BCL6 – regulated by AhR/ARNT and wild-type *MEF2B* – drives expression of germinal center markers *MYBL1* and *LMO2*

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SUPPLEMENTAL METHODS

Gene expression analyses

RNA was prepared using the RNeasy Mini kit including the RNase Free DNase Set (Qiagen). TaqMan probes (Applied Biosystems) were used to quantify human *AhR* (Hs00169233_m1), *ARNT* (Hs01121918_m1), *BCL6* (Hs00153368_m1), *CGGBP1* (Hs00383191_m1), *CHMP2B* (Hs01045897_m1), *CTXN3* (Hs00416961_m1), *CYP1A1* (Hs01054797_g1), *GAPDH* (Hs02758991_g1), *ITM2B* (Hs00222753_m1), *LMO2* (Hs00153473_m1), *MEF2B* (Hs04188747_m1), *MYBL1* (Hs00277143_m1), *RB1* (Hs01078066_m1), *SOCS1* (Hs00705164s1) and *SOCS2* (Hs00919620_m1) expression levels with *TATA box binding protein* (*TBP*) as endogenous control. Relative expression levels were calculated using the $\Delta\Delta$Ct-method.

Preparation of recombinant retroviral supernatants and retroviral transduction

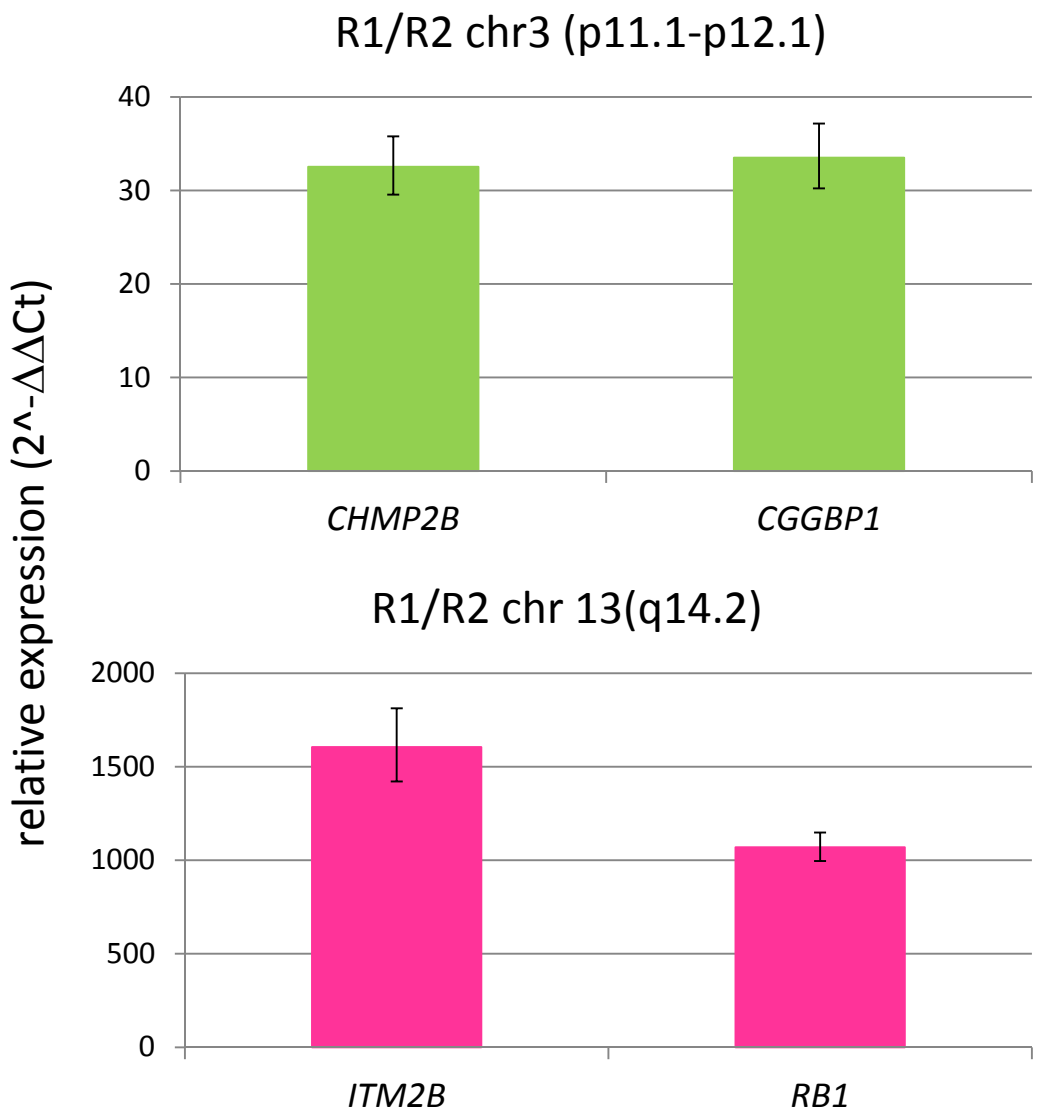
Retroviral supernatants were generated by calcium phosphate co-transfection of 293T cells using MSCV-BCL6-IRES-GFP (obtained from Addgene, Cambridge, MA, USA (http://www.addgene.org) or MSCV-IRES-GFP (vector control), M57 for gag/pol and pMD.g. Medium was replaced after 12 h by RPMI 1649 medium + 10% fetal calf serum for an additional 12 h. Retroviral supernatant was collected in RPMI 1640, twice within 24 h, pooled, cleared by low-speed centrifugation and filtered through a 0.45-mm filter. Viral supernatants were centrifuged for 10 to 16 h at 10,000 rpm at 10°C for concentration of viral particles.

Each construct was transduced into $5x10^5$ U-2932 R2 cells at a multiplicity of infection (MOI) of about 1. Cells were cultivated for 4 d and GFP+ cells were sorted by a BD FACS Aria (Becton Dickinson). RNA of sorted cells was isolated 10 d after sorting using TRIzol reagent (Invitrogen, Karlsruhe, Germany).

Whole exome sequencing

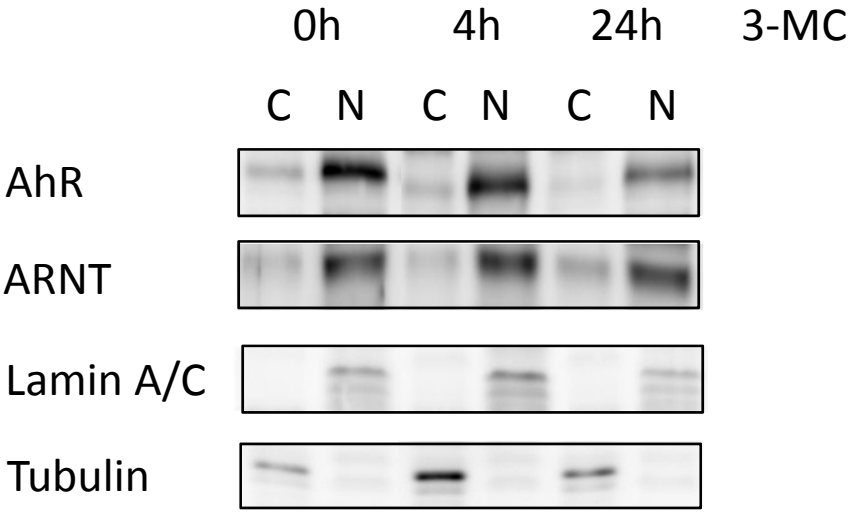
Paired-end exome (SureSelect XT Human All Exon V5 + UTR, Agilent, Santa Clara, CA, USA) sequencing of U29332R1 and U2932R2 on HiSeq2500 (Illumina, San Diego, CA, USA) resulted in 44 and 53 million reads resulting in 119 and 143 mean coverage, respectively. After data preprocessing (STAR 2.4.0b, samtools 0.1.19, picard 1.121) variants were identified via GATK (3.2.2) tools and mutation effects revealed via Ensembl VEP.

Suppl. Fig. 1: Subclone-specific gene expression

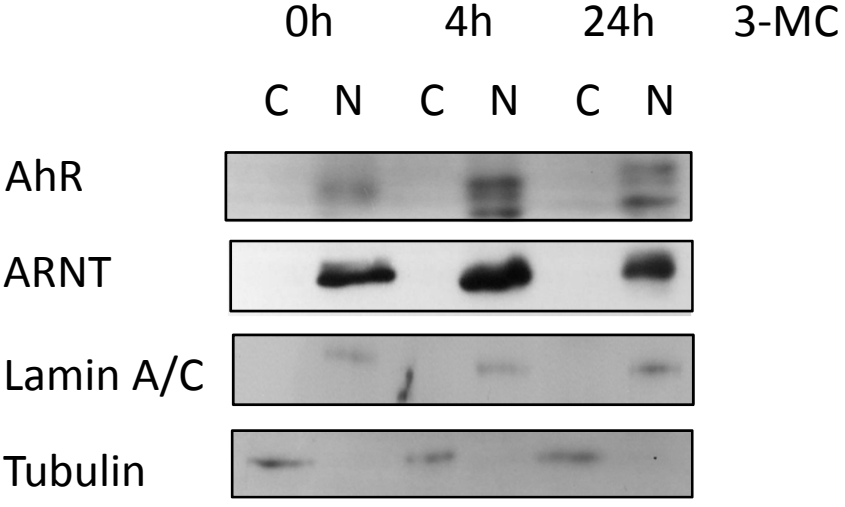


Suppl. Fig. 2: Nuclear localization of AhR/ARNT

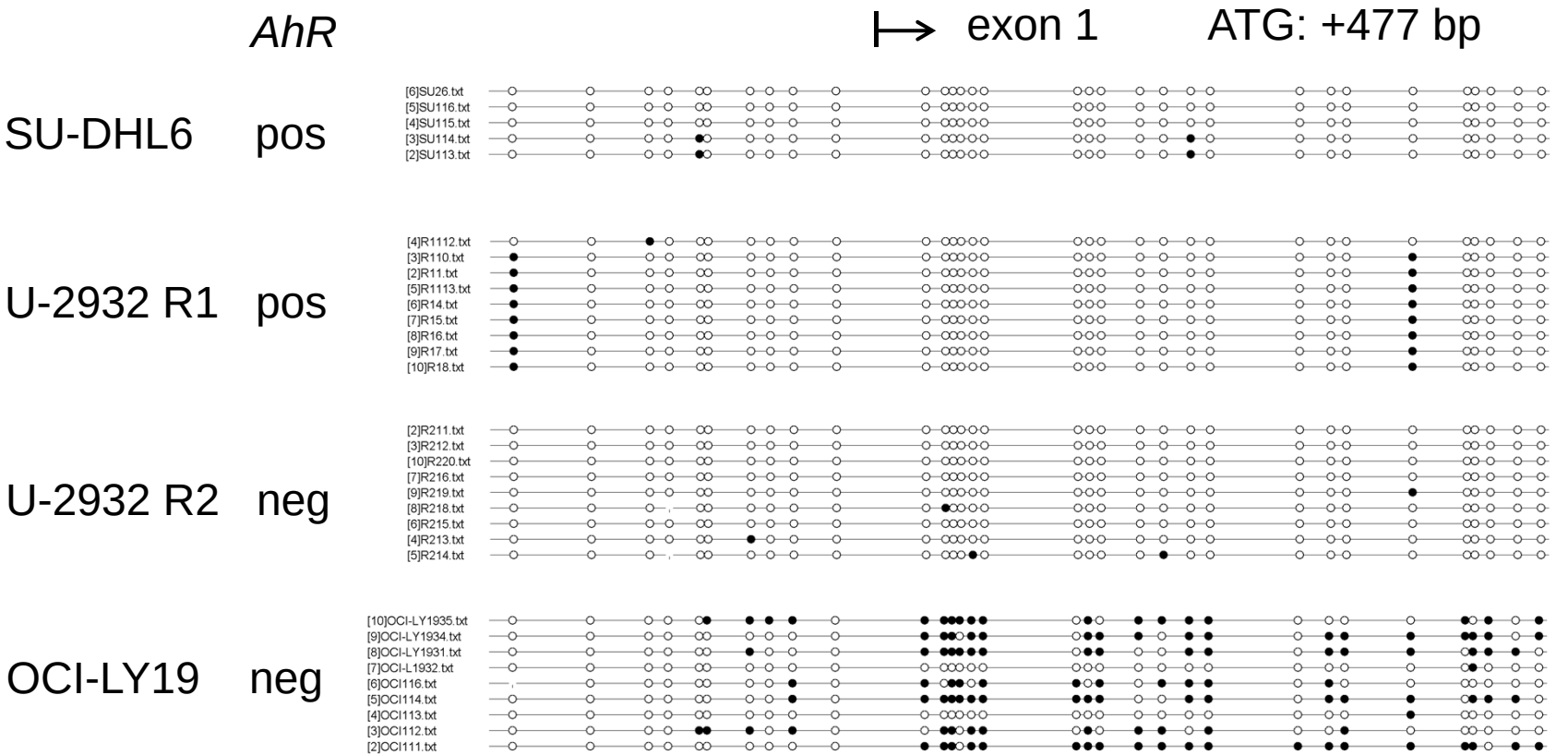
U-2932 R1



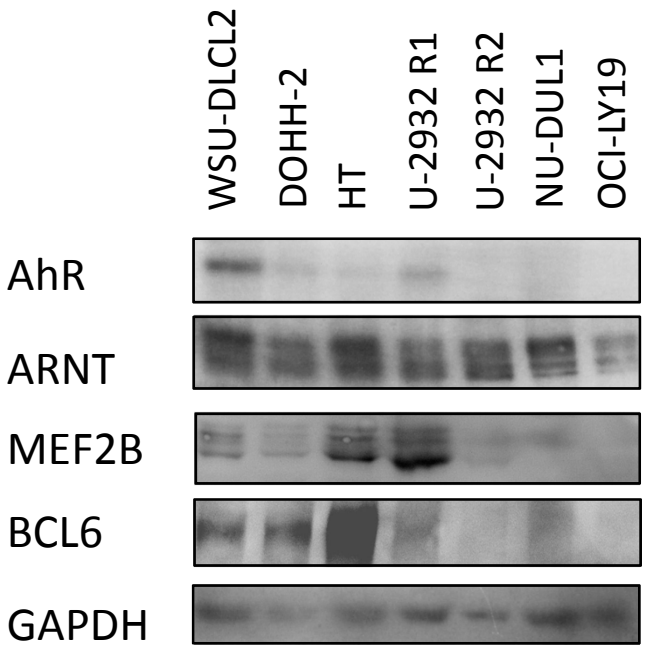
U-2932 R2



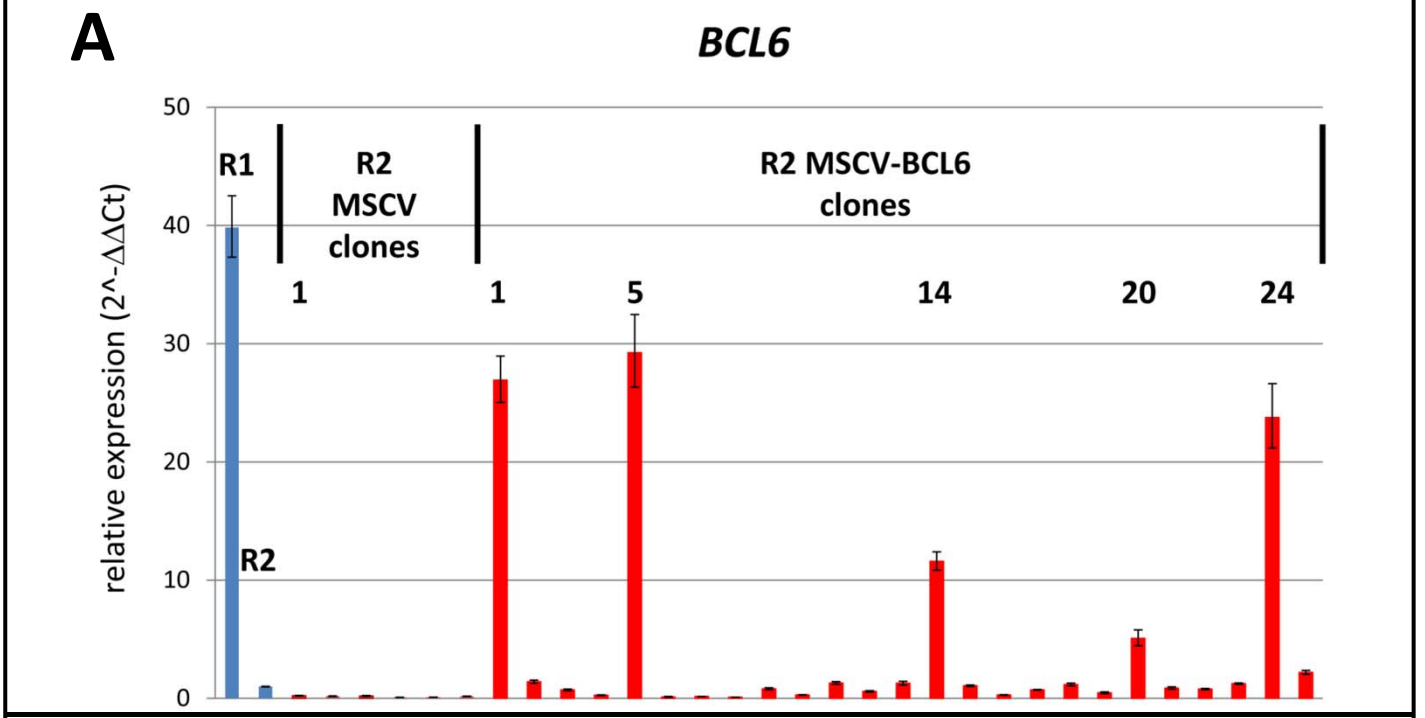
Suppl. Fig. 3: Bisulfite sequencing of the *AhR* promoter

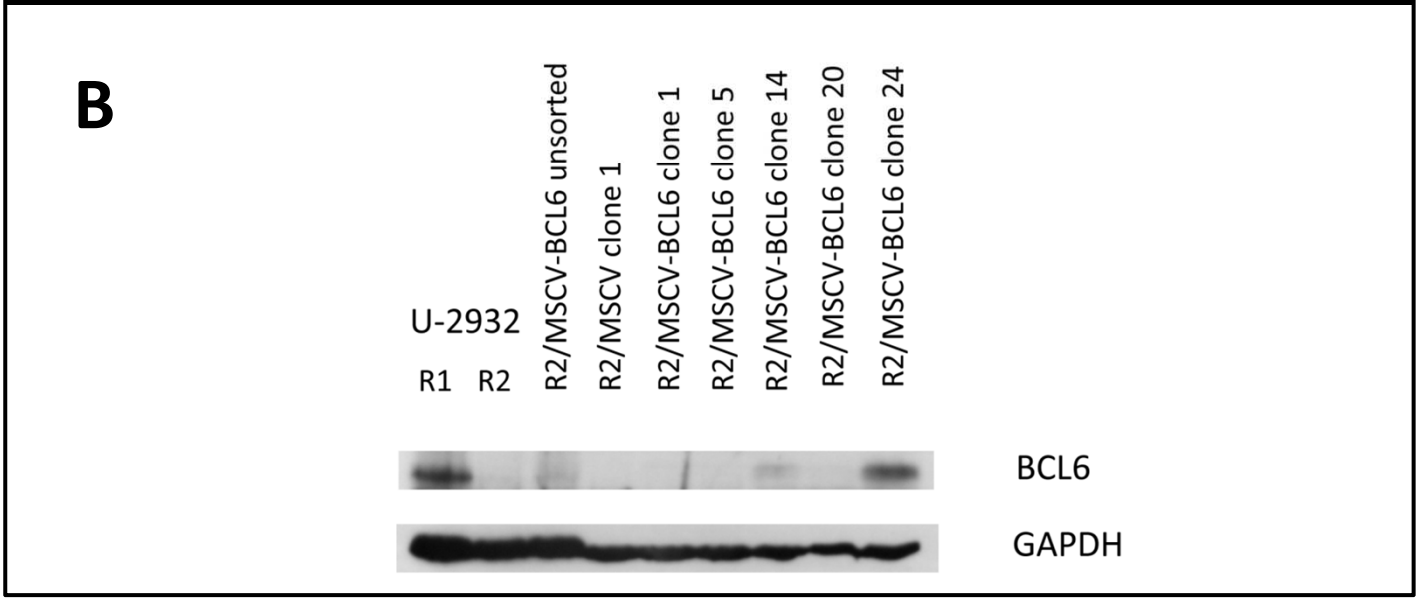


Suppl. Fig. 4: Protein expression in DLBCL cell lines



Suppl. Fig. 5: *BCL6* mRNA (A) and protein (B) expression





Supplementary Table 1 Primer sequences for real-time PCR

ABL1	FRW	5′-GTG GCC AGT GGA GAT AAC AC-3′
	REV	5′-CGC AAT TCC CAG ATT TCT ATC-3′
CDCP1	FRW	5′-GTC TCC GGC TTC AGC ATT G-3′
	REV	5′-ACC TAA TCA GAT AGC AGG GAG-3′
CGGBP1	FRW	5′-ATT ACT TCC AGA ATG AAC TGT TGT T-3′
	REV	5′-GCT GTT ACT ACA AAT CGC TCC-3′
CHMP2B	FRW	5′-CTA TCT ATA TTT GAT GTG TTC CCT T-3′
	REV	5′-GTG GAT CCA TCT TCT TGT TAA CT-3′
EPHA6	FRW	5′-CTC TTC TGA AAT GTA AGT GTT CG-3′
	REV	5′-CGC CCA CTA CAG ACT TCT C-3′
FLT1	FRW	5′-TCT GAC CTG TGA AGC AAC AGT-3′
	REV	5′-TAC AGA GCA CTT CGG CTT ATG-3′
ITM2B	FRW	5′-ACC TGT CTC ATG CTG AAT TGC-3′
	REV	5′-CCA CAG TAG TAC ACG TCA TCT-3′
KPNA3	FRW	5′-AGT GGT CCA ATT GAG TGC TGT-3′
	REV	5′-CCA GGT AAC ACA ACT GAG GAA-3′
RB1	FRW	5′-CTT GGA CTT GTA ACA TCT AAT GG-3′
	REV	5′-CCT CCC TCC ACA GTC TCA A-3′

PCR was performed for 40 cycles with 60°C annealing temperature.

Supplemental Table 2 Statistics

```
##############
#
Statistics referring to Figure 4
#
##############
#
# fishers exact test

stat.fig4a ← matrix(c(8, 5, 0, 10),
      nrow = 2,
      dimnames = list(AhR = c("AhR pos", "AhR neg"),
      MEF2B = c("MEF2B pos", "MEF2B neg")))
stat.fig4a

fisher.test(stat.fig4a, alternative = "greater")

# #
# Fisher's Exact Test for Count Data
#
# data:  stat.fig4a
# p-value = 0.002625
# alternative hypothesis: true odds ratio is greater than 1
# 95 percent confidence interval:
#  2.872487      Inf
# sample estimates:
# odds ratio
#        Inf


stat.fig4b ← matrix(c(12, 1, 1, 9),
      nrow = 2,
      dimnames = list(
            MEF2B = c("MEF2B pos", "MEF2B neg"),
            BCL6= c("BCL6 pos", "BCL6 neg")))
stat.fig4b

fisher.test(stat.fig4b, alternative = "greater")

##
# Fisher's Exact Test for Count Data
#
# data:  stat.fig4b
# p-value = 0.0001145
```

```
# alternative hypothesis: true odds ratio is greater than 1
# 95 percent confidence interval:
#  5.951049      Inf
# sample estimates:
# odds ratio
#   67.95602
#
```

```
Statistics referring to Supp. Table 3:

##############
#
#  McNemar's chi-squared test for symmetry of rows and columns
#
##############

M ← as.table(rbind(c(9, 2), c(15, 34)))
dimnames(M) ← list(ploidy = c("hyper (>2n)","hypo (<2n)"),
      expression=c("high", "low"))
chisq.test(M)

#
# Pearson's Chi-squared test with Yates' continuity correction
#
# data:  M
# X-squared = 7.7968, df = 1, p-value = 0.005234

mcnemar.test(M)

#
# McNemar's Chi-squared test with continuity correction
#
# data:  M
# McNemar's chi-squared = 8.4706, df = 1, p-value = 0.003609
#
```

Online Supplementary Table 3: 221 genes with > 10x expression difference between R1 and R2

Probe Set ID	Fold change([	Regulation([M	[MZ10110.1_CD20++CI	[MZ10110.1_	[MZ10110.2_CD20-	[MZ10110.2_	Gene Symbol	Entrez Gene	Alignments	RefSeq Transc	UniGene ID	R1/R2
228937_at	14.198563	up	144	2n	10	1n	C13orf31 = LACC1	144811	5405-43366067 (+) // 77.	NM_153218.2	Hs.210586	14.2
225915_at	11.7097225	up	194	2n	17	0n	CAB39L	81617	0786-48873649 (-) // 99	M_001079670	Hs.87159	11.7
200985_s_at	13.136413	up	819	2n	62	1n	CD59	966	36991-33700589 (-) // 9	NM_000611.5	Hs.278573	13.1
233647_s_at	26.878677	up	205	2n	8	0n	CDADC1	81602	9890-48739922 (+) // 10	NM_030911.1	Hs.388220	26.9
1552511_a_at	15.192938	up	95	2n	6	1n	CPA6	57094	5893-68821174 (-) // 98.	NM_020361.4	Hs.658850	15.2
218858_at	56.610584	up	592	2n	10	1n	DEPDC6 = DEPTOR	64798	145-121131937 (+) // 95	NM_022783.2	Hs.112981	56.6
241808_at	10.954515	up	52	2n	5	1n	FAM164A = ZC2HC1A	51101	970-79794549 (+) // 94.5	NM_016010.1	Hs.271876	11.0
202304_at	38.210648	up	489	2n	13	0n	FNDC3A	22862	0641-48681729 (+) // 97	M_001079673	Hs.508010	38.2
205848_at	10.262643	up	95	2n	9	1n	GAS2	2620	2930-22791122 (+) // 98	NM_005256.2	Hs.632151	10.3
218692_at	17.044813	up	301	2n	18	1n	GOLSYN = SYBU	55638	5590-110773009 (-) // 97	M_001099743	Hs.390738	17.0
217732_s_at	50.68264	up	1523	2n	30	0n	ITM2B	9445	5306-47733521 (+) // 95	NM_021999.3	Hs.643683	50.7
218656_s_at	21.477571	up	408	2n	19	1n	LHFP	10186	5029-39075201 (-) // 97.	NM_005780.2	Hs.507798	21.5
204249_s_at	51.092422	up	814	2n	16	1n	LMO2	4005	36700-33870412 (-) // 9	NM_005574.2	Hs.34560	51.1
202998_s_at	21.540615	up	549	2n	25	1n	LOXL2	4017	0640-23317575 (-) // 99.	NM_002318.2	Hs.626637	21.5
213906_at	89.83103	up	487	2n	5	1n	MYBL1	4603	5964-67667947 (-) // 94.	M_001080416	Hs.445898	89.8
212915_at	129.20955	up	992	2n	8	1n	PDZRN3	23024	4273-73756762 (-) // 97	NM_015009.1	Hs.719126	129.2
230673_at	11.983309	up	204	2n	17	1n	PKHD1L1	93035	155-110611735 (+) // 87	NM_177531.4	Hs.170128	12.0
203132_at	14.637268	up	160	2n	11	0n	RB1	5925	5911-47954023 (+) // 97	NM_000321.2	Hs.408528	14.6
208456_s_at	15.369736	up	765	2n	50	1n	RRAS2	22800	3 // p32.3 /// chr11:1425	M_001102669	Hs.502004	15.4
212845_at	15.896698	up	229	2n	14	1n	SAMD4A	23034	8610-54329780 (+) // 97	NM_015589.3	Hs.98259	15.9
204529_s_at	72.54462	up	824	2n	11	1n	TOX	9760	0530-60194321 (-) // 98.	NM_014729.2	Hs.491805	72.5
227198_at	-21.028719	down	50	1n	1042	2n	AFF3	3899	0149-99531503 (-) // 78.	M_001025108	Hs.444414	0.0
201218_at	-30.02685	down	19	1n	565	2n	CTBP2	1488	// q21.1 /// chr10:12666	M_001083914	Hs.501345	0.0
226184_at	-25.351238	down	10	1n	248	2n	FMNL2	114793	327-153214584 (+) // 97	NM_052905.3	Hs.654630	0.0
212446_s_at	-19.500639	down	8	1n	164	2n	LASS6 = CERS6	253782	5555-169340107 (+) // 97	NM_203463.1	Hs.718403	0.1
218181_s_at	-13.064496	down	24	1n	310	2n	MAP4K4	9448	5386-101877582 (+) // 98	NM_004834.3	Hs.719073	0.1
219855_at	-27.172165	down	18	1n	500	2n	NUDT11	55190	603-51256100 (-) // 77.2	NM_018159.3	Hs.200016	0.0
214615_at	-10.074078	down	6	1n	57	2n	P2RY10	27334	7556-78104066 (+) // 89.	NM_014499.2	Hs.296433	0.1
212190_at	-15.919967	down	18	1n	280	2n	SERPINE2	5270	3109-224612567 (-) // 93	NM_006216.2	Hs.38449	0.1
230597_at	-12.029298	down	14	1n	172	2n	SLC7A3	84889	2156-70062743 (-) // 96.	M_001048164	Hs.175220	0.1
224587_at	-19.24841	down	222	1n	4267	2n	SUB1	10923	416-32639942 (+) // 96.	NM_006713.2	Hs.229641	0.1
235749_at	-11.509959	down	5	2n	60	5n	UGCGL2 = UGGT2	55757	5163-95436687 (-) // 91.	NM_020121.2	Hs.193226	0.1
224588_at	-176.12349	down	23	1n	3983	2n	XIST	7503	7215-72978273 (-) // 92.	NR_001564.1	Hs.529901	0.0
228988_at	-16.949287	down	22	1n	371	2n	ZNF711	7552	162-84415060 (+) // 99.	NM_021998.4	Hs.326801	0.1
205681_at	44.35439	up	4504	3n	102	2n	BCL2A1	597	0289-78050593 (-) // 99.	NM_004049.3	Hs.227817	44.4
209030_s_at	14.292792	up	916	5n	64	2n	CADM1	23705	9558-114880338 (-) // 9	M_001098517	Hs.370510	14.3
202295_s_at	14.733625	up	2880	3n	195	2n	CTSH	1512	1170-77024406 (-) // 99.	NM_004390.3	Hs.148641	14.7
214724_at	17.564274	up	229	6n	13	2n	DIXDC1	85458	3335-111397913 (+) // 9	M_001037954	Hs.655626	17.6
1552531_a_at	49.541157	up	2725	3n	55	2n	NLRP11	204801	3581-61021415 (-) // 97.	NM_145007.2	Hs.375039	49.5
209694_at	11.091936	up	2498	6n	225	2n	PTS	5805	2373-111609686 (+) // 9	NM_000317.2	Hs.503860	11.1
231899_at	17.677458	up	141	5n	8	2n	ZC3H12C	85463	2904-109547774 (+) // 9	NM_033390.1	Hs.376289	17.7
223268_at	-17.09965	down	326	2n	5567	3n	C11orf54	28970	20108-93135898 (+) // 83	NM_014039.2	Hs.8360	0.1
204735_at	-13.903835	down	34	2n	469	3n	PDE4A	5141	4636-10441306 (+) // 97	NM_006202.2	Hs.89901	0.1
206011_at	-11.198894	down	35	3n	390	2n	CASP1	834	1444-104410640 (-) // 8	NM_001223.3	Hs.2490	0.1
209524_at	-16.817415	down	41	3n	692	2n	HDGFRP3	50810	6577-81667325 (-) // 96.	NM_016073.2	Hs.513954	0.1
209392_at	-28.913513	down	10	2n	285	1n	ENPP2	5168	506-120720251 (-) // 99	M_001040092	Hs.190977	0.0
205413_at	-27.565903	down	7	2n	181	1n	MPPED2	744	8349-30558616 (-) // 97.	NM_001584.1	Hs.289795	0.0
202431_s_at	-15.649786	down	236	2n	3695	1n	MYC	4609	511-128822629 (+) // 98	NM_002467.3		0.1
209598_at	-46.3171	down	8	2n	386	1n	PNMA2	10687	3112-26422365 (-) // 69.	NM_007257.5	Hs.591838	0.0
204011_at	-11.119356	down	10	2n	106	1n	SPRY2	10253	08114-79813087 (-) // 96	NM_005842.2	Hs.18676	0.1
226524_at	17.069777	up	2326	12n	136	1n	C3orf38	285237	837-88289434 (+) // 97.	NM_173824.2	Hs.518099	17.1
237613_at	12.675493	up	297	5n	23	3n	FOXR1	283150	5509-118357207 (+) // 9	NM_181721.2	Hs.116679	12.7
212560_at	80.996086	up	4596	5n	57	3n	SORL1	6653	6842-121009681 (+) // 9	NM_003105.4	Hs.368592	81.0
238846_at	19.034685	up	371	16n	19	14n	TNFRSF11A	8792	5088-58205879 (+) // 99.	NM_003839.2	Hs.204044	19.0
206861_s_at	13.51673	up	1221	13n	90	1n	CGGBP1	8545	7252-88190803 (-) // 95.	M_001008390	Hs.444818	13.5
202536_at	10.015122	up	2227	13n	222	1n	CHMP2B	25978	124-87387339 (+) // 97.	NM_014043.3	Hs.476930	10.0
241348_at	14.291068	up	1388	12n	97	1n	ZNF654	55279	5066-88276498 (+) // 72.	NM_018293.2	Hs.591650	14.3
213792_s_at	-13.369286	down	44	3n	582	4n	INSR	3643	7047-7244942 (-) // 97.6	NM_000208.2	Hs.465744	0.1
204567_s_at	-13.911304	down	13	2n	186	2n	ABCG1	9619	2447-42590421 (+) // 98	NM_004915.3	Hs.124649	0.1
204639_at	18.115915	up	943	2n	52	2n	ADA	100	1577-42713757 (-) // 99.	NM_000022.2	Hs.654536	18.1
201792_at	-16.111355	down	79	2n	1270	2n	AEBP1	165	0650-44120683 (+) // 94	NM_001129.3	Hs.439463	0.1
224499_s_at	-11.630042	down	124	2n	1443	2n	AICDA	57379	7024-8656706 (-) // 91.8	NM_020661.1	Hs.149342	0.1
223136_at	22.541872	up	138	1n	6	1n	AIG1	51390	3774-143703134 (+) // 96	NM_016108.2	Hs.567501	22.5
210517_s_at	-17.75434	down	14	1n	250	1n	AKAP12	9590	3515-151719601 (+) // 99	NM_005100.2	Hs.371240	0.1
204205_at	-42.11873	down	14	2n	575	2n	APOBEC3G	60489	3081-37813693 (+) // 99	NM_021822.1	Hs.660143	0.0
200602_at	-95.560875	down	8	2n	787	2n	APP	351	4732-26464956 (-) // 95.	NM_000484.2	Hs.434980	0.0
219127_at	11.2269335	up	194	2n	17	2n	ATAD4 = PRR15L	79170	4334-43390109 (-) // 97.8	NM_024320.2	Hs.368260	11.2
203140_at	42.26567	up	4862	4n	115	4n	BCL6	604	1865-188946169 (-) // 97	NM_001706.3	Hs.478588	42.3
212993_at	-14.033887	down	6	2n	80	2n	BTBD14A = NACC2	138151	3205-138042179 (-) // 91	NM_144653.3	Hs.112895	0.1
228434_at	12.936694	up	455	2n	35	2n	BTNL9	153579	0495-180421127 (+) // 6	NM_152547.3	Hs.546502	12.9
239977_at	-18.05297	down	14	2n	248	2n	C12orf42	374470	9862-102220322 (-) // 9	M_001099336	Hs.534649	0.1
1559584_a_at	-26.313713	down	6	2n	156	2n	C16orf54	283897	62.93 // /// chr16:29396	NM_175900.3	Hs.331095	0.0
238480_at	-10.853435	down	37	2n	397	2n	C18orf17 = TTC39C	125488	9090-19969890 (+) // 77	NM_153211.2	Hs.653395	0.1
219463_at	-33.999924	down	24	2n	814	2n	C20orf103 = LAMP5	24141	3297-9459171 (+) // 100	NM_012261.2	Hs.22920	0.0
223204_at	97.02253	up	549	2n	6	2n	C4orf18 = FAM198B	51313	5184-159267461 (-) // 95	M_001031700	Hs.567498	97.0
224990_at	-18.186203	down	150	2n	2719	2n	C4orf34	201895	6232-39316977 (-) // 81	NM_174921.1	Hs.576320	0.1
1552386_at	-22.785168	down	9	2n	204	2n	C5orf29 = GAPT	202309	082-57827943 (+) // 66.	NM_152687.2	Hs.547697	0.0
1552448_a_at	95.1449	up	1756	2n	18	2n	C8orf12	83656	3320-11333577 (+) // 67	XR_041853.1		95.1
230900_at	19.160563	up	139	2n	7	2n	CCDC110	256309	3334-186616553 (-) // 9	NM_152775.2	Hs.41101	19.2
200953_s_at	-13.935302	down	13	2n	185	2n	CCND2	894	198-4284777 (+) // 97.5	NM_001759.2	Hs.376071	0.1
206337_at	-11.366155	down	62	2n	700	2n	CCR7	1236	3580-35975250 (-) // 99.	NM_001838.2	Hs.370036	0.1
226702_at	12.993053	up	84	2n	6	2n	CMPK2	129607	5897-6907555 (-) // 92.3	NM_207315.2	Hs.7155	13.0
213050_at	21.099983	up	291	2n	14	2n	COBL	23242	1403-51351990 (-) // 99.	NM_015198.3	Hs.99141	21.1
211032_at	31.829222	up	266	2n	8	2n	COBLL1	22837	3211-165406896 (-) // 97	NM_014900.3	Hs.470457	31.8
205544_s_at	10.917972	up	86	2n	8	2n	CR2	1380	4317-205729852 (+) // 9	M_001006658	Hs.445757	10.9
229228_at	10.490457	up	70	2n	7	2n	CREB5	9586	565-28832033 (+) // 95.	M_001011666	Hs.437075	10.5
202551_s_at	-12.722332	down	9	2n	119	2n	CRIM1	51232	5900-36631781 (+) // 96.	NM_016441.1	Hs.699247	0.1
207030_s_at	-13.455472	down	47	2n	637	2n	CSRP2	1466	0 // q21.2 /// chr3:13211	NM_001321.1	Hs.530904	0.1
201059_at	14.791426	up	340	2n	23	2n	CTTN	2017	2297-69960328 (+) // 98	NM_005231.3	Hs.596164	14.8
231391_at	64.89294	up	654	2n	10	2n	CTXN3	613212	1751-127022225 (+) // 91	M_001048252	Hs.66194	64.9
202157_s_at	-74.50294	down	32	2n	2366	2n	CUGBP2 = CELF2	10659	47448-11413251 (+) // 9	M_001025076	Hs.309288	0.0
244407_at	18.102419	up	105	2n	6	2n	CYP39A1	51302	7233-46728029 (-) // 87.9	NM_016593.3	Hs.387367	18.1
206588_at	26.522898	up	188	2n	7	2n	DAZL	1618	3306-16621942 (-) // 99.	NM_001351.2	Hs.131179	26.5
206414_s_at	14.735279	up	225	2n	15	2n	DDEF2 = ASAP2	8853	344-9463257 (+) // 96.9	NM_003887.1	Hs.555902	14.7
204720_s_at	29.958982	up	580	2n	19	2n	DNAJC6	9829	024-65654140 (+) // 98.	NM_014787.2	Hs.647643	30.0
215565_at	10.005174	up	313	2n	31	2n	DTNB	1838	709-25504389 (+) // 33.	NM_021907.3	Hs.307720	10.0
219517_at	16.656925	up	4323	2n	260	2n	ELL3	80237	52113-41856476 (-) // 98	NM_025165.2	Hs.706346	16.7
217820_s_at	11.285909	up	144	2n	13	2n	ENAH	55740	02 // q28 /// chr1:22374	M_001008493	Hs.497893	11.3
220161_s_at	12.840984	up	532	2n	41	2n	EPB41L4B	54566	2259-111109507 (-) // 95	NM_018424.2	Hs.591901	12.8
214053_at	-34.96982	down	17	2n	582	2n	ERBB4	2066	8690-211950488 (-) // 9	M_001042599	Hs.390729	0.0
221601_s_at	-18.397343	down	43	2n	783	2n	FAIM3	9214	4280-205161966 (-) // 9	NM_005449.3	Hs.58831	0.1
212981_s_at	12.561367	up	93	2n	7	2n	FAM115A	9747	0.2 // q35 /// chr7:14317	NM_014719.1		12.6
209683_at	-17.094202	down	7	2n	127	2n	FAM49A	81553	4600-16668769 (-) // 88.	NM_030797.2	Hs.467769	0.1
209696_at	21.431818	up	1597	2n	74	2n	FBP1	2203	455-96441419 (-) // 99.8	NM_000507.3	Hs.494496	21.4
231472_at	-24.580168	down	13	1n	317	1n	FBXO15	201456	1585-69900242 (-) // 97.	NM_152676.1	Hs.664011	0.0
203562_at	16.022903	up	156	1n	10	1n	FEZ1	9638	0859-124871274 (-) // 9	NM_005103.3	Hs.224008	16.0
201540_at	-10.104974	down	58	1n	583	1n	FHL1	2273	7 // q26.3 /// chr3:1711	NM_001449.3	Hs.435369	0.1
212288_at	65.28747	up	3373	2n	52	2n	FNBP1	23048	286-131845294 (-) // 91.	NM_015033.2	Hs.189409	65.3
206018_at	46.420795	up	931	2n	20	2n	FOXG1	2290	06012-28308612 (+) // 8	NM_005249.3	Hs.695962	46.4
223278_at	19.522276	up	189	2n	10	2n	GJB2	2706	9610-19661919 (-) // 99.	NM_004004.4	Hs.524894	19.5
231771_at	16.681095	up	226	2n	14	2n	GJB6	10804	4101-19695622 (-) // 98.	NM_006783.3	Hs.511757	16.7
204875_s_at	10.40114	up	909	2n	87	2n	GMDS	2762	9077-2190730 (-) // 99.9	NM_001500.2	Hs.144496	10.4
204115_at	-33.759506	down	12	2n	413	2n	GNG11	2791	294-93393757 (+) // 97.	NM_004126.3	Hs.83381	0.0
209170_s_at	-13.152082	down	20	1n	266	1n	GPM6B	2824	2019-13745074 (-) // 90	M_001001994	Hs.495710	0.1
200696_s_at	10.969669	up	447	2n	41	2n	GSN	2934	1945-123134941 (+) // 97	NM_000177.4	Hs.522373	11.0
218450_at	19.265621	up	226	2n	12	2n	HEBP1	50865	9077-13044393 (-) // 96.	NM_015987.3	Hs.642618	19.3
203394_s_at	10.437844	up	264	4n	25	4n	HES1	3280	6399-195339090 (+) // 9	NM_005524.2	Hs.250666	10.4
203290_at	13.184316	up	1296	2n	98	2n	HLA-DQA1	3117	p1:3992092-3998304 (+)	NM_002122.3	Hs.387679	13.2
206858_s_at	12.713767	up	183	2n	14	2n	HOXC6	3223	3460-52710787 (+) // 97.	NM_004503.3	Hs.549040	12.7
211548_s_at	-15.916002	down	7	2n	117	2n	HPGD	3248	3186-175680194 (-) // 95	NM_000860.3	Hs.596913	0.1
205466_s_at	-59.636383	down	8	2n	452	2n	HS3ST1	9957	540-11010837 (-) // 99.3	NM_005114.2	Hs.507348	0.0
208937_s_at	14.086286	up	887	2n	63	2n	ID1	3397	5830-29657582 (+) // 95.	NM_002165.2	Hs.504609	14.1
209291_at	26.488232	up	337	2n	13	2n	ID4	3400	5596-19950407 (+) // 96.	NM_001546.2	Hs.519601	26.5
229450_at	-21.002394	down	8	1n	167	1n	IFIT3	3437	0155-91090705 (+) // 70.	M_001031683	Hs.714337	0.0
240915_at	21.708317	up	318	not in assay	15	not in assay	IGHG1	3500	0557-106240947 (-) // 57.	36 // q32.33	Hs.510635	21.7
231929_at	-17.341434	down	40	2n	701	2n	IKZF2	22807	2666-213575416 (-) // 9	M_001079526	Hs.604950	0.1
206502_s_at	-74.36406	down	9	2n	693	2n	INSM1	3642	5764-20299590 (+) // 88.	NM_002196.2	Hs.89584	0.0
226189_at	31.277441	up	146	2n	5	2n	ITGB8	3696	9960-20421907 (+) // 80.	NM_002214.2	Hs.592171	31.3
207110_at	-16.165817	down	13	2n	217	2n	KCNJ12	3768	9201-21260985 (+) // 99	NM_021012.4		0.1
232762_at	10.918845	up	170	2n	16	2n	KIAA1217	56243	7696-24849562 (+) // 73	M_001098500	Hs.445885	10.9
228476_at	-16.877846	down	37	2n	616	2n	KIAA1407	57577	675-115236687 (-) // 97.	NM_020817.1	Hs.477159	0.1
233002_at	13.483457	up	87	2n	6	2n	KIAA1622 = PPP4R4	57718	0482-93815825 (+) // 99.	NM_020958.2	Hs.259599	13.5
229310_at	38.449238	up	700	2n	18	2n	KLHL29	114818	348-23784980 (+) // 89.	M_001717454	Hs.130593	38.4
209894_at	11.825644	up	73	2n	6	2n	LEPR	3953	3836-65873698 (+) // 99	M_001003679	Hs.705413	11.8
213880_at	-10.24193	down	5	2n	55	2n	LGR5	8549	5028-70266353 (+) // 98	NM_003667.2	Hs.658889	0.1
217892_s_at	14.929028	up	579	2n	39	2n	LIMA1	51474	5839-48963539 (-) // 99.	NM_016357.4	Hs.525419	14.9
209204_at	-10.6160555	down	67	2n	710	2n	LMO4	8543	5738-87583851 (+) // 87.	NM_006769.2	Hs.436792	0.1
226884_at	-16.911322	down	5	2n	89	2n	LRRN1	57633	7910-3864900 (+) // 79.5	NM_020873.5	Hs.163244	0.1
206163_at	29.355616	up	177	1n	6	1n	MAB21L1	4081	6339-34948788 (-) // 86.	NM_005584.2	Hs.584776	29.4
235278_at	-26.843306	down	24	2n	634	2n	MACROD2	140733	0536-15981842 (+) // 94	M_001033087	Hs.661576	0.0
228262_at	56.421345	up	456	1n	8	1n	MAP7D2	256714	905-19936189 (-) // 97.4	NM_152780.2	Hs.127951	56.4
226225_at	45.439125	up	329	2n	7	2n	MCC	4163	5699-112388450 (-) // 94	M_001085377	Hs.593171	45.4
1559942_at	13.64577	up	979	2n	72	2n	MDFIC	29969	0144-114350941 (+) // 70	NM_199072.3	Hs.427236	13.6
204059_s_at	12.170219	up	679	2n	56	2n	ME1	4199	7975-84197499 (-) // 95.	NM_002395.3	Hs.21160	12.2
203510_at	18.959251	up	198	2n	10	2n	MET	4233	9694-116225669 (+) // 94	NM_000245.2	Hs.132966	19.0
203637_s_at	15.034996	up	133	1n	9	1n	MID1	4281	5165-10548459 (-) // 99.	NM_000381.2	Hs.27695	15.0
204959_at	-148.79947	down	9	2n	1403	2n	MNDA	4332	7791-157085894 (+) // 99	NM_002432.1	Hs.153837	0.0
219959_at	21.948507	up	302	3n	14	3n	MOCOS	55034	1479-32102682 (+) // 99	NM_017947.2	Hs.405028	21.9
226818_at	-72.031265	down	15	2n	1102	2n	MPEG1	219972	32561-58734705 (-) // 91	M_001039396	Hs.718450	0.0
214770_at	-11.645864	down	5	2n	59	2n	MSR1	4481	9655-16079874 (-) // 89	NM_002445.3	Hs.147635	0.1
225782_at	-13.782038	down	6	2n	85	2n	MSRB3	253827	4357-64146954 (+) // 86	M_001031679	Hs.339024	0.1
202086_at	-27.690495	down	18	2n	511	2n	MX1	4599	0023-41753006 (+) // 97	NM_002462.2	Hs.517307	0.0
212338_at	12.175663	up	78	2n	6	2n	MYO1D	4642	1969-28127155 (-) // 99.	NM_015194.1	Hs.658000	12.2
203072_at	11.054021	up	545	2n	49	2n	MYO1E	4643	5901-57452363 (-) // 99.	NM_004998.2	Hs.654506	11.1
203216_s_at	118.84086	up	1044	2n	9	2n	MYO6	4646	5768-76682664 (+) // 99.	NM_004999.3	Hs.149387	118.8
221933_at	10.482242	up	127	1n	12	1n	NLGN4X	57502	068-6155888 (-) // 97.24	NM_020742.2	Hs.21107	10.5
238605_at	-113.323265	down	11	3n	1268	3n	NOL4	8715	4870-29685849 (-) // 98.	NM_003787.3	Hs.514795	0.0
204105_s_at	-23.194178	down	16	2n	377	2n	NRCAM	4897	5329-107884006 (-) // 99	M_001037132	Hs.21422	0.0
228855_at	14.809055	up	242	2n	16	2n	NUDT7	283927	3102-76333655 (+) // 90	M_001105663	Hs.719356	14.8
219032_x_at	-10.804561	down	118	2n	1277	2n	OPN3	23596	3537-239870234 (-) // 8	NM_014322.2	Hs.719236	0.1
202733_at	10.996932	up	221	2n	20	2n	P4HA2	8974	5201-131590458 (-) // 98	M_001017973	Hs.519568	11.0
200897_s_at	12.555234	up	397	2n	32	2n	PALLD	23022	5795-170086141 (+) // 97	NM_016081.3	Hs.151220	12.6
1557166_at	-10.534743	down	9	1n	90	1n	PDCD4	27250	2478-112625588 (+) // 9	NM_014456.3	Hs.711490	0.1
219304_s_at	49.656025	up	925	2n	19	2n	PDGFD	80310	3130-103539971 (-) // 9	NM_025208.4	Hs.352298	49.7
209621_s_at	41.760113	up	1274	2n	31	2n	PDLIM3	27295	0089-186693629 (-) // 97	NM_014476.2	Hs.85862	41.8
220595_at	37.313416	up	306	2n	8	2n	PDZRN4	29951	53496-40254651 (+) // 93	NM_013377.3	Hs.380044	37.3
222392_x_at	25.298113	up	488	1n	19	1n	PERP	64065	3615-138470401 (-) // 9	NM_022121.2	Hs.201446	25.3
204525_at	-14.757885	down	11	2n	158	2n	PHF14	9678	0068-11109807 (+) // 96.	M_001007157	Hs.655688	0.1
207469_s_at	12.968806	up	352	1n	27	1n	PIR	8544	2846-15421377 (-) // 98.	M_001018109	Hs.495728	13.0
219014_at	-69.51511	down	51	2n	3565	2n	PLAC8	51316	864-84254913 (-) // 96.7	NM_016619.1	Hs.546392	0.0
213222_at	19.95349	up	470	2n	24	2n	PLCB1	23236	1295-8813547 (+) // 98.5	NM_015192.2	Hs.431173	20.0
210139_s_at	10.74367	up	101	2n	9	2n	PMP22	5376	73834-15106550 (-) // 97	NM_000304.2	Hs.372031	10.7
238117_at	10.59452	up	145	2n	14	2n	PPOX	5498	3847-159414427 (+) // 96	NM_000309.3	Hs.517373	10.6
203355_s_at	-155.90785	down	6	2n	960	2n	PSD3	23362	2490-18769600 (-) // 98	NM_015310.3	Hs.434255	0.0
240413_at	-49.85956	down	10	2n	516	2n	PYHIN1	149628	3110-157213462 (+) // 69	NM_152501.3	Hs.710248	0.0
205174_s_at	61.621754	up	1424	2n	23	2n	QPCT	25797	5372-37453968 (+) // 97.	NM_012413.3	Hs.79033	61.6
227036_at	-16.463549	down	7	2n	120	2n	RASAL2	9462	2815-176714608 (+) // 97	NM_004841.2	Hs.715627	0.1
214369_s_at	-28.771168	down	17	2n	498	2n	RASGRP2	10235	4913-64268415 (-) // 92	M_001098670	Hs.99491	0.0
1568752_s_at	162.04091	up	1167	2n	7	2n	RGS13	6003	0283-190895615 (+) // 78	NM_002927.3	Hs.497220	162.0
213566_at	-13.059918	down	8	2n	111	2n	RNASE6	6039	9083-20320460 (+) // 96	NM_005615.4	Hs.23262	0.1
232060_at	-112.23754	down	6	2n	705	2n	ROR1	4919	7898-64419765 (+) // 98	M_001083592	Hs.654491	0.0
200962_at	-15.81767	down	54	2n	854	2n	RPL31	6160	5167-101002650 (+) // 89	NM_000993.4	Hs.469473	0.1
1554413_s_at	12.410187	up	145	2n	12	2n	RUNDC2C//SNX29P2	00509///4403	7909-29284222 (+) // 70	12391.1///NR_	Hs.443656	12.4
232231_at	29.854166	up	489	2n	16	2n	RUNX2	860	3234-45626796 (+) // 70.	M_001015051	Hs.535845	29.9
211474_s_at	15.617707	up	471	2n	30	2n	SERPINB6	5269	4.39 // p33 /// chr6:2893	NM_004568.4	Hs.519523	15.6
238567_at	13.2705555	up	219	2n	16	2n	SGPP2	130367	4729-223132019 (+) // 95	NM_152386.2	Hs.591604	13.3
229485_x_at	-34.578606	down	9	2n	311	2n	SHISA3	152573	97790-42099261 (+) // 97	M_001080505	Hs.370904	0.0
210135_s_at	-10.917975	down	11	2n	119	2n	SHOX2	6474	538-159303586 (-) // 88.	NM_003030.3	Hs.55967	0.1
206181_at	15.368424	up	370	2n	24	2n	SLAMF1	6504	5512-158883493 (-) // 99	NM_003037.2	Hs.523660	15.4
222838_at	10.995907	up	212	2n	19	2n	SLAMF7	57823	5699-158991229 (+) // 80	NM_021181.3	Hs.517265	11.0
213664_at	21.58005	up	149	2n	7	2n	SLC1A1	6505	5152-4577468 (+) // 95.3	NM_004170.4	Hs.444915	21.6
210993_s_at	-64.4726	down	14	2n	934	2n	SMAD1	4086	406-146698556 (+) // 99	M_001003688	Hs.604588	0.0
203874_s_at	-21.52611	down	8	1n	163	1n	SMARCA1	6594	08414-128480107 (-) // 9	NM_003069.3	Hs.152292	0.0
213624_at	21.026327	up	152	1n	7	1n	SMPDL3A	10924	597-123172805 (+) // 99	NM_006714.2	Hs.486357	21.0
213139_at	40.304195	up	346	2n	9	2n	SNAI2	6591	879-49996705 (-) // 94.0	NM_003068.3	Hs.360174	40.3
210001_s_at	13.282465	up	225	2n	17	2n	SOCS1	8651	5807-11256889 (-) // 94.	NM_003745.1	Hs.50640	13.3
227697_at	18.22486	up	99	2n	5	2n	SOCS3	9021	4453-73864922 (-) // 88.	NM_003955.3	Hs.527973	18.2
201417_at	-35.191326	down	51	2n	1785	2n	SOX4	6659	0978-21706829 (+) // 90	NM_003107.2	Hs.643910	0.0
226342_at	12.254973	up	499	2n	41	2n	SPTBN1	6711	0999-54743023 (+) // 98.	NM_003128.2	Hs.503178	12.3
214597_at	24.521452	up	213	2n	9	2n	SSTR2	6752	2755-68679655 (+) // 82	NM_001050.2	Hs.514451	24.5
203767_s_at	-35.64348	down	12	1n	427	1n	STS	412	496-7282851 (+) // 88.85	NM_000351.4	Hs.522578	0.0
230560_at	10.3778515	up	78	2n	8	2n	STXBP6	29091	48704-24349175 (-) // 96	NM_014178.6	Hs.508958	10.4
224724_at	19.319445	up	396	2n	21	2n	SULF2	55959	3498-45799001 (-) // 99.	NM_018837.2	Hs.162016	19.3
212956_at	-10.750348	down	69	2n	743	2n	TBC1D9	23158	385-141811532 (-) // 97.	NM_015130.2	Hs.480819	0.1
226388_at	-10.9952345	down	16	2n	178	2n	TCEA3	6920	141-23623820 (-) // 86.8	NM_003196.1	Hs.446354	0.1
243198_at	13.763108	up	305	2n	22	2n	TEX9	374618	1796-54508303 (+) // 97	NM_198524.1	Hs.511476	13.8
203221_at	-10.603576	down	23	2n	244	2n	TLE1	7088	419-83493032 (-) // 98.6	NM_005077.3	Hs.197320	0.1
226186_at	18.237108	up	140	2n	8	2n	TMOD2	29767	2097-49895857 (+) // 76	NM_014548.2	Hs.659839	18.2
206641_at	12.780529	up	6749	2n	528	2n	TNFRSF17	608	6464-11969426 (+) // 99	NM_001192.2	Hs.2556	12.8
228737_at	-12.284545	down	14	2n	174	2n	TOX2	84969	0709-42131666 (+) // 91.	M_001098796	Hs.26608	0.1
211796_s_at	-20.411964	down	57	2n	1170	2n	TRBC1///TRBC2	28638///2863	9477-142210338 (+) // 99.	26 // q34		0.0
210055_at	-10.935785	down	9	2n	102	2n	TSHR	7253	1527-80682394 (+) // 98	NM_000369.2	Hs.160411	0.1
217979_at	36.57624	up	963	2n	26	2n	TSPAN13	27075	9960-16790684 (+) // 98.	NM_014399.3	Hs.364544	36.6
238462_at	-18.09624	down	10	1n	177	1n	UBASH3B	84959	8981-122190395 (+) // 9	NM_032873.4	Hs.444075	0.1
1556096_s_at	68.03379	up	567	2n	8	2n	UNC13C	440279	4519-52708095 (+) // 98	M_001080534	Hs.657273	68.0
225093_at	-15.029277	down	26	1n	384	1n	UTRN	7402	3605-145215861 (+) // 9	NM_007124.2	Hs.133135	0.1
235343_at	-13.5374975	down	8	2n	106	2n	VASH2	79805	1079-211231548 (+) // 97	NM_024749.2	Hs.96885	0.1
201426_s_at	-39.70185	down	54	2n	2154	2n	VIM	7431	0935-17319597 (+) // 94.	NM_003380.2	Hs.642813	0.0
243087_at	10.907009	up	99	2n	9	2n	WDR63	126820	4787-85371409 (+) // 96.	NM_145172.2	Hs.97933	10.9
204712_at	-35.479584	down	9	2n	333	2n	WIF1	11197	0675-63801350 (-) // 97.	NM_007191.3	Hs.284122	0.0
226676_at	-33.713364	down	13	6n	436	6n	ZNF521	25925	5887-21060219 (-) // 99.	NM_015461.1	Hs.116935	0.0

Supplementary Table 4 Correlation *BCL6* and *BCL6* target gene expression in B-NHL cell lines

Probe set ID	Gene symbol	FARAGE	Karpas-1106P	U-2940	U-2932 R1	U-2932 R2	NU-DHL1	OCI-LY19	SU-DHL8	mean
203140_at	*BCL6*	4.21	4.60	3.75	4.38	-1.08	0.69	0.47	-1.54	1.93
205681_at	*BCL2A1*	5.01	2.93	3.98	4.17	-1.45	-5.00	-4.79	-3.75	0.14
228434_at	*BTNL9*	3.81	3.04	2.01	1.11	-3.08	0.00	-1.60	-4.97	0.04
1552448_a_a	*C8orf12*	-4.36	-1.93	-4.69	2.51	-3.69	-4.32	-4.79	-5.01	-3.28
228592_at	*MS4A1*	4.92	5.91	5.22	5.05	3.59	3.47	1.20	0.07	3.68
204581_at	*CD22*	1.69	1.75	0.69	1.15	-2.14	1.50	0.52	-1.43	0.47
206150_at	*CD27*	0.97	0.02	0.40	2.36	-0.75	-1.22	-0.03	-3.11	-0.17
205692_s_at	*CD38*	0.47	-0.02	-2.71	0.77	-1.21	-0.03	0.26	3.20	0.09
200985_s_at	*CD59*	1.96	1.47	1.28	1.98	-2.03	-0.11	-0.60	-1.43	0.32
231391_at	*CTXN3*	-4.29	-4.82	-5.10	1.34	-4.30	-4.91	-5.14	-4.90	-4.01
204720_s_at	*DNAJC6*	0.30	1.25	-0.05	0.98	-3.58	-1.48	-0.37	-1.12	-0.51
219517_at	*ELL3*	2.79	4.06	2.84	4.11	0.19	-1.26	-1.22	-0.06	1.43
220161_s_at	*EPB41L4B*	-3.41	2.67	1.44	0.95	-2.68	-3.70	-3.18	-4.18	-1.51
212288_at	*FNBP1*	3.35	4.76	3.02	3.30	-2.47	3.39	1.92	0.63	2.24
206018_at	*FOXG1*	-4.51	-4.19	-4.69	2.79	-3.81	-4.03	-5.02	-4.86	-3.54
204875_s_at	*GMDS*	1.38	-1.42	-1.46	1.80	-1.00	-0.20	0.96	-0.34	-0.03
203394_s_at	*HES1*	-2.36	-4.44	-4.69	0.34	-3.75	0.22	-3.50	-5.04	-2.90
208937_s_at	*ID1*	-3.23	-3.71	-2.96	2.10	-1.77	-3.32	-4.39	-3.43	-2.59
209291_at	*ID4*	-4.94	-4.48	-4.46	1.06	-4.56	-2.96	-4.23	-4.58	-3.65
218656_s_at	*LHFP*	0.00	1.32	-3.18	0.70	-3.47	-4.91	-0.53	-4.41	-1.81
217892_s_at	*LIMA1*	1.86	2.35	2.10	1.14	-2.64	0.09	-0.97	-2.53	0.17
204249_s_at	*LMO2*	4.46	3.99	3.77	2.06	-3.47	0.34	3.59	-2.51	1.53
1559942_at	*MDFIC*	0.53	-0.15	1.61	1.83	-1.45	-1.22	-5.14	-3.07	-0.88
238576_at	*MOCOS*	-4.80	-3.84	-3.70	-1.96	-4.82	-3.41	-4.64	-4.74	-3.99
213906_at	*MYBL1*	0.83	2.45	1.63	1.16	-5.12	-4.09	-1.80	-0.26	-0.65
1552531_a_a	*NLRP11*	-2.92	-0.33	-2.96	3.30	-2.06	-2.22	-3.59	-1.44	-1.53
209621_s_at	*PDLIM3*	-3.47	-2.44	-4.35	2.33	-3.17	-3.46	-3.14	-4.36	-2.76
205174_s_at	*QPCT*	2.55	3.12	3.03	2.88	-3.52	-3.75	-3.69	-4.36	-0.47
1568752_s_at	*RGS13*	2.94	2.56	3.05	3.11	-5.39	-2.79	-4.08	1.06	0.06
208456_s_at	*RRAS2*	1.18	2.02	0.94	1.84	-2.11	0.11	-2.97	-0.86	0.02
212560_at	*SORL1*	3.73	3.19	1.71	4.32	-2.54	-0.60	2.58	-4.10	1.04
243198_at	*TEX9*	1.90	0.10	-0.02	0.04	-3.81	-4.81	-3.42	-2.30	-1.54
217979_at	*TSPAN13*	2.93	-0.50	-4.01	2.28	-3.36	3.11	3.96	3.47	0.99

LEGENDS SUPPLEMENTAL FILES

Supplemental Figure 1 - Subclone-specific gene expression. Quantitative RT-PCR was performed to test mRNA levels in the U-2932 subclones R1 and R2. U-2932 R2 was used as reference. Note that structural aberrations on chr 3 and chr 13 correlate with the R1-restricted overexpression of target genes: U-2932 subclone R1 has 32x higher mRNA expression levels of *CHMP2B* and *CGGBP1* than R2, *ITM2B* and *RB1* is >1000x fold higher expressed in R1 than in R2.

Supplemental Figure 2 - Nuclear localization of AhR/ARNT. AhR localized in the nucleus of U-2932 R1 and R2 cells, without stimulation with the ligand 3-methyl-cholantrene (3-MC) (2 μM, 0 h – 24 h). Note that AhR expression in R2 was extremely low, detectable only after long exposure. C: cytoplasm; N: nucleus. Protein expression was determined by Western blot analysis.

Supplemental Figure 3 – Bisulfite sequencing of the *AhR* promoter. Parts of the AhR promoter region were sequenced after bisulfite converson of DNA in the two *AhR*-positive (SU-DHL6, U-2932 R1) and *AhR* negative (U-2932 R2, OCI-LY19) cell lines. CpGs are represented as open dots (unmethylated) of filled dots (methylated).

Supplemental Figure 4 - Expression of AhR, ARNT, MEF2B and BCL6 in DLBCL cell lines. Protein expression was determined by Western blot analysis. GAPDH was used as endogenous control.

Supplemental Figure 5 - Expression of *BCL6* in U-2932 R1, R2, and in R2 clones transfected with MSCV and MSCV-BCL6. A) *BCL6* mRNA and B) protein

expression was determined using qRT-PCR and Western blot analysis. Note that only a minority of MSCV-BCL6-IRES-GFP clones expressed *BCL6,* although all clones were GFP-positive. After cryopreservation, recloning of R2-MSCV clone 24 was necessary to obtain BCL6 positive subclones.

Supplemental Table 1 - Primers for quantitative genomic PCR. PCR was performed for 40 cycles with 60°C annealing temperature.

Supplemental Table 2 – Statistical evaluation of results. R-programmed statistical analyis.

Supplemental Table 3 - Genes with >10x expression differences between R1 and R2. mRNA expression was determined by microarray analysis. Colored: Genes showing numerical disparities. Green: true negative (34); yellow: true positive (9); red: false positive (2); blue: false negative (5); grey: not included in statistical analysis because neither R1 nor R2 were diploid. Numerical differences between the two subclones predict differences in gene expression (sensitivity 0.64, specificity 0.94, accuracy 0.78). McNemar´s chi-squared test with continuity correction rejected non-correlation of the two parameters with a p-value of 0.0036 compared to 0.05 as level of significance.

Supplemental Table 4 – Positive *BCL6* target genes. Expression array analysis reveals a positive correlation between the expression of *BCL6* and positive candidate target genes of Fig. 5 (sensitivity 0.77, specificity 0.83, accuracy 0.80). Red: expression above average; green: expression below average.