24-dehydrocholesterol reductase
210239_at	2.38	2.38E-02	iroquois homeobox 5
235425_at	2.79	2.57E-02	shugoshin-like 2 (S. pombe)
210407_at	2.13	2.71E-02	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform
239946_at	2.41	3.33E-02	KIAA0922
236293_at	2.38	3.78E-02	ras homolog gene family, member H
218974_at	2.13	3.88E-02	sine oculis binding protein homolog (Drosophila)
243808_at	2.23	3.88E-02	cyclin-dependent kinase 6
227884_at	2.14	4.38E-02	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa
243589_at	2.43	4.49E-02	KIAA1267
243031_at	2.15	4.71E-02	reticulon 4
210387_at	3.22	4.94E-02	histone cluster 1, H2bi; histone cluster 1, H2bg; histone cluster 1, H2be; histone cluster 1, H2bf; histone cluster 1, H2bc

Table S4: Molecular characteristics of T-ALL patients with respect to *BCL11b* expression

Characteristics		*BCL11b*-low Q1	*BCL11b*-high Q2-4	P-value
n		49	146	
Gene mRNA expression levels				
IGFBP7	n	48	141	0.02
	Median	1.4	0.5	
	Range	0-45.3	0-79.1	
BAALC	n	34	130	n.s.
	Median	0.1	0.1	
	Range	0-7.2	0-160.3	
ERG	n	45	124	n.s.
	Median	6.1	7.3	
	Range	0-62.7	0-136.7	
WT1	n	49	135	n.s.
	Median	0	0	
	Range	0-0.4	0-1.5	
GATA3	n	28	74	<0.01
	Median	2.1	5.7	
	Range	0.1-15.6	0.2-42.7	
Mutations				
WT1 mut/total (%)		8/49 (16.3%)	16/146 (11%)	n.s.
NOTCH1 mut/total (%)		10/18 (55.6%)	43/67 (64.1%)	n.s.
TCR rearrangement				
clonal/total (%)		16/32 (50)	44/55 (80)	0.01

Table S5: Molecular characteristics of thymic T-ALL patients with respect to *BCL11b* expression

Characteristics	***BCL11b*-low** **Q1**	***BCL11b*-high** **Q2-4**	**P-value**
T-ALL			
n	18	94	
Gene mRNA expression levels			
BAALC			n.s.
Median	0	0.1	
Range	0.0-0.3	0.0-10.4	
ERG			n.s.
Median	1.1	1.2	
Range	0.2-7.8	0.1-6.6	
IGFBP7			n.s.
Median	0.3	0.4	
Range	0.0-16.2	0.0-12.5	
WT1			n.s.
Median	0	0	
Range	0.0-0.1	0.0-0.6	
GATA3			<0.01
Median	1.6	5.1	
Range	0.3-5.7	1.2-25.3	
Mutations			
WT1 no (%)	3/18 (17%)	10/94 (11%)	n.s.
NOTCH1 no (%)	4/5 (80%)	30/40 (75%)	n.s.
TCR rearrangement			n.s.
clonal/total (%)	7/13 (54%)	23/38 (61%)	

Table S6: *BCL11b* exon 4 mutations in T-ALL

BCL11b, transcript NM_138576.2

T-ALL ID	Base change	AS change	Location
3	C792T	L470F	ZF3
3	C844T	P454L	ZF2
4	G851A	R472A	ZF3
5	1128 ins(TT)	E590fs	fs
29	C780T	T450M	ZF2
30	C844T	L470F	ZF3
31	1705 ds(16bp)	P783fs	fs
31	C797A	Y455*	stop, ZF3
34	355ds	F317fs	fs
38	G851A	R472A	ZF3
40	C780T	T450M	ZF2
41	G320T	G306C	ZF1
50	498ds	S358fs	fs
53	90ds	Q238fs	ZF1
57	G718T	E430*	stop, ZF1
76	1109 ins(GG)	A584fs	fs
87	C865T	T476M	ZF3
99	C850T	R472C	ZF3
101	G812C	C460S	ZF3
105	C780T	T450M	ZF2
108	C499A	S358*	stop
110	A1903G	Q848R	-
111	611ds	F395fs	fs
120	817ds	D461fs	ZF3
139	828ds	S465fs	ZF3

Abbreviations: ds: deletion, ins: insertion, fs: frame shift, bp: base pair, *: stop of translation, ZF= zinc finger

Table S7: Clinical characteristics of GMALL T-ALL patients with respect to *BCL11b* mutations

Characteristics	***BCL11b wt***	***BCL11b mut***	**P-value**
n	126 (86%)	21 (14%)	n.s.
***BCL11b* Expression**			n.s.
Median	0.5	0.8	
Range	0.0-12.3	0.0-2.7	
Age			n.s.
15-35 yrs	72	13	
36-55 yrs	47	7	
56-65 yrs	7	1	
Sex			n.s.
Female %	21%	29%	
WBC, x 10^9/l			n.s.
<30,000	52	6	
30-100,000	44	10	
>100,000	25	5	
T-ALL subtyp			0.03
Early n (%)	33 (26%)	1 (5%)	
Mature n (%)	23 (18%)	2 (9.5%)	
Thymic n (%)	70 (56%)	18 (85.5%)	
Response to induction therapy*			
CR n (%)	116 (96%)	18 (86%)	n.s.
ED n (%)	2 (2%)	1 (5%)	n.s.
Failure n (%)	3 (2%)	2 (10%)	n.s.

Abbreviations: CR = complete remission, ED = early death

*evaluable = in 142 patients information of response to induction therapy was available

Table S8: Members of the German Multicenter Study Group for Adult ALL

Augsburg: Zentralklinikum (G. Schlimok, D. Oruzio, C. Schmid)
Berlin: Charité Campus Benjamin Franklin (E. Thiel, S. Schwartz)
Berlin: Vivantes-Klinikum (J. Beyer, M. Hackenthal)
Berlin: Charité Campus Virchow (R. Arnold, T. Terwey)
Berlin: Charité Campus Buch (W.-D. Ludwig, R. Ratei)
Berlin: Vivantes Klinikum Neukölln (M. de Wit, A. Grüneisen, B. Kallinich)
Berlin: St.-Hedwig-Krankenhaus (K,-M. Derwahl, H. Englisch, B. Oldenkott)
Bielefeld: Franziskus-Hospital (H.J. Weh, A. Zumsprekel)
Bochum: Knappschaftskrankenhaus (W. Schmiegel, C. Teschendorf)
Bremen: Klinikum Mitte (B. Hertenstein, S. Kaun)
Bremen: Evangelische Diakonissenanstalt (K. H. Pflüger, J. Kullmer)
Bremerhaven: Ev. Diakonissenanstalt (H.-H. Heidtmann, A. Pott)
Chemnitz: Klinikum (M. Haenel, A. Morgner)
Cottbus: Carl-Thiem-Klinikum (H.B. Steinhauer, N. Peter, K. Petzold)
Dessau: Städt. Klinikum (A. Florschütz, O. Kellner)
Dortmund: St. Johannes-Hospital (H. Pielken, H. Hindahl, V. Hagen)
Dresden: Klinikum Carl Gustav Carus (G. Ehninger, R. Naumann, M. Schaich)
Duisburg: St. Johannes-Hospital (C. Aul, A. Giagounidis)
Düsseldorf: Universitätsklinik (R. Haas, G. Kobbe)
Erlangen: Universität Erlangen-Nürnberg (A. Mackensen, B. Spriewald)
Essen: Universitätsklinikum (U. Dührsen, A. Hüttmann)
Essen-Werden: Kliniken Essen Süd (P. Reimer, F.-K. Baur, M. Wattad)
Frankfurt: Universitätsklinikum (H. Serve, N. Gökbuget)
Frankfurt: Städt. Klinikum Frankfurt-Höchst (G. Derigs, M. Oestreicher)
Freiburg: Universitätsklinikum (M. Lübbert, F. Kaul)
Gießen: Universitätsklinikum (M. Rummel, W. Blau)
Greifswald: Ernst-Moritz-Arndt-Universität (G. Dölken, C. Busemann)
Hagen: Katholisches Krankenhaus (W. Lindemann, V. Rethwisch)
Halle/Saale: Martin-Luther-Univ. Halle-Wittenberg (H.-J. Schmoll, H.-H. Wolf)
Hamburg: Asklepios Klinik St. Georg (N. Schmitz, R. Stuhlmann)
Hamburg: Asklepios-Klinik Altona (D. Braumann, H. Salwender)
Hameln: Kreiskrankenhaus (H. Schmidt, F.Krebbel)
Hamm: Evangelisches Krankenhaus (J. Schubert, E. Lange)
Hanau: Städt. Klinikum (M. Burk, A. Sendler)
Hannover: Medizinische Hochschule (A. Ganser, H. Diedrich)
Heidelberg: Universitätsklinikum (A. Ho, J. Dengler)
Homburg/Saar: Med. Universitätsklinik und Poliklinik (M. Pfreundschuh, G. Held)
Karlsruhe: Städt. Klinikum (M. Bentz, S. Wilhelm)
Kassel: Klinikum (M. Wolf, B. Ritter)
Kiel: Universitätsklinikum, Campus Kiel (M. Kneba, S. Irmer)
Köln: Universitätsklinik (M. Hallek, K.-A. Kreuzer)
Krefeld: Klinikum (T. Frieling. M. Planker)
Lemgo: Klinikum Lippe-Lemgo (F. Hartmann, T. Hesse)
Leverkusen: Klinikum (N. Niederle, M. Kreß)
Lübeck: Universitätsklinikum, Campus Lübeck (T. Wagner, S. Peters)
Magdeburg: Otto-von-Guericke-Universität (T. Fischer, M. Mohren)
Mainz: Universitätskliniken (C. Huber, J. Beck)
Mannheim: Klinikum (W.-K. Hofmann, N. Härtel)
Marburg: Klinikum Lahnberge (A. Neubauer, N. Hagner)
Minden: Klinikum (M. Griesshammer, A. Renzelmann)
München: Krankenhaus München-Schwabing (C. Nerl, Th. Lipp, S. Zewen)
München: Klinikum Rechts der Isar (C. Peschel, F. Schneller)
Münster: Universitätsklinikum (W. Berdel, M. Stelljes)
Nürnberg: Klinikum Nord (M. Wilhelm, K. Wendelin)
Offenburg: Klinikum (F. Hirsch, I. Dresel)
Oldenburg: Klinikum (C.-H. Köhne, M. Lange)
Passau: Klinikum (T. Südhoff, T. Nitsch)
Potsdam: Klinikum Ernst von Bergmann (G. Maschmeyer, A. Scholz)
Regensburg: Universitätsklinikum (A. Reichle, D. Ditz)
Rostock: Medizinische Fakultät der Universität (M. Freund, C. Junghanss)

Stuttgart: Robert Bosch-Krankenhaus (W. Aulitzky, L. Leimer)
Stuttgart: Diakonissenkrankenhaus (E. Heidemann, J. Kaesberger)
Trier: Krankenhaus d. Barmherzigen Brüder (C. B. Kölbel, G. Pollmeier)
Tübingen: Universitätsklinikum (L. Kanz, M. Schmalzing)
Ulm: Medizinische Universitätsklinik (H. Döhner, M. Schmid)
Wuppertal: Helios-Klinikum (A. Raghavachar, T. Binder)
Würzburg: Universitätsklinikum (H. Einsele, M. Topp)
Zwickau: Heinrich-Braun-Krankenhaus (U. Kreibich, W. Zschille)

Supplemental Methods

Statistical analysis

The nonparametric Mann-Whitney U test was applied for continuous variables. The Chi Square test, resp. Fisher test was used for frequency tables. Complete remission (CR) after induction therapy was defined according to standard criteria[2]. Patients who died during the induction period were classified as early death and the remaining patients were classified as failure. Relapse was defined by presence of PB blasts, more than 5% leukemic blasts in BM samples or extramedullary leukemia in patients with previously documented CR. OS was assessed from first day of treatment until death or last follow-up. Remission duration was measured from the date of first CR until the date of relapse. Relapse-free patients were censored at the end of the follow-up, while patients with stem cell transplantation in first CR, patients that left the study or died in CR were censored at the respective dates. Estimated probability of OS and remission duration was calculated using the Kaplan-Meier method, and the log-rank test evaluated differences between survival distributions. The statistical analysis was carried out using the SAS program (SAS-PC, Version 9, SAS Institute, Cary, NC), GraphPad Prism software version 5.0 (GraphPad Software, La Jolla, CA, USA), and IBM SPSS Statistics software version 18 (IBM, Armonk, NY, USA).

Reference List

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2. European Leukemia Net., European Leukemia Trial Registry Trial: ALL GMALL 07/2003. 2013; [Accessed September 3, 2013]. http://www.leukemia-net.org/trial/download/public/ALL_GMALL07-03_ShortProtEN.pdf?id=489