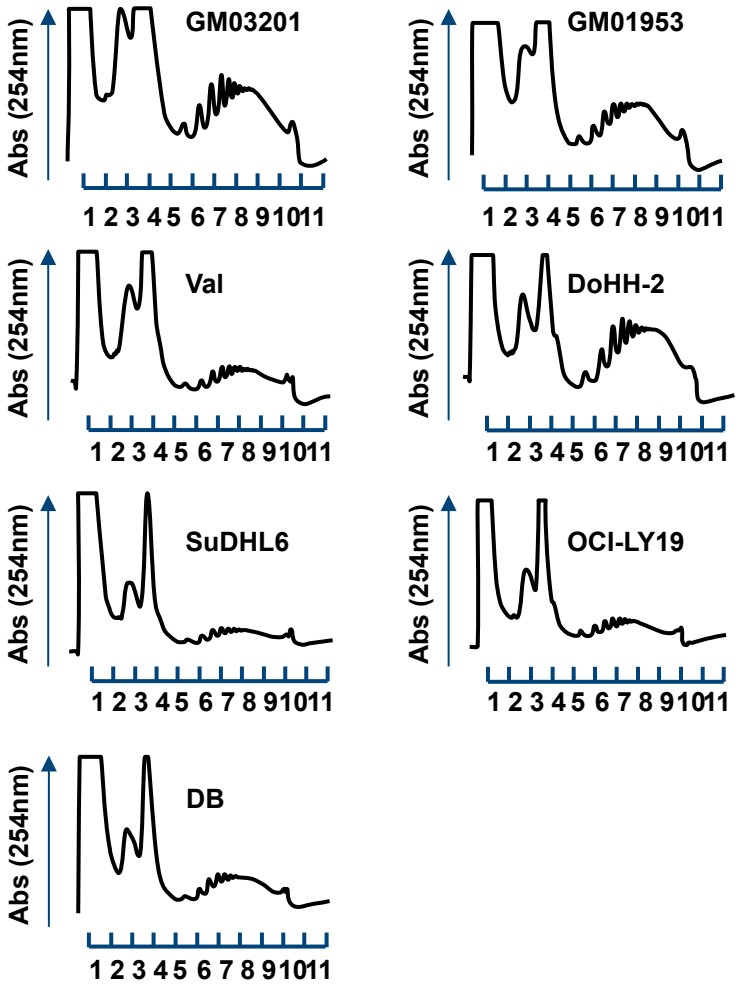
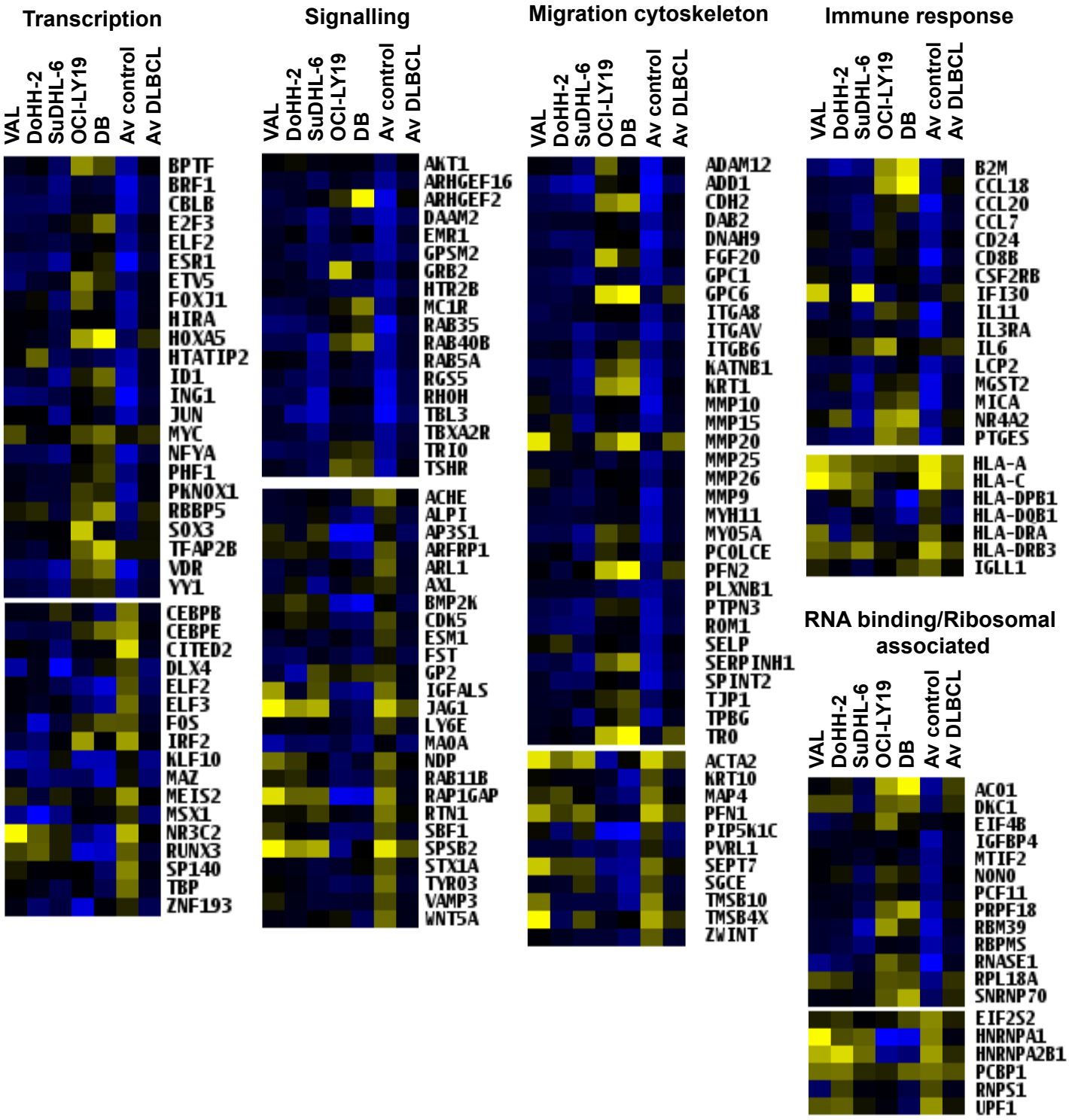
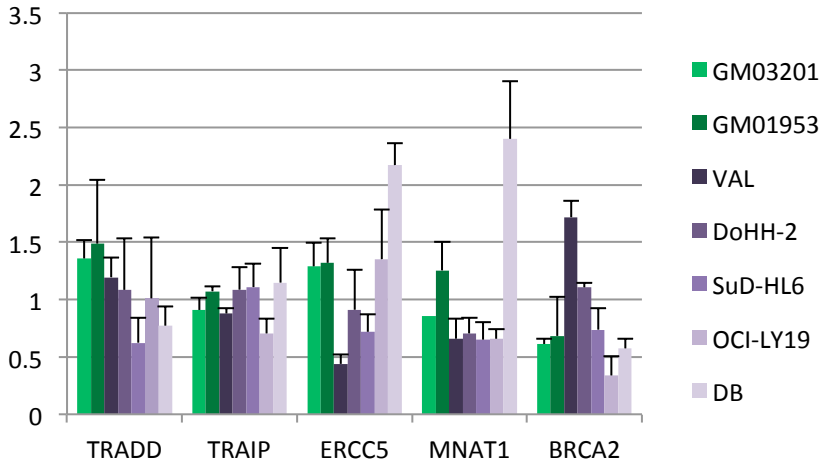


Supplementary Figure 1: Gradient profiles of DLBCL cell lines
Lysates of 5 DLBCL cell lines (Val, DoHH-2, SuDHL6, OCI-LY19 and DB) and 2 controls (GM03201 and GM01953) were applied on 10-60% (w/v) sucrose gradients. They were separated into 11 fractions and absorbance at 254nm was measured.

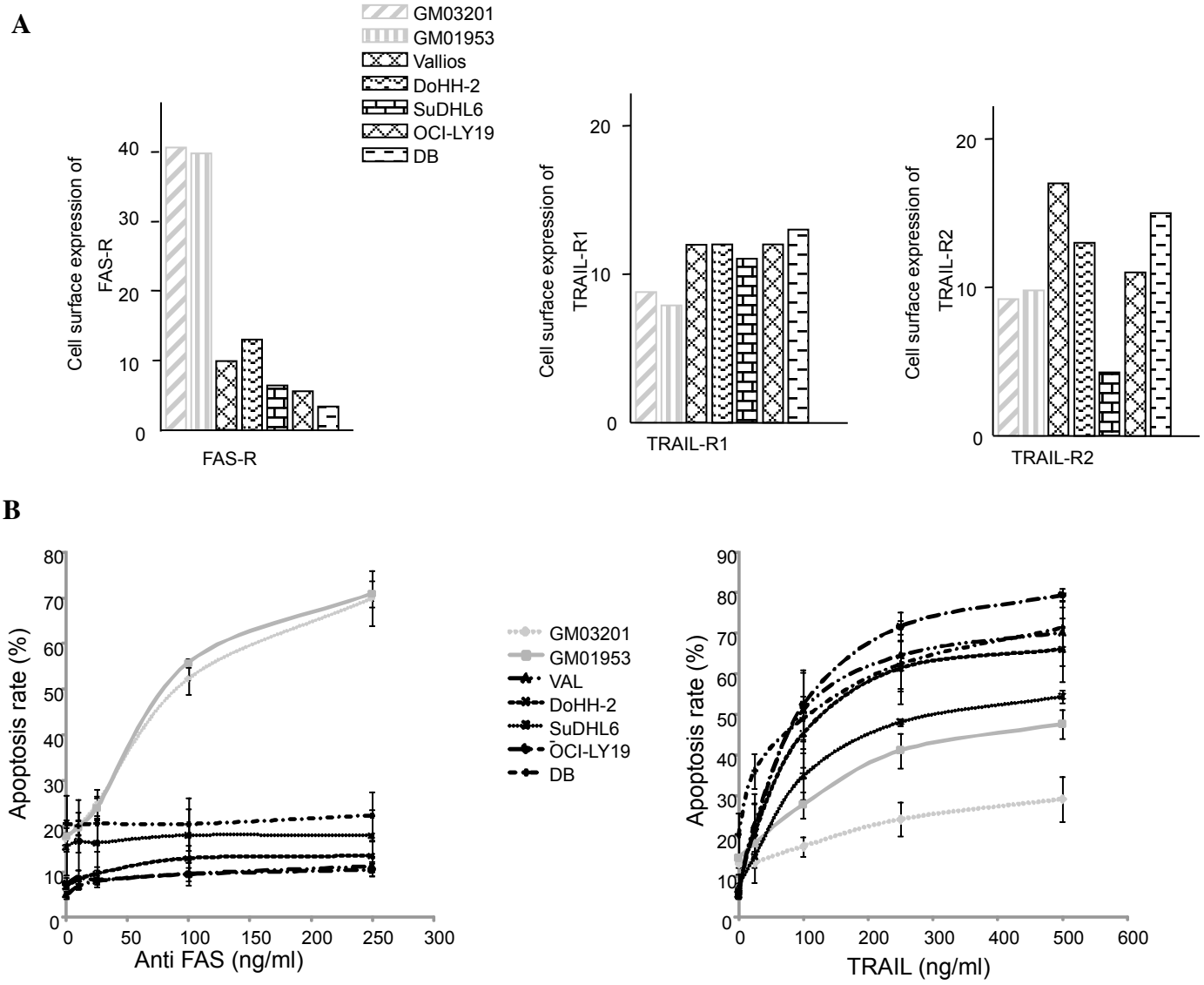


Supplementary Figure 2: Heat map showing changes in RNA association with polysomes in DLBCL compared to controls

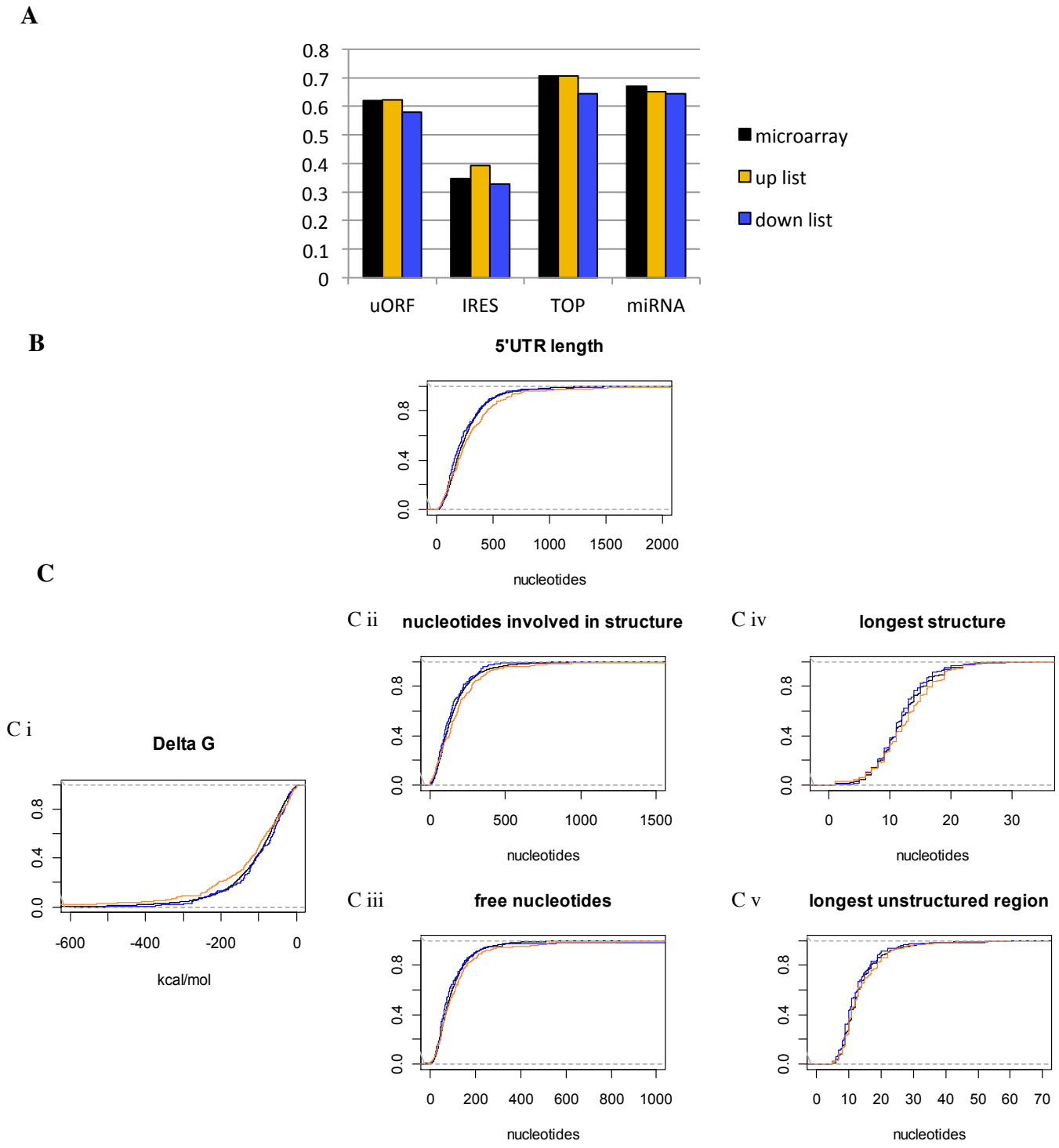
Selected candidate mRNAs that displayed significantly increased quantile ranking DLBCL cell lines compared to control B-cells. Genes are clustered into functional groups. A colour scale has been used to represent the ratio of mRNA in subpolysome to polysome fractions. Transformed from the log2[Polysome:Subpolysome] where blue indicates subpolysome associated and yellow signifies that the mRNA is predominately polysome associated.



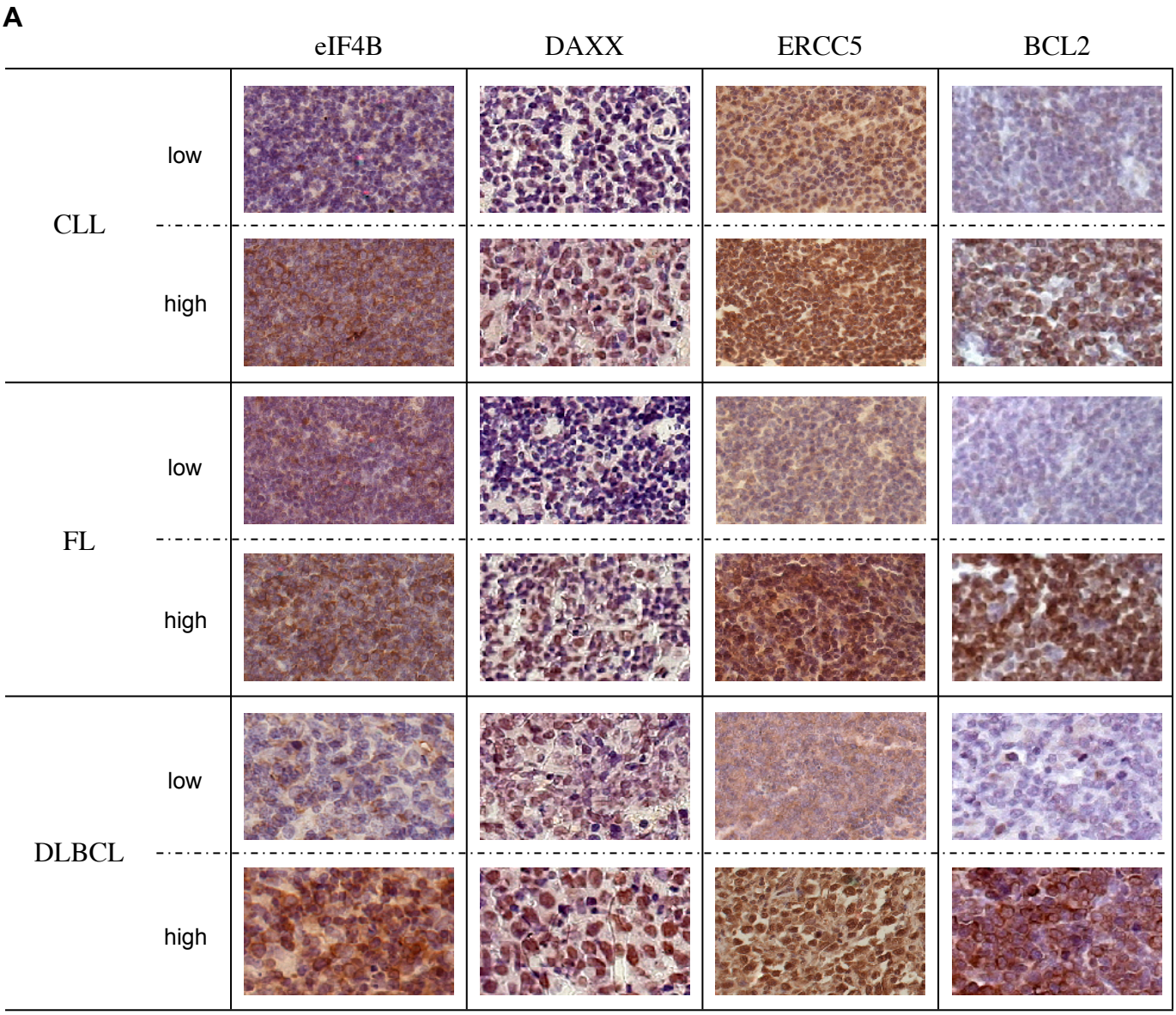
Supplementary Figure 3: Evaluation of total RNA contents by quantitative RT-PCR
Error bars represent standard deviations on 3 independent experiments.

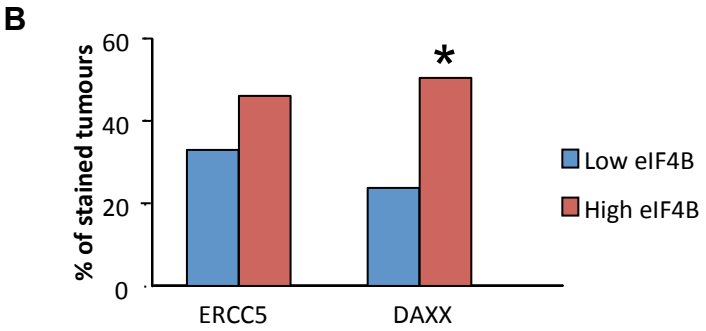


Supplementary Figure 4: Sensitivity of DLBCL derived cell lines to FAS-induced apoptosis
(A) Surface expression of TRAIL receptors TRAIL-R1 and TRAIL-R2. TRAIL-R1 is slightly more expressed in DLBCL cell lines than in the controls.
(B) DLBCL (VAS, DoHH-2, SuDHL-6, OCI-LY19 and DB) and control (GM03201 and GM01953) were treated by increasing doses of TRAIL or an anti-FAS antibody, and apoptosis measured by flow cytometry following annexin/PI staining. DLBCL cell lines were almost completely resistant to Fas activation but as sensitive as the controls to TRAIL.



Supplementary Figure 5: Contribution of 5' UTR features to translation dysregulation
(A) Contribution of 5' UTR and 3' UTR features to translation dysregulation:
The cDNA microarray data were analysed and the percentage of mRNA containing uORF, IRES and TOP-like sequences in the 5' UTR (in-house Perl scripts) and predicted miRNA target sites in the 3' UTR (conserved targets of conserved miRNA families from TargetScan; http://www.targetscan.org) were calculated for those mRNAs in the "up" and "down" lists and those in the full microarray set. No significant changes between the full microarray set and the lists were seen (χ^2 tests; p-values ranging from 0.1 to 0.99).
(B) Cumulative densitiy plot showing the distribution of the 5'UTR length in the "up list" (in yellow), the "down list (in blue) and the rest of mRNA in the microarray (in black).
(C) Analysis of the most stable structure for 5'UTR (as given by mfold)
(Ci) shows the cumulative distribution of the delta G of this structure in the "up list" (in yellow), the "down list (in blue) and the rest of mRNA in the microarray (in black).
(Cii) and (Ciii) show respectively the distribution of number of paired nucleotide and the number of free nucleotide in those structures.
(Civ) and (Cv) show respectively the distribution of the size of the longest string of nucleotides involved in a hairpin and the size of the longest string of nucleotides in an unstructured region.

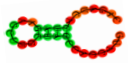
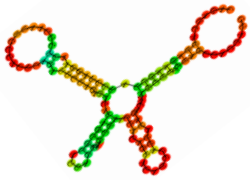
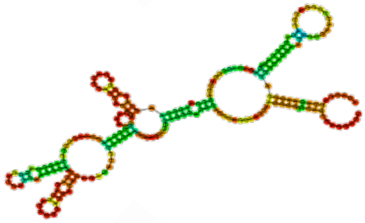
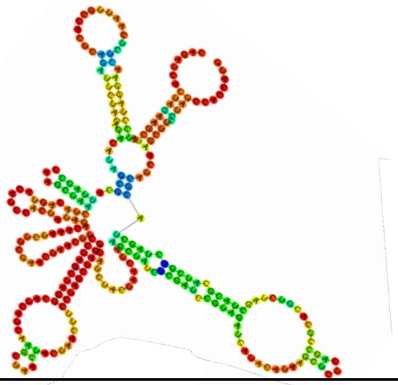
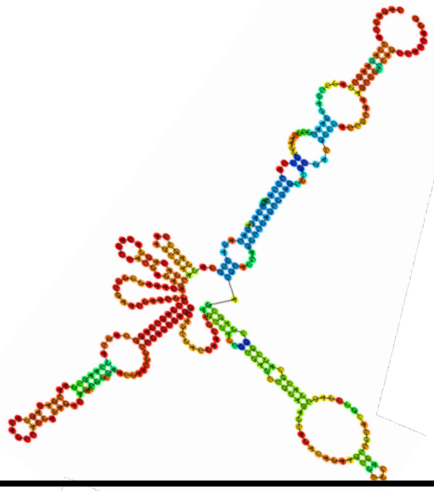




Supplementary Figure 6: Tissue microarray analysis
(A) Section examples
Tumours sections stained with different antibodies on the tissue microarrays.
Tissue microarrays were hybridized with primary antibodies against eIF4B, DAXX, ERCC5 or BCL2, then with a biotinylated secondary, streptavidin peroxydase and a DAB reaction was performed (brown staining). Nuclei were counterstained with haematoxylin (blue). For each antibodies, examples of CLL, FL and DLBCL tumours expressing low or high levels of the protein are shown.
(B) Histogram showing the connection between eIF4B expression and ERCC5 and DAXX.
The proportion of tumours expressing high levels of ERCC5 and DAXX is higher in the sections that express eIF4B. Chi-sqare tests were preformed and showed that the connexion between DAXX and eIF4B expression is statistically significant (*, $p<0.05$)

	brand	reference	dilution for Western blot	dilution for immunohistochemistry
4EBP1	cell signaling	9644	1/1000	
4EBP1 (P)	cell signaling	9459	1/1000	
eIF2 alpha	cell signaling	9722	1/1000	
eIF2 alpha (P)	cell signaling	3597	1/1000	
eIF4B	cell signalling	3592	1/1000	
eIF4E	cell signaling	4952	1/1000	
eIF4E (P)	cell signaling	9741	1/1000	
RPS6	cell signaling	2217	1/1000	
FAS	cell signaling	4233	1/1000	
BCL2	cell signaling	2872	1/1000	
BCLxL	cell signaling	2762	1/1000	
β-Tubulin	cell signaling	2146	(1/5000)	
actin	Sigma	clone AC15	1/10000	
MNAT1	abcam	ab65125	(1/1000)	1/25
ERCC5	abcam	ab46	(1/500)	
TRAIP	abcam	ab47543	(1/1000)	
c-Myc	Epitomics	1472	1/1000	
eIF4B	Epitomics	clone EP2299Y		1/150
DAXX	Upstate	07-471	1/1000	1/300

Supplementary Table 1: Provenance of antibodies and dilutions used

Insert length (bases)	SEQUENCE 5' ⇒ 3' (encompassing AUG)	FREE ENERGY	PREDICTED STRUCTURE
27	CAGATCACTAGAAGCTTGCTAGCC ACCATG	-2.39 kcal/ mol.	
115	CAGATCACTAGAAGCTATCCTAGG AACTCTCAATTGCCACTCAGATTCT AGAGACATAGCGCATTAGCCAAGC TAACTACAGTACATCCACTATAGAC AAAGCTTCCTAGCCACCATG	-22,23 kcal/ mol	
217	CAGATCACTAGAAGCTATCCTAGG AACTCTCAATTGCCACTCAGATTCT AGAGACATAGCGCATTAGCCAAGC TAACTACAGTACATCCACTATAGAC AAATCTTCGAACTAACTTCCTAGCT AGGCATCATCAAGCTAACTACAGTA CATCCACTATAGACAGATCTTCGAA CTAACTTCCTAGCTAGGCATCTACT AACTAAGCTTCCTAGCCACCATG	-44,92 kcal/mol	
265	CAGATCACTAGAAGCTATCCTAGG AACTCTCAATTGCCACTCAGATTCT AGAGACATAGCGCATTAGCCAAGC TAACTACAGTACATCCACTATAGAC AAATCTTCGAACTAACTTCCTAGCT AGGCATCATCAAGCTAACTACTAAC TTCCTAGCTAGGCATCTACTAACTA AGCTATCTCGATCCGTAGATCATAC ATAAGCTCTCAGCCGCACGTCTAG CTACGCATCGGCTAGCTACGCATC AAGCTTCCTAGCCACCATG	-58.30 kcal/mol.	
327	CAGATCACTAGAAGCTATCCTAGG AACTCTCAATTGCCACTCAGATTCT AGAGACATAGCGCATTAGCCAAGC TAACTACAGTACATCCACTATAGAC AAATCTTCGAACTAACTTCCTAGCT AGGCATCATCAAGCTAACTACAGTA CATCCACTATAGACAGATCTTCGAA CTAACTTCCTAGCTAGGCATCTACT AACTAAGCTATCTCGATCCGTAGAT CATACATAAGCTCTCAGCCGCACG TCTAGCTACGCATCGGCTAGCTAC GCATCAGTCCTAGCTGAGCTCGCT ACGTTCACCGCAAAGCTTCCTAGC CACCATG	-71.95 kcal/mol	

Supplementary Table 2: Length and structure of the 5'UTRs subcloned in pRL vector

Reporter vectors with long 5'UTRs were derived from a modified pRL-CMV (Promega) presenting an HA tag at the 5' end of the luciferase coding region.

To generate pRL27, a deletion was performed between NheI and HindIII sites using the Quikchange XL site directed mutagenesis kit (Stratagene) and oligonucleotides DEL1-F (5'GTTTAGTGAACCGTCAGATCACTAGAAGCTTGCTAGCCACCATGGCTTACCCCG3') and DEL1-R (5'GGGTAAGCCATGGTGGCTAGCAAGCTTCTAGTGATCTGAC GGTTCACTAAAC3'). Oligonucleotide DeL1-F introduces a NcoI site at the luciferase AUG initiation codon. NcoI / HindIII digestion of pRL27 and double strand oligonucleotides insertion generated reporter constructs harboring variable 5' untranslated region from 115 to 350 nucleotides. The 17 nucleotides region upstream the luciferase AUG start codon remained unchanged in all vectors. Resulting plasmids namely pRL115, pRL217, pRL265 or pRL327 were checked by DNA sequencing. Sequences, folding and free energy of the thermodynamic prediction of the variable 5' UTRs are provided. The empty pGL3 vector expressing *Firefly luciferase* was use as an internal control in this case.

	Apoptosis					DNA repair			
	TRADD	FAS	DAXX	BCL-2	TRAIP	c-MYC	ERCC5	BRCA2	MNAT1
GM03201	4.246	1.622	0.011	0.029	0.085	0.352	0.238	0.032	0.357
GM01953	2.416	1.418	0.018	0.243	0.486	0.308	0.173	0.007	0.825
VAL	0.094	0.457	0.436	1.915	0.637	1.014	1.138	0.790	0.890
DoHH-2	0.065	0.414	1.169	2.158	0.871	1.678	1.312	1.771	0.711
SuD-HL6	0.042	1.129	2.457	0.222	1.783	1.206	1.800	1.774	1.109
OCI-LY19	0.023	0.975	1.558	1.019	2.479	1.450	1.998	2.076	1.489
DB	0.114	0.984	1.353	1.414	0.658	0.992	0.341	0.549	1.619
p-value	***0.001***	***0.017***	***0.026***	***0.045***	***0.084***	***0.004***	***0.035***	***0.019***	***0.064***

	Validations in tumour samples			
	eIF4B	BCL-2	DAXX	ERCC5
Tonsil 1	0.252	0.352	0.420	0.632
Tonsil 2	0.146	0.312	0.197	0.368
DLBCL 1	2.119	1.214	2.301	1.253
DLBCL 2	2.219	0.909	1.575	1.463
DLBCL 3	0.290	1.077	0.421	1.016
DLBCL 4	0.888	1.910	1.340	1.425
DLBCL 5	1.087	1.225	0.747	0.843
p-value	***0.019***	***0.003***	***0.020***	***0.016***

	translation initiation											
	eIF4G	eIF4B total	eIF4B-P	eIF4B-P/ total	eIF4A	eIF4E total	eIF4E-P	eIF4B-P/ total	eIF4H	eIF2α	eIF2α-P	eIF2α P/ total
GM03201	0.377	0.472	0.431	0.913	0.415	0.783	0.855	1.092	0.805	0.836	0.816	0.976
GM01953	0.819	0.303	0.325	1.074	0.367	0.883	1.009	1.143	0.677	0.623	0.511	0.819
VAL	1.380	1.185	1.701	1.436	0.498	1.148	1.174	1.023	1.566	1.003	1.005	1.002
DoHH-2	1.727	1.360	0.863	0.635	0.473	1.150	1.159	1.008	1.167	1.414	0.983	0.695
SuD-HL6	1.379	1.252	0.941	0.751	4.195	0.686	0.756	1.102	1.033	1.268	0.702	0.554
OCI-LY19	0.704	1.202	0.941	0.783	0.491	1.111	0.818	0.736	0.667	0.963	1.065	1.105
DB	0.614	1.227	1.798	1.466	0.560	1.239	1.229	0.992	1.086	0.892	1.918	2.150
p-value	***0.098***	***0.00003***	***0.026***	***0.474***	***0.260***	***0.108***	***0.302***	***0.111***	***0.098***	***0.042***	***0.120***	***0.342***

	mTOR signaling							
	PI3K	PKB total	PKB-P	PKB-P/ total	mTOR	4EBP1 total	4EBP1-P	4EBP-P/ total
GM03201	0.254	0.500	0.013	0.025	0.193	0.453	0.172	0.380
GM01953	0.225	0.612	0.018	0.030	0.319	0.796	0.321	0.403
VAL	0.428	0.768	0.353	0.459	0.902	0.493	0.475	0.962
DoHH-2	0.425	0.625	0.661	1.058	1.490	1.651	1.561	0.945
SuD-HL6	0.388	0.579	0.877	1.515	0.870	0.868	0.914	1.053
OCI-LY19	0.461	0.878	0.776	0.884	1.389	1.811	2.017	1.114
DB	0.322	0.725	0.697	0.961	0.935	1.017	0.801	0.788
	0.005	***0.075***	***0.003***	***0.010***	***0.006***	***0.127***	***0.055***	***0.001***

Supplementary Table 3: Quantification of Western blots from figures 2, 3D and 5A
The blots were quantified with Image J software. The values obtained were normalised first to tubulin, then to the average value for the 7 cell lines. P-values were obtained by performing a unpaired t.test comparing the 5 DLBCL cell lines (or patient samples) to the 2 controls. For phosphorylated proteins, the relative ratio between phosphorylated and total proteins (p/total) was also calculated.

	eIF4B				DAXX				ERCC5			
	analysed	negative	positive	p-value	*analysed*	negative	positive	p-value	*analysed*	positive	negative	p value
DLBCL	***153***	**41** (26.8%)	**112** (73.2%)		***153***	**80** (52.3%)	**73** (47.7%)		***134***	**70** (52.2%)	**64** (47.8%)	
Age at diagnosis												
<65 years	*65*	**20** (30.8%)	**45** (69.2%)	0.47	*66*	**39** (59.1%)	**27** (40.9%)	0.27	*54*	**26** (48.1%)	**28** (51.9%)	0.55
≥65 years	*87*	**21** (24.1%)	**66** (75.9%)		*87*	**41** (47.1%)	**46** (52.9%)		*77*	**44** (57.1%)	**33** (42.9%)	
Gender												
male	*87*	**23** (26.4%)	**64** (73.6%)	0.94	*86*	**41** (47.7%)	**45** (52.3%)	0.39	*74*	**40** (54.1%)	**34** (45.9%)	0.75
female	*65*	**18** (27.7%)	**47** (72.3%)		*67*	**39** (58.2%)	**28** (41.8%)		*57*	**30** (52.6%)	**27** (47.4%)	
International prognosis index												
<=2	*41*	**10** (24.4%)	**31** (75.6%)	0.73	*45*	**29** (64.4%)	**16** (35.6%)	0.10	*31*	**18** (58.1%)	**13** (41.9%)	0.52
>=3	*33*	**8** (24.2%)	**25** (75.8%)		*35*	**12** (34.3%)	**23** (65.7%)		*28*	**13** (46.4%)	**15** (53.6%)	
cell origin (HANS classification)												
GC-like	*40*	**6** (15%)	**34** (85%)	0.09	*42*	**22** (52.4%)	**20** (47.6%)	0.99	*35*	**16** (45.7%)	**19** (54.3%)	0.44
non GC-like	*85*	**26** (30.6%)	**59** (69.4%)		*80*	**45** (56.3%)	**35** (43.8%)		*74*	**40** (54.1%)	**34** (45.9%)	
FL	***65***	**30** (46.2%)	**35** (53.8%)		***73***	**66** (90.4%)	**7** (9.6%)		***29***	**17** (58.6%)	**12** (41.4%)	
Age at diagnosis												
<65 years	*44*	**20** (45.5%)	**24** (54.5%)	0.93	*53*	**50** (94.3%)	**3** (5.7%)	0.33	*20*	**12** (60%)	**8** (40%)	0.09
≥65 years	*20*	**9** (45%)	**11** (55%)		*19*	**15** (78.9%)	**4** (21.1%)		*8*	**0** (0%)	**8** (100%)	
Gender												
male	*21*	**11** (52.4%)	**10** (47.6%)	0.57	*27*	**25** (92.6%)	**2** (7.4%)	0.70	*10*	3 (30%)	**7** (70%)	0.47
female	*44*	**19** (43.2%)	**25** (56.8%)		*46*	**41** (89.1%)	**5** (10.9%)		*19*	**9** (47.4%)	**10** (52.6%)	
grade												
1	*21*	**9** (42.9%)	**12** (57.1%)		*26*	**25** (96.2%)	**1** (3.8%)		*12*	**4** (33.3%)	**8** (66.7%)	
2	*33*	**15** (45.5%)	**18** (54.5%)	0.63	*34*	**30** (88.2%)	**4** (11.8%)	0.43	*13*	**8** (61.5%)	**5** (38.5%)	0.07
3	*11*	**6** (54.5%)	**5** (45.5%)		*13*	**11** (84.6%)	**2** (15.4%)		*4*	**0** (0%)	**4** (100%)	
CLL	***46***	**21** (45.7%)	**25** (54.3%)		***44***	**40** (90.9%)	**4** (9.1%)		***30***	**22** (73.3%)	**8** (26.7%)	
Age at diagnosis												
<65 years	*20*	**11** (55%)	**9** (45%)	0.40	*18*	**17** (94.4%)	**1** (5.6%)	0.60	*14*	**10** (71.4%)	**4** (28.6%)	0.87
≥65 years	*25*	**10** (40%)	**15** (60%)		*25*	**22** (88%)	**3** (12%)		*16*	**12** (75%)	**4** (25%)	
Gender												
male	*33*	**16** (48.5%)	**17** (51.5%)	0.74	*32*	**30** (93.8%)	**2** (6.3%)	0.58	*21*	**15** (71.4%)	**6** (28.6%)	0.84
female	*12*	**5** (41.7%)	**7** (58.3%)		*11*	**9** (81.8%)	**2** (18.2%)		*8*	**6** (75%)	**2** (25%)	

Supplementary Table 4: Composition of the tissue microarrays

The table shows the number of tumours sections immunostained with anti-ERCC5, anti-eIF4B and anti-DAXX antibodies that could be analysed for each tumour type: Diffuse Large B-cell lymphoma (DLBCL), Follicular Lymphoma (FL) and Chronic Lymphocytic leukemia (CLL). Clinical features such as gender or age do not impact on the expression for the studied proteins. ERCC5, eIF4B and DAXX do not significantly correlate either with the grade of FL, the International prognosis Index for DLBCL or the cell or origin classification in Ganglionary Cell like (GC) and non GC DLBCL.

Chi-square tests were used to generate p-values.