Supplementary Table S1. Cox regression analysis of BM involvement, IPI score, and COO classification for PFS and OS.

	PFS			OS		
Variable	**RR**	**95% CI**	***P* value**	**RR**	**95% CI**	***P* value**
BM involvement						
Negative	1			1		
Concordant	1.497	1.121-1.998	0.006	1.396	1.030-1.894	0.032
Discordant	1.236	0.843-1.811	0.278	0.648	0.400-1.052	0.079
COO						
GCB	1			1		
Non-GCB	1.383	1.084-1.765	0.009	1.398	1.073-1.822	0.013
IPI score						
Low (0-1)	1			1		
Intermediate (2-3)	1.974	1.420-2.743	<0.001	2.691	1.817-3.984	<0.001
High (4-5)	3.114	2.122-4.571	<0.001	4.432	2.844-6.906	<0.001

RR indicates relative risk.

Supplementary Table S2. COX regression analysis of treatment, age, and ECOG PS for PFS and OS in patients with concordant BM involvement

	PFS			OS		
Variable	RR	95% CI	P value	RR	95% CI	P value
Treatment						
Regular therapy	1			1		
Intensive therapy	0.375	0.206-0.684	0.001	0.364	0.186-0.711	0.003
Age						
≤60 years	1			1		
>60 years	1.136	0.737-1.752	0.564	1.368	0.850-2.205	0.197
ECOG PS						
0,1	1			1		
≥2	2.441	1.637-3.639	<0.001	2.545	1.675-3.865	<0.001

ECOG indicates Eastern Cooperative Oncology Group; PS, performance status; PFS, progression-free survival; OS, overall survival; BM, bone marrow; RR indicates relative risk.

Supplementary Table S3. Genes differentially expressed between concordant BM involvement patients with high BM-adjusted IPI and low BM-adjusted IPI

Genes up-regulated in concordant BM involvement patients with high BM-adjusted IPI		
Gene Symbol	**Gene Title**	**Gene ID**
MLLT6	PHD Finger Domain Containing	4302
ATPIF1	ATPase Inhibitory Factor 1	93974
C1QBP	Complement C1q Binding Protein	708
COPS9	COP9 Signalosome Subunit 9	150678
POLR1D	RNA Polymerase I Subunit D	51082
COMMD6	COMM Domain Containing 6	170622
SUGT1	MIS12 Kinetochore Complex Assembly Cochaperone	10910
TMA7	Translation Machinery Associated 7 Homolog	51372
SNRPD1	Small Nuclear Ribonucleoprotein D1 Polypeptide	6632
RPS21	Ribosomal Protein S21	6227
CCT3	Chaperonin Containing TCP1 Subunit 3	7203
SERBP1	SERPINE1 mRNA Binding Protein 1	26135
ATP5J	ATP synthase, H+ transporting, Mitochondrial Fo Complex Subunit F6	522
CACYBP	Calcyclin Binding Protein	27101
ATP5I	ATP Synthase, H+ transporting, Mitochondrial Fo Complex Subunit E	521
EXOSC7	Exosome Component 7	23016
RPS4X	Ribosomal Protein S4, X-linked	6191
POLR3G	RNA Polymerase III Subunit G	10622
RPL5	Ribosomal Protein L5	6125
RPL23A	Ribosomal Protein L23a	6147
RPS20	Ribosomal Protein S20	6224
SSBP1	Single Stranded DNA Binding Protein 1	6742
GSK3B	Glycogen Synthase Kinase 3 beta	2932
YWHAZ	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein zeta	7534
COTL1	Coactosin Like F-actin Binding Protein 1	23406
CSPP1	Centrosome and Spindle Pole Associated Protein 1	79848
EHD1	EH Domain Containing 1	10938
FCRLA	Fc Receptor Like A	84824
GTF2H2	General Transcription Factor IIH Subunit 2	2966
MCM4	Minichromosome Maintenance Complex Component 4	4173
MRPL39	Mitochondrial Ribosomal Protein L39	54148
Genes down-regulated in concordant BM involvement patients with high BM-adjusted IPI		
Gene Symbol	**Gene Title**	**Gene ID**
CTSB	Cathepsin B	1508
CCPG1	Cell Cycle Progression 1	9236
HEATR3	Heat Repeat Containing 3	55027
GPHN	Gephyrin	10243
AXL	AXL Receptor Tyrosine Kinase	558

FBXO32	F-box Protein 32	114907
LDLRAD3	Low Density Lipoprotein Receptor Class A Domain Containing 3	143458
SLC11A2	Solute Carrier Family 11 Member 2	4891
FRMD3	FERM Domain Containing 3	257019
TF	Transferrin	7018
WFDC8	WAP Four-Disulfide Core Domain 8	90199
TLK1	Tousled Like Kinase 1	9874
TLR7	Toll Like Receptor 7	51284
GOLGA4	Golgin A4	2803
LINC00528	Long Intergenic non-Protein Coding RNA 528	200298
RBFOX1	RNA Binding Protein, Fox-1 Homolog 1	54715
GTPBP1	GTP Binding Protein 1	9567
ETV7	ETS Variant 7	51513
ZNF438	Zinc Finger Protein 438	220929
ADAM2	ADAM Metallopeptidase Domain 2	2515
THAP6	THAP Domain Containing 6	152815
LINS1	Lines Homolog 1	55180
ZNF599	Zinc Finger Protein 599	148103
PNKD	Paroxysmal non-Kinesigenic Dyskinesia	25953
JAK1	Janus Kinase 1	3716

Supplementary Table S4. Genes differentially expressed between concordant BM involvement patients with MYC$^+$ and MYC$^-$

Genes up-regulated in concordant BM involvement patients with MYC$^+$		
Gene Symbol	**Gene Title**	**Gene ID**
METTL15	Methyltransferase Like 15	196074
NUP35	Nucleoporin 35	129401
RITA1	RBPJ Interacting and Tubulin Associated 1	84934
FAM161A	Family with Sequence Similarity 161 Member A	84140
RB1	RB Transcriptional Corepressor 1	5925
OR7E47P	Olfactory Receptor Family 7 Subfamily E Member 47 Pseudogene	26628
OR1A2	Olfactory Receptor Family 1 Subfamily A Member 2	26189
TXLNG	Taxilin Gamma	55787
SLC15A4	Solute Carrier Family 15 Member 4	121260
PAWR	Pro-apoptotic WT1 Regulator	5074
OR7E37P	Olfactory Receptor Family 7 Subfamily E Member 37 Pseudogene	100506759
PRMT5	Protein Arginine Methyltransferase 5	10419
ZNF22	Zinc Finger Protein 22	7570
DIMT1	DIM1 Dimethyladenosine Transferase 1 Homolog	27292
Genes down-regulated in concordant BM involvement patients with MYC$^+$		
Gene Symbol	**Gene Title**	**Gene ID**
N4BP2L1	NEDD4 Binding Protein 2 Like 1	90634
CHD2	Chromodomain Helicase DNA Binding Protein 2	1106
PBXIP1	PBX Homeobox Interacting Protein 1	57326
PARD6A	Par-6 Family Cell Polarity Regulator alpha	50855
NEAT1	Nuclear Paraspeckle Assembly Transcript 1 (non-protein coding)	283131
TSR3	TSR3, Acp Transferase Ribosome Maturation Factor	115939
ENGASE	Endo-beta-N-Acetylglucosaminidase	64772
MALAT1	Metastasis Associated Lung Adenocarcinoma Transcript 1 (non-protein coding)	378938
ARF1	ADP Ribosylation Factor 1	375
APOL2	Apolipoprotein L2	23780
ANGEL1	Angel Homolog 1	23357
LOC283859	Unknown	Unknown

Supplementary Figure legends

Supplementary Figure S1. Survival curves for OS and PFS according to type of BM involvement in DLBCL risk-stratified patients. (a) Comparisons of OS and PFS according to type of BM involvement in high-risk IPI cohort. (b) Comparisons of OS and PFS according to type of BM involvement in non-GCB cohort.

Supplementary Figure S2. Survival curves for OS according to clinical and pathologic features in DLBCL patients with positive BM involvement.

Supplementary Figure S3. The BM-adjusted IPI for risk stratification in DLBCL patients with positive BM involvement. (a) The training set. (b) The validation set.

Supplementary Figure S4. Impact on OS of molecular pathologic parameters in concordant vs negative BM groups. Con indicates concordant BM involvement; Neg, negative BM involvement; *BCL2*-R, *BCL2* rearrangement; WT-*TP53,* wide-type *TP53*; MUT-*TP53*, mutant-type *TP53*; *MYC*-R, *MYC* rearrangement; DPL, BCL2/MYC double-positive lymphoma; DHL, *BCL2/MYC* double-hit lymphoma.

Figure S1

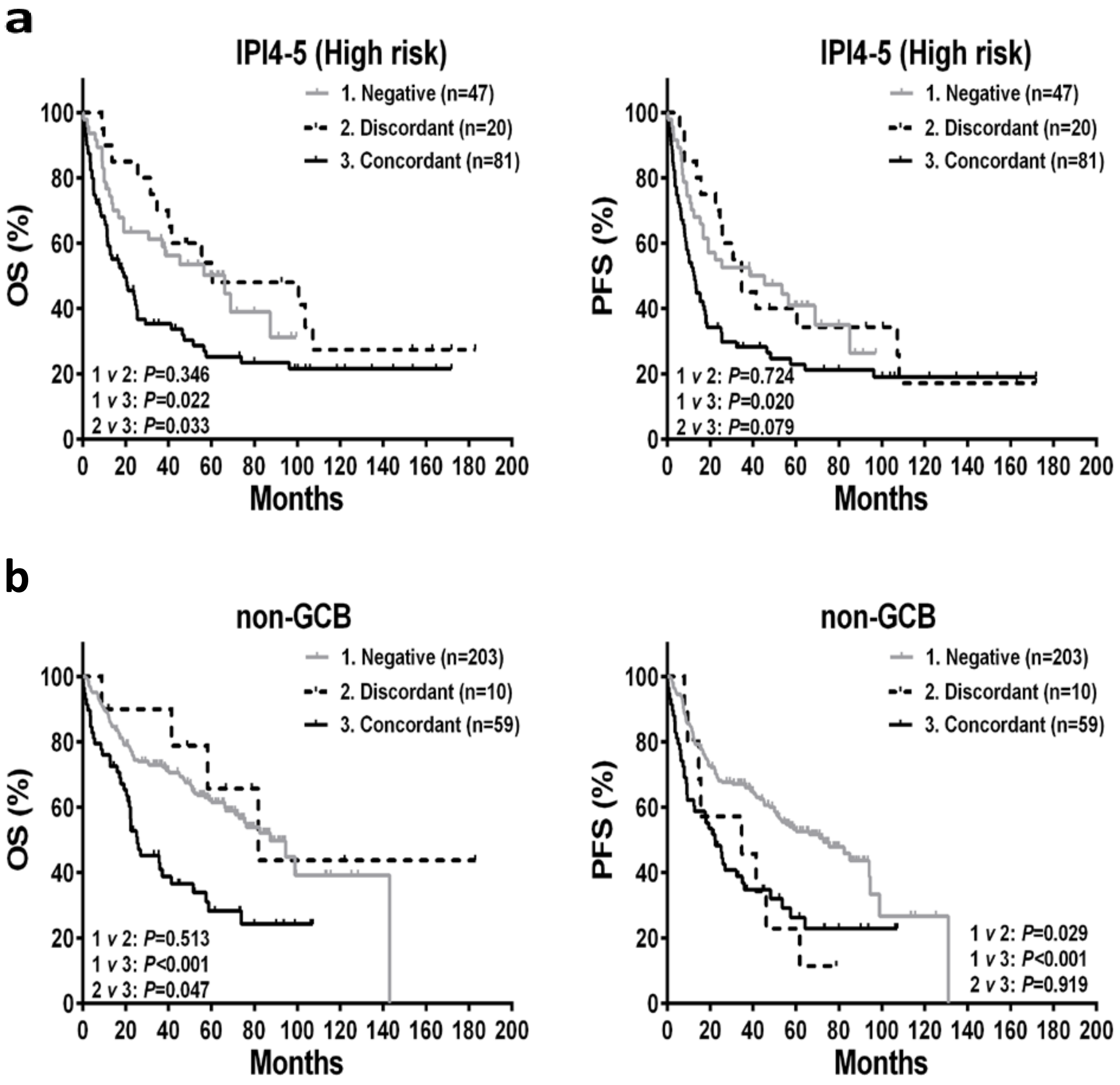

a
IPI4-5 (High risk)
1. Negative (n=47)
2. Discordant (n=20)
3. Concordant (n=81)
OS (%)
1 v 2: P=0.346
1 v 3: P=0.022
2 v 3: P=0.033
Months
IPI4-5 (High risk)
1. Negative (n=47)
2. Discordant (n=20)
3. Concordant (n=81)
PFS (%)
1 v 2: P=0.724
1 v 3: P=0.020
2 v 3: P=0.079
Months
b
non-GCB
1. Negative (n=203)
2. Discordant (n=10)
3. Concordant (n=59)
OS (%)
1 v 2: P=0.513
1 v 3: P<0.001
2 v 3: P=0.047
Months
non-GCB
1. Negative (n=203)
2. Discordant (n=10)
3. Concordant (n=59)
PFS (%)
1 v 2: P=0.029
1 v 3: P<0.001
2 v 3: P=0.919
Months
0
20
40
60
80
100
0
20
40
60
80
100
120
140
160
180
200

Figure S2

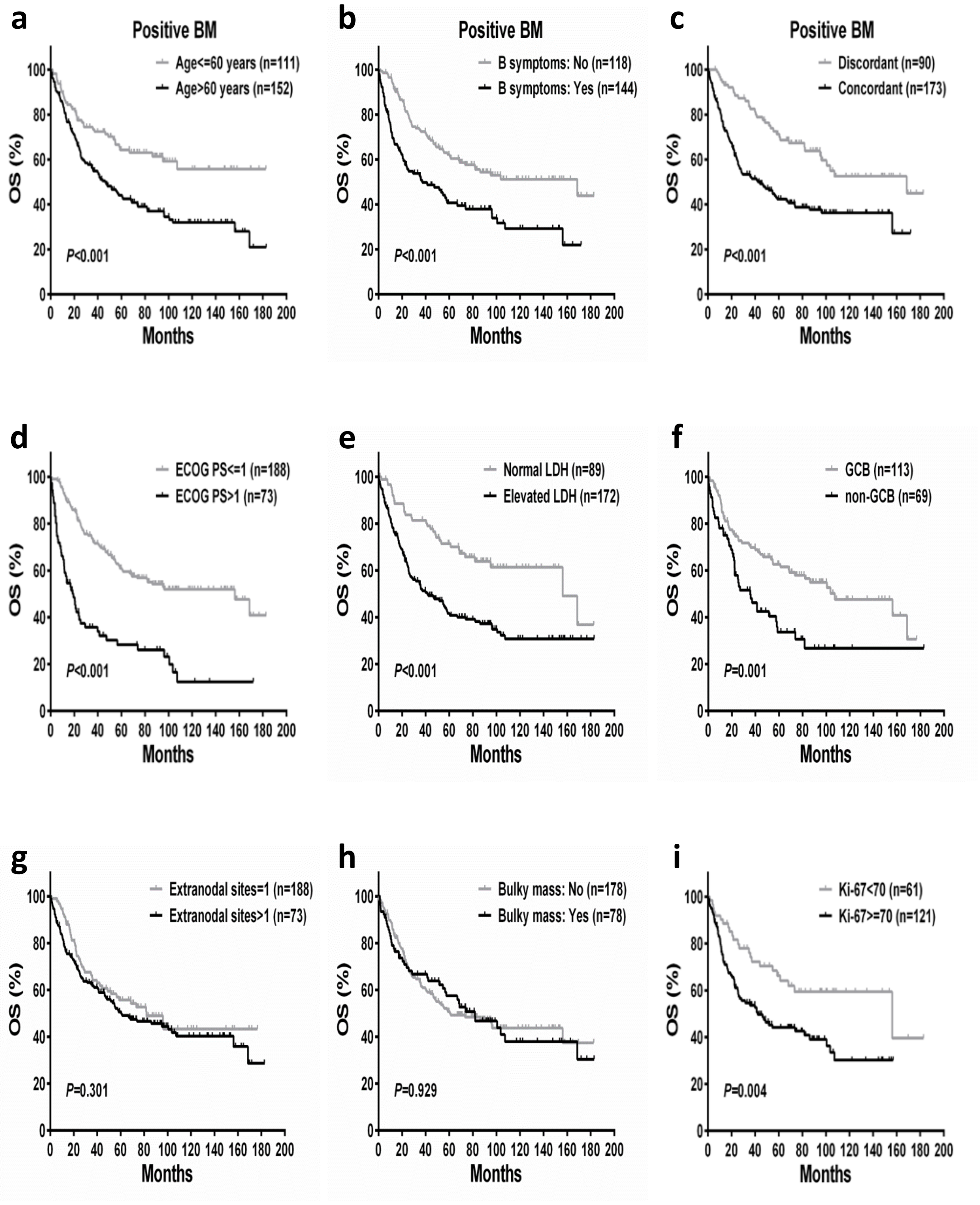
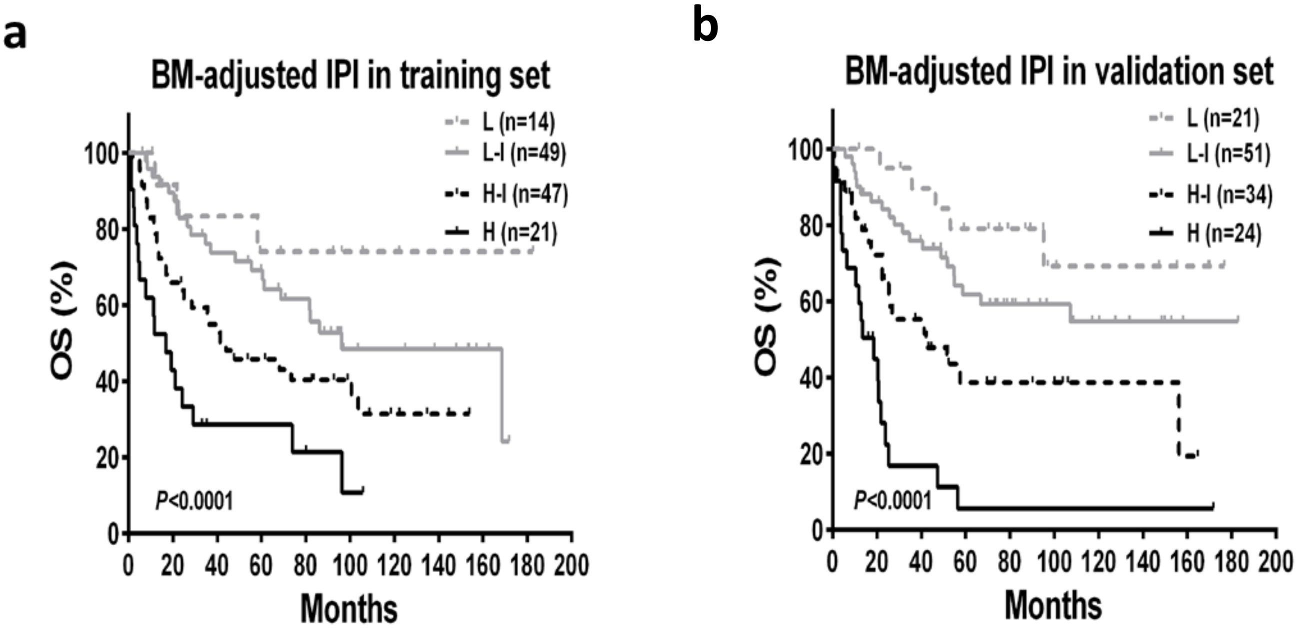

a
Positive BM
Age<=60 years (n=111)
Age>60 years (n=152)
P<0.001
b
Positive BM
B symptoms: No (n=118)
B symptoms: Yes (n=144)
P<0.001
c
Positive BM
Discordant (n=90)
Concordant (n=173)
P<0.001
d
ECOG PS<=1 (n=188)
ECOG PS>1 (n=73)
P<0.001
e
Normal LDH (n=89)
Elevated LDH (n=172)
P<0.001
f
GCB (n=113)
non-GCB (n=69)
P=0.001
g
Extranodal sites=1 (n=188)
Extranodal sites>1 (n=73)
P=0.301
h
Bulky mass: No (n=178)
Bulky mass: Yes (n=78)
P=0.929
i
Ki-67<70 (n=61)
Ki-67>=70 (n=121)
P=0.004
OS (%)
0
20
40
60
80
100
Months
0
20
40
60
80
100
120
140
160
180
200

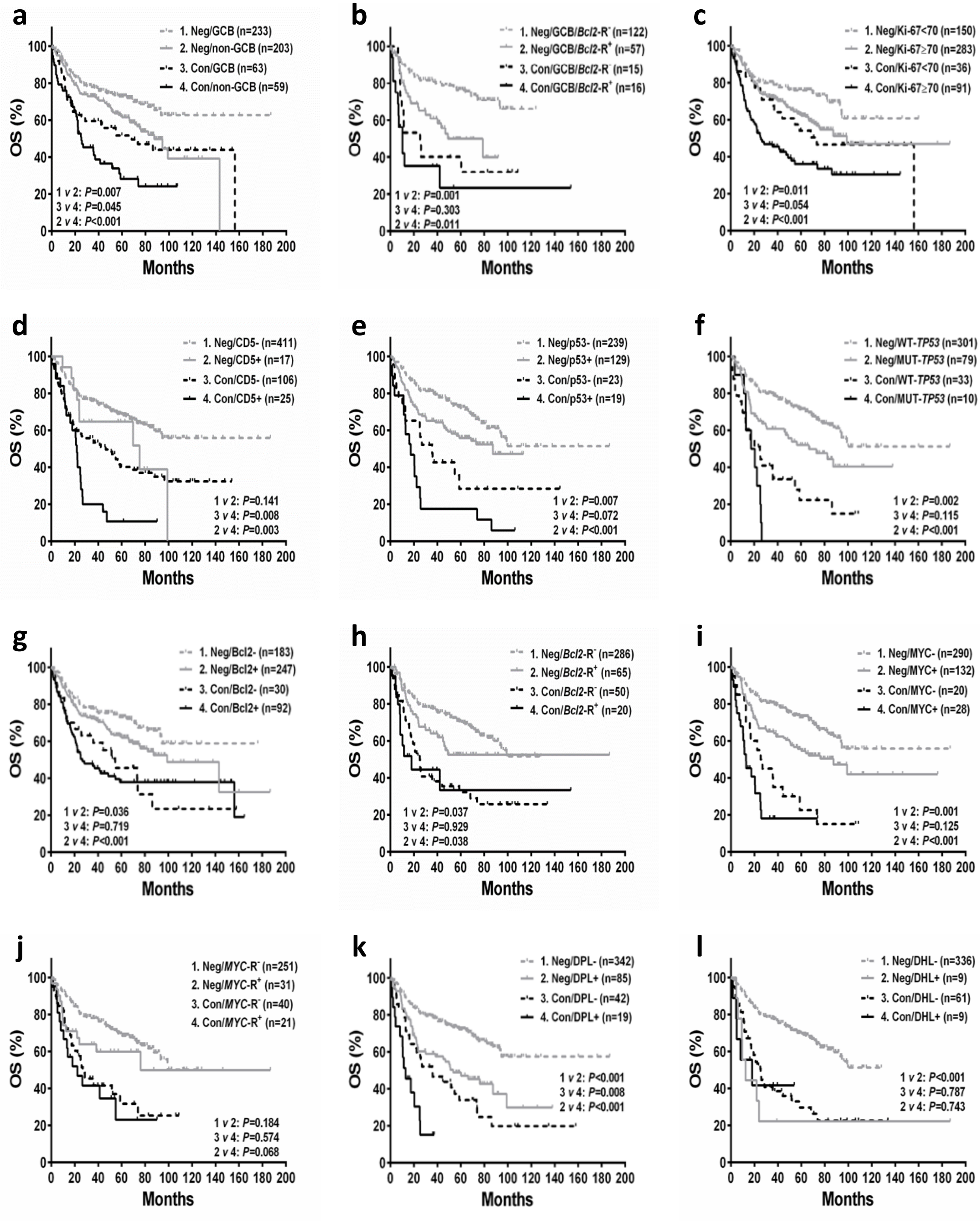
Figure S3



BM-adjusted IPI in training set

BM-adjusted IPI in validation set

Figure S4


a
1. Neg/GCB (n=233)
2. Neg/non-GCB (n=203)
3. Con/GCB (n=63)
4. Con/non-GCB (n=59)
1 v 2: P=0.007
3 v 4: P=0.045
2 v 4: P<0.001
b
1. Neg/GCB/Bcl2-R- (n=122)
2. Neg/GCB/Bcl2-R+ (n=57)
3. Con/GCB/Bcl2-R- (n=15)
4. Con/GCB/Bcl2-R+ (n=16)
1 v 2: P=0.001
3 v 4: P=0.303
2 v 4: P=0.011
c
1. Neg/Ki-67<70 (n=150)
2. Neg/Ki-67≥70 (n=283)
3. Con/Ki-67<70 (n=36)
4. Con/Ki-67≥70 (n=91)
1 v 2: P=0.011
3 v 4: P=0.054
2 v 4: P<0.001
d
1. Neg/CD5- (n=411)
2. Neg/CD5+ (n=17)
3. Con/CD5- (n=106)
4. Con/CD5+ (n=25)
1 v 2: P=0.141
3 v 4: P=0.008
2 v 4: P=0.003
e
1. Neg/p53- (n=239)
2. Neg/p53+ (n=129)
3. Con/p53- (n=23)
4. Con/p53+ (n=19)
1 v 2: P=0.007
3 v 4: P=0.072
2 v 4: P<0.001
f
1. Neg/WT-TP53 (n=301)
2. Neg/MUT-TP53 (n=79)
3. Con/WT-TP53 (n=33)
4. Con/MUT-TP53 (n=10)
1 v 2: P=0.002
3 v 4: P=0.115
2 v 4: P<0.001
g
1. Neg/Bcl2- (n=183)
2. Neg/Bcl2+ (n=247)
3. Con/Bcl2- (n=30)
4. Con/Bcl2+ (n=92)
1 v 2: P=0.036
3 v 4: P=0.719
2 v 4: P<0.001
h
1. Neg/Bcl2-R- (n=286)
2. Neg/Bcl2-R+ (n=65)
3. Con/Bcl2-R- (n=50)
4. Con/Bcl2-R+ (n=20)
1 v 2: P=0.037
3 v 4: P=0.929
2 v 4: P=0.038
i
1. Neg/MYC- (n=290)
2. Neg/MYC+ (n=132)
3. Con/MYC- (n=20)
4. Con/MYC+ (n=28)
1 v 2: P=0.001
3 v 4: P=0.125
2 v 4: P<0.001
j
1. Neg/MYC-R- (n=251)
2. Neg/MYC-R+ (n=31)
3. Con/MYC-R- (n=40)
4. Con/MYC-R+ (n=21)
1 v 2: P=0.184
3 v 4: P=0.574
2 v 4: P=0.068
k
1. Neg/DPL- (n=342)
2. Neg/DPL+ (n=85)
3. Con/DPL- (n=42)
4. Con/DPL+ (n=19)
1 v 2: P<0.001
3 v 4: P=0.008
2 v 4: P<0.001
l
1. Neg/DHL- (n=336)
2. Neg/DHL+ (n=9)
3. Con/DHL- (n=61)
4. Con/DHL+ (n=9)
1 v 2: P<0.001
3 v 4: P=0.787
2 v 4: P=0.743
OS (%)
0
20
40
60
80
100
Months
0 20 40 60 80 100 120 140 160 180 200