Supporting Information

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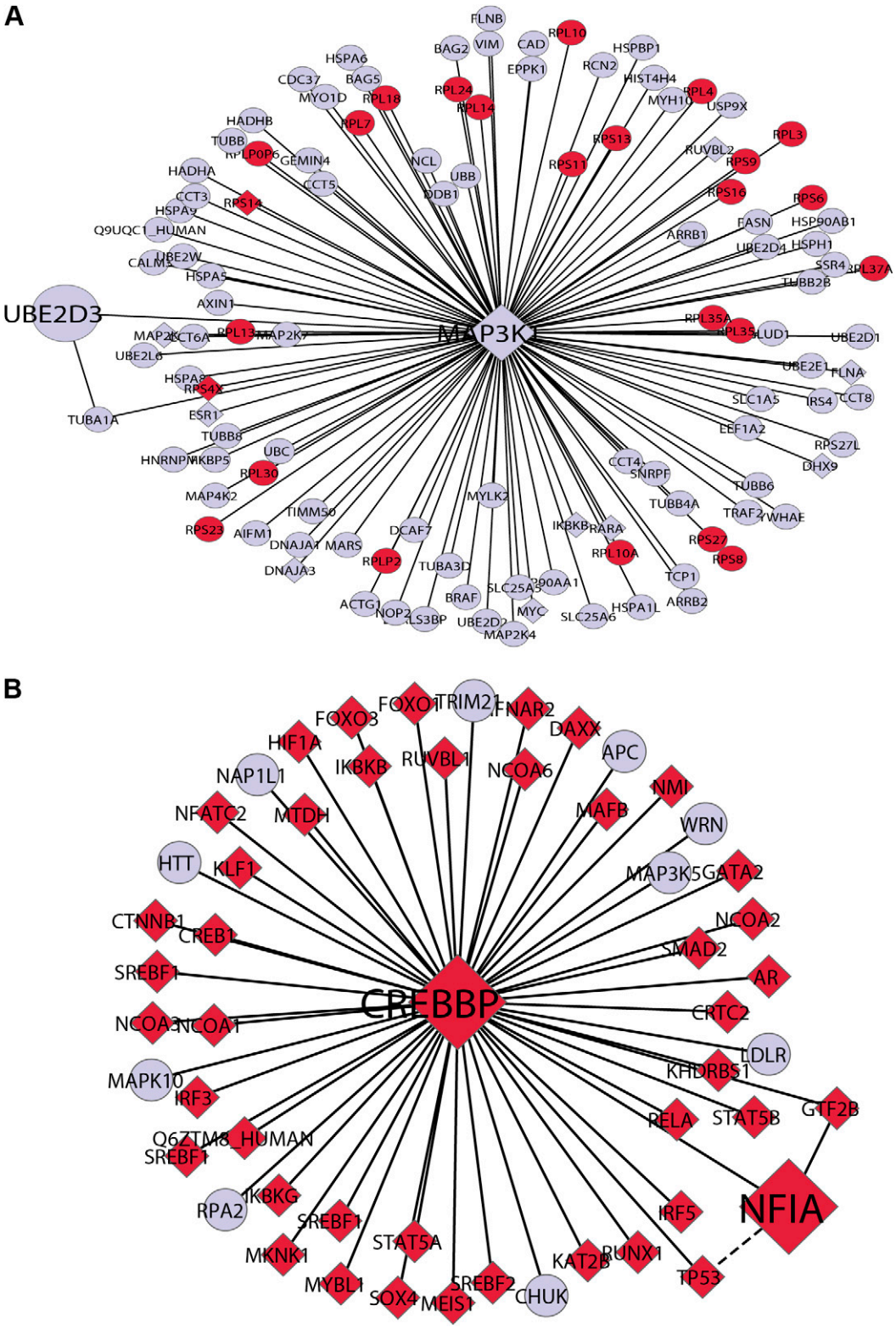

Fig. S1. Local protein interaction networks for the human orthologs of top-ranked CIS genes (*A*) MAP3K1 and (*B*) CREBBP.

Table S1. List of 77 CIS identified in *SB*-induced MB

CIS	Chromosome	No. of tumors with CIS*	Unique insertion sites†	GKC *P* value adjusted by chromosome	Entrez Gene ID
Crebbp	16	21	25	$<1.00 \times 10^{-9}$	12914
Gm10801	2	17	10	$<1.00 \times 10^{-9}$	—
Map3k1	13	9	18	$<1.00 \times 10^{-9}$	26401
Nfia	4	22	31	1.26×10^{-9}	18027
Zdhhc9	X	2	9	2.68×10^{-8}	208884
Tspan7	X	9	11	8.75×10^{-5}	21912
CIS1:49971756	1	5	10	0.0002	—
Mirg	12	2	10	0.0007	100040724
Adk	14	17	41	0.0009	54169
Tjp1	7	14	20	0.0017	21872
Slc7a14	3	8	12	0.0029	241919
Fam117b	1	6	8	0.0033	72750
Ubr5	15	13	31	0.0037	70790
CIS3:112660566	3	6	8	0.0046	—
Dgki	6	4	8	0.0050	320127
CISY:1712661	Y	3	4	0.0063	—
Cdkn2a	4	7	7	0.0067	12578
CIS13:87242495	13	34	66	0.0069	—
Zfp521	18	9	9	0.0073	225207
Pten	19	10	10	0.0083	19211
Uchl1	5	30	41	0.0084	22223
U7	13	12	16	0.0091	—
CIS13:82919990	13	8	15	0.0094	—
Gm14481	X	3	9	0.0098	—
Rims1	1	15	23	0.0105	116837
Ube2d3	3	2	6	0.0110	66105
Zfp148	16	17	17	0.0124	22661
Auts2	5	11	14	0.0129	319974
Fbxo41	6	16	19	0.0131	330369
Rap1gds1	3	21	25	0.0133	229877
Trim33	3	10	11	0.0139	94093
Nr6a1	2	5	7	0.0145	14536
Nfix	8	18	19	0.0154	18032
Pcsk2	2	11	12	0.0157	18549
Ptn	6	6	10	0.0185	19242
Edil3	13	36	85	0.0190	13612
Dyrk1a	16	10	12	0.0192	13548
Dcaf12	4	11	12	0.0197	68970
Nrg3	14	19	26	0.0216	18183
Srgap2	1	12	13	0.0226	14270
CIS18:79544777	18	1	9	0.0231	—
Atp9b	18	15	19	0.0233	50771
Arhgap5	12	11	12	0.0244	11855
CIS13:88276844	13	14	27	0.0248	—
Kdm6a	X	10	13	0.0250	22289
Wac	18	10	11	0.0262	225131
Vsnl1	12	11	16	0.0264	26950
3110070M22Rik	13	6	7	0.0267	67304
Zbtb20	16	11	13	0.0271	56490
Fut9	4	12	18	0.0280	14348
CIS8:59405464	8	4	8	0.0282	—
CIS14:109712676	14	1	7	0.0291	—
Setbp1	18	7	7	0.0297	240427
5033411D12Rik	13	29	79	0.0300	192136
Zfp644	5	13	13	0.0303	52397
Dennd4b	3	9	11	0.0308	229541
U6	16	5	10	0.0315	—
Cdh12	15	12	22	0.0316	215654
Dph3b-ps	13	15	28	0.0320	620949
Zeb1	18	18	21	0.0328	21417
CT010465.1	13	22	44	0.0341	—
Brd4	17	8	10	0.0341	57261

Table S1. Cont.

CIS	Chromosome	No. of tumors with CIS*	Unique insertion sites†	GKC *P* value adjusted by chromosome	Entrez Gene ID
Magi1	6	12	15	0.0350	14924
U6	6	31	41	0.0369	—
Gm14575	X	33	48	0.0371	100416098
Rab3c	13	15	34	0.0381	67295
Kdm1a	4	8	9	0.0389	99982
Cux1	5	15	18	0.0395	13047
Akap6	12	13	14	0.0401	238161
AC134596.1	12	12	17	0.0442	—
Lrrc68	7	6	6	0.0445	232947
Grlf1	7	8	8	0.0448	232906
Add3	19	8	8	0.0450	27360
Plcxd3	15	8	16	0.0453	239318
Arid1b	17	12	14	0.0456	239985
Ppp2r5e	12	7	7	0.0461	26932
U4	13	10	19	0.0483	—

*Number of independent tumors with insertion within the locus.
†Number of nonredundant *SB* insertions within the locus.

Table S2. Human orthologs of CIS-derived candidate genes

Mouse gene	Human Uniprot ID	Mouse gene	Human Uniprot ID
Add3	ADDG_HUMAN	Nr6a1	NR6A1_HUMAN
Akap6	AKAP6_HUMAN	Nrg3	NRG3_HUMAN
Arhgap5	RHG05_HUMAN	Pcsk2	NEC2_HUMAN
Arid1b	ARI1B_HUMAN	Plcxd3	PLCX3_HUMAN
Atp9b	ATP9B_HUMAN	Ppp2r5e	2A5E_HUMAN
Auts2	AUTS2_HUMAN	Pten	PTEN_HUMAN
Brd4	BRD4_HUMAN	Ptn	PTN_HUMAN
Cdh12	CAD12_HUMAN	Rab3c	RAB3C_HUMAN
Cdkn2a	CD2A1_HUMAN	Rap1gds1	GDS1_HUMAN
Crebbp	CBP_HUMAN	Rims1	RIMS1_HUMAN
Cux1	CUX1_HUMAN	Setbp1	SETBP_HUMAN
Dcaf12	DCA12_HUMAN	Slc7a14	S7A14_HUMAN
Dennd4b	DEN4B_HUMAN	Srgap2	SRGP2_HUMAN
Dgki	DGKI_HUMAN	Tjp1	ZO1_HUMAN
Dyrk1a	DYR1A_HUMAN	Trim33	TRI33_HUMAN
Edil3	EDIL3_HUMAN	Tspan7	TSN7_HUMAN
Fam117b	F117B_HUMAN	Ube2d3	UB2D3_HUMAN
Fbxo41	FBX41_HUMAN	Ubr5	UBR5_HUMAN
Fut9	FUT9_HUMAN	Uchl1	UCHL1_HUMAN
Kdm1a	KDM1A_HUMAN	Vsnl1	VISL1_HUMAN
Kdm6a	KDM6A_HUMAN	Wac	WAC_HUMAN
Magi1	MAGI1_HUMAN	Zbtb20	ZBT20_HUMAN
Map3k1	M3K1_HUMAN	Zdhhc9	ZDHC9_HUMAN
Nfia	NFIA_HUMAN	Zeb1	ZEB1_HUMAN
Nfix	NFIX_HUMAN		

Table S3. Rand Index results for clustering human MB molecular subtypes based on expression data in GSE21140

Clustering method	CCG	CCG + PCA (5)	CCG + network + PCA (9)	Pei signature
Average linkage	0.499	0.627	0.569	0.681
Ward	0.461	0.469	0.685	0.699
K-means	0.492	0.502	0.661	0.724
Ward + Sil	0.526	0.465	0.497	0.699
K-means + Sil	0.404	0.366	0.475	0.724

CCG, CIS candidate genes; PCA, principal component analysis. Numbers in parentheses represent the number of principal components.