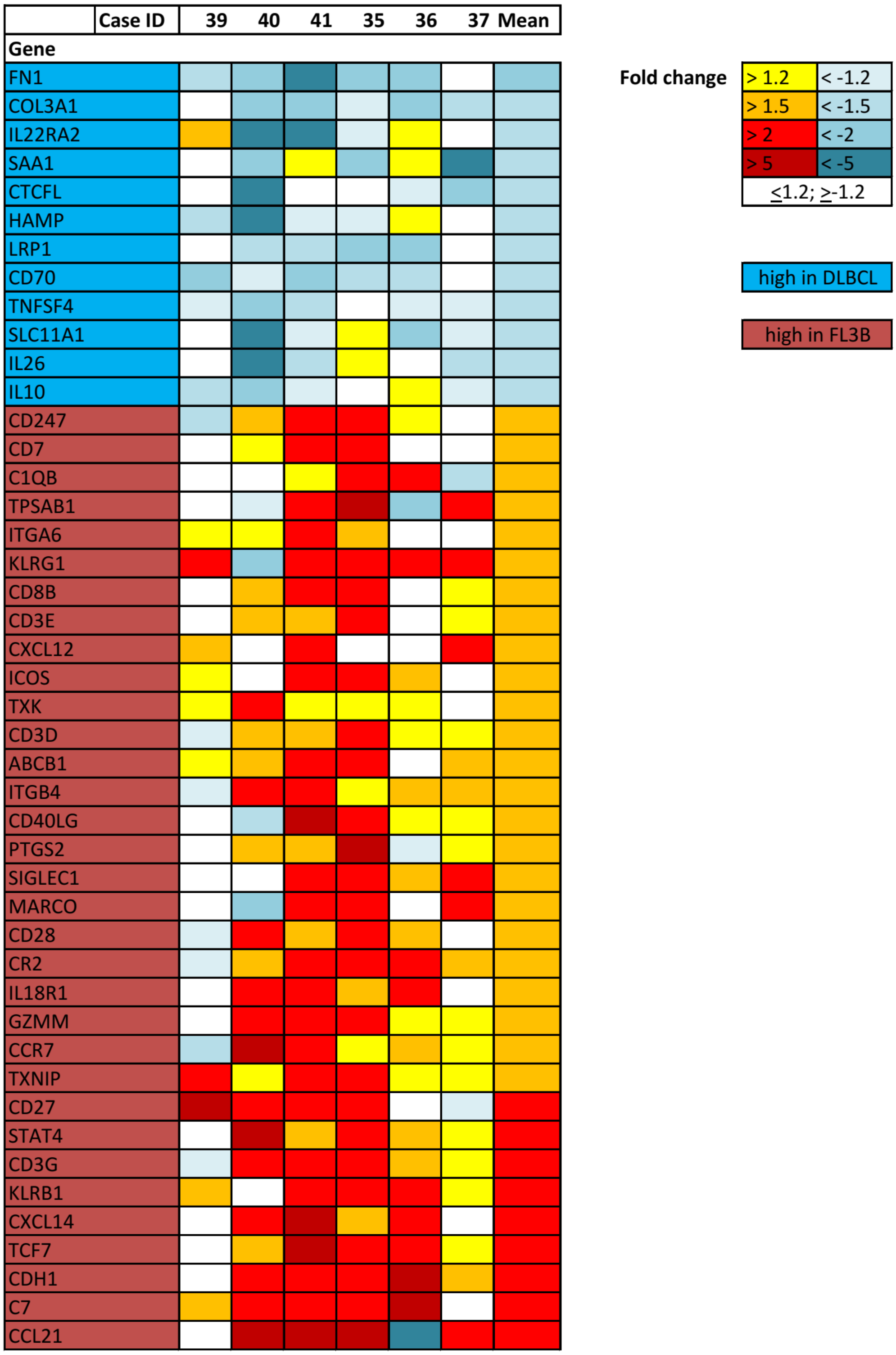
Supplementary material



Supplementary Figure 1: Fold changes of differentially expressed genes between follicular FL3B and DLBCL component of the same patient, in 6 patients with both components available. Individual cases are indicated by the case ID. The fold changes of each individual case and of the geometric mean expression levels over all 6 cases are displayed in color codes as indicated in the legend.

Supplementary Table 1: Overview of regions covered by the AmpliSeq Panel

gene	Ref-Seq	analyzed region*	gene	Ref-Seq	analyzed region*
ARID1A	NM_006015, NM_139135	CDS	*MEF2B*	NM_001145785	CDS
CARD11	NM_NM032415	CDS	*MYC*	NM_002467	CDS
CCND3	NM_001287427, NM_001760	CDS	*MYD88*	NM_001172567	L265
CD79B	NM_000626	CDS	*NOTCH1*	NM_017617	E25-E34
CREBBP	NM_004380	CDS	*NOTCH2*	NM_024408	E32-E34
CXCR4	NM_002467	CDS	*PIK3CD*	NM_001350234	CDS
EP300	NM_001429	CDS	*PIM1*	NM_001243186	CDS
EZH2	NM_001203247	E4, E14, E16	*PRDM1*	NM_001198, NM_182907	CDS
FADD	NM_003824	CDS	*PTEN*	NM_001304717	CDS
FASLG	NM_002015	CDS	*PTPRD*	NM_002839	E30-E35
FOXO1	NM_001349339	CDS	*RHOA*	NM_001664	CDS
GNA13	NM_006572	CDS	*SF3B1*	NM_001005526, NM_012433	E14-E18
ID3	NM_002167	CDS	*SOCS1*	NM_003745	CDS
IRF4	NM_001195286, NM_002460	CDS	*TBL1XR1*	NM_024665	E9-E12
IRF8	NM_002163	E1,E2, E7, E8	*TCF3*	NM_001136139, NM_003200	CDS
KMT2C	NM_170606	CDS	*TNFAIP3*	NM_001270507, NM_001270508, NM_006290	CDS
KMT2D	NM_003482	CDS	*TNFRSF14*	NM_001270949, NM_001270950, NM_001270951, NM_003839	CDS
MAP2K1	NM_002755	E1-E6	*TP53*	NM_000546, NM_001126112, NM_001126113, NM_001126114, NM_001126115, NM_001126116, NM_001126117, NM_001126118	CDS

*:coding and intron bondaries

Supplemantary Table 2: List of potential protein changing variants identified by targeted resequencing.(see excel file)

In column B those variants common in all analyzed components and those only identified in single comments are visible. Column C-E shows the different components of each samples and if a variant was identified this specific component (yes: variant was identified, no: variant could be not identified, NA: the component was not present in that sample). Those, variants initially identified as discrepant between the components of that sample but with low frequency (<10%) in the sequencing data are described as “low”. The chromosomal position according the genome build hg19 is provided.

Supplementary Table 3: Clinical characteristics and treatment response in follicular lymphoma grade 3B (FL3B) with or without a diffuse large B-cell lymphoma (DLBCL) in comparison with patients with DLBCL without FL 3B

	FL3B alone		**FL3B with DLBCL**		**DLBCL, NOS alone**	
Number of patients	17		16		551	
Median age (range)	51 years (29-72)		57 years (29-76)		62 years (18-80)[*]	
Baseline characteristics	Number	Percent	Number	Percent	Number	Percent
Male sex	13	76.5%	7	43.8%	309	56.1%
Age ≥ 60 years	5	29.4%	6	37.5%	307[**]	55.7%
ECOG performance status > 1	1	5.9%	0	0.0%	56	10.2%
Lactate dehydrogenase > ULN	10	58.8%	7	43.8%	306	55.5%
Ann Arbor stage III or IV	11	64.7%	10	62.5%	316	57.4%
Extranodal manifestations > 1	2	11.8%	3	18.8%	180	32.7%
Bone marrow infiltration	1	5.9%	0	0.0%	39	7.1%
B symptoms	5	29.4%	1	6.3%	168	30.5%
International Prognostic Index						
Low	9	53.0%	8	50.0%	200	36.4%
Low-intermediate	3	17.6%	3	18.8%	143	26.0%
High-intermediate	4	23.5%	5	31.2%	117	21.3%
High	1	5.9%	0	0.0%	90	16.3%
Treatment response						
Overall response	16	94.1%	15	93.8%	461	83.7%
Complete remission	12	70.6%	10	62.5%	346	62.8%

[*] p=0.031 (Kruskal-Wallis test); [**] p=0.039 (chi^2 test). ECOG: Eastern Cooperative Oncology Group; ULN: upper limit of normal.

Supplementary Table 4: Genetic variants in FL3B and FL3B+DLBCL

Gene	**FL3B+DLBCL (n=16)**	**FL3B (n=11)**	**p-value (Fisher´s exact test)**
ARID1A	1	1	>0.9999
CD79B	1	0	>0.9999
CARD11	1	1	>0.9999
CREBBP	6	0	0.0536
FASLG	0	1	0.4074
FOXO1	2	0	0.4986
GNA13	1	0	>0.9999
ID3	1	0	>0.9999
IRF8	1	0	>0.9999
KMT2C	5	1	0.3497
KMT2D	6	2	0.4048
MEF2B	2	1	>0.9999
MYC	3	0	0,2479
MYD88	0	2	0.1567
NOTCH1	2	0	0.4986
NOTCH2	3	1	0.6239
PIK3CD	1	0	>0.9999
PIM1	2	1	>0.9999
PRDM1	1	0	>0.9999
PTEN	2	0	0.4986
SF3B1	1	0	>0.9999
SOCS1	3	0	0,2479
TBL1XR1	1	1	>0.9999
TNFAIP3	2	0	0.4986
TNFRSF14	2	1	>0.9999
TP53	3	3	0.6618