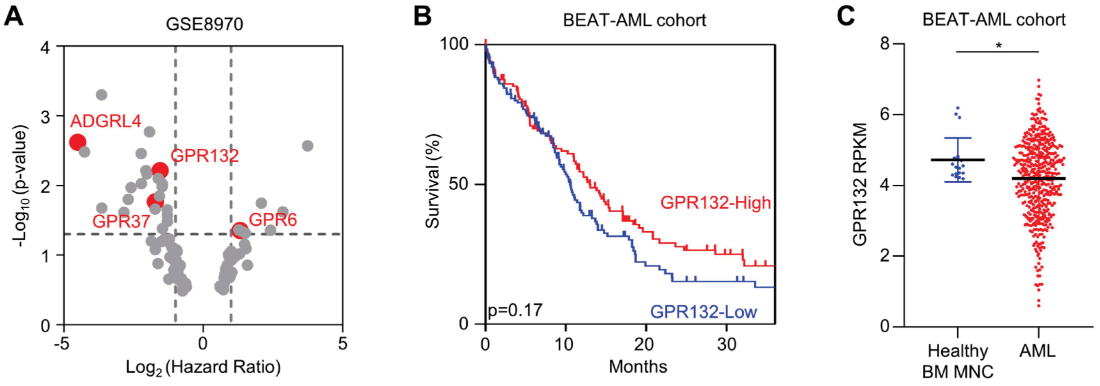
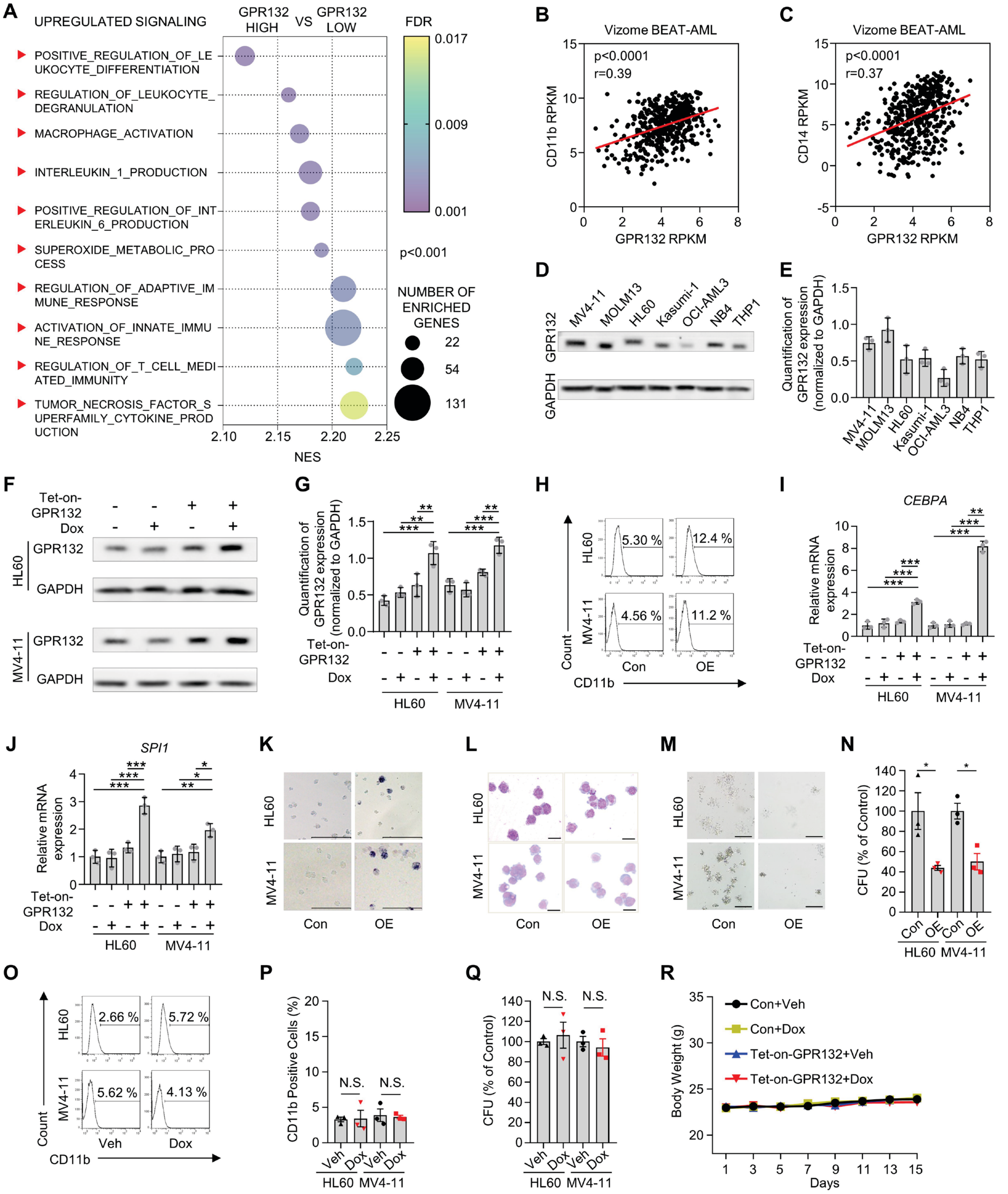


Supplementary figure 1: related to Figure 1

(A) Volcano plot depicting hazard ratios (High versus low expressing group) and p-values of orphan GPCRs in AML patients. Data was obtained from GEO database: GSE8970.

(B) Kaplan-Meier plot for AML patients in the BEAT-AML cohort, stratified by median *GPR132* expression (n=138 for High group, n=138 for Low group).

(C) Dot plot depicting *GPR132* expression in AML blasts (n=451) and healthy bone-marrow mononuclear cells (n=19). Data was obtained from the BEAT-AML dataset. Student’s t-tests were performed, *P < 0.05. BM MNC, bone-marrow mononuclear cell.



Supplementary figure 2: related to Figure 2

(A) Gene Set Enrichment Analysis of TCGA-LAML dataset comparing *GPR132* HIGH and *GPR132* LOW. Scattergrams of gene sets upregulated in *GPR132* HIGH and gene set enrichment plots were shown.

(B-C) Gene expression correlation between *GPR132* and *CD11b* (B) or *CD14* (C) in AML (BEAT-

AML dataset). Two-sided Pearson’s correlation analysis was performed.

(D-E) Western blotting (D) and corresponding quantification (E) of GPR132 expression in a panel of AML cell lines. Three independent experiments were performed. Data were shown as mean ± SD (n=3).

(F-G) Western blotting (F) and corresponding quantification (G) of GPR132 expression in Tet-On AML cells. HL60 and MV4-11 cells were treated with or without doxycycline (1 μg/mL) for 48 h. *GPR132* Tet-On AML cells were established by stably transfecting with the Tet-On expression vector for inducible *GPR132* overexpression. Three independent experiments were performed. Data were shown as mean ± SD (n=3). One-way analysis of variance (ANOVA) with Tukey's multiple comparison tests were performed (n = 3), **P < 0.01, ***P < 0.001.

(H) Representative flow cytometric histogram of myeloid differentiation marker CD11b expression using Tet-On AML cells (HL60 and MV4-11) with (OE) or without (Con) doxycycline treatment (1 μg/mL) for 72 h.

(I-J) Boxplots of the mRNA expression of *CEBPA* (I) and *SPI1* (J) using Tet-On AML cells (HL60 and MV4-11) with (OE) or without (Con) doxycycline treatment (1 μg/mL) for 12 h. One-way ANOVA with Tukey's multiple comparison tests were performed, *P < 0.05, **P < 0.01, ***P < 0.001.

(K) NBT reduction analysis showing formazan formation in Tet-On AML cells (HL60 and MV4-11) with (OE) or without (Con) doxycycline exposure (1 μg/mL) for 72 h. Scale bars represent 80 μm.

(L) Representative Wright–Giemsa staining images showing the mature myeloid cell morphology of Tet-On AML cells (HL60 and MV4-11) following doxycycline treatment (1 μg/mL, 72 h). Scale bars represent 20 μm.

(M) Representative images of colony formation for Tet-On AML cells. Cells were cultured in semi-solid medium and treated with 1 μg/mL doxycycline to induce GPR132 overexpression. Colonies were photographed under a microscope on day 7. Scale bars represent 400 μm.

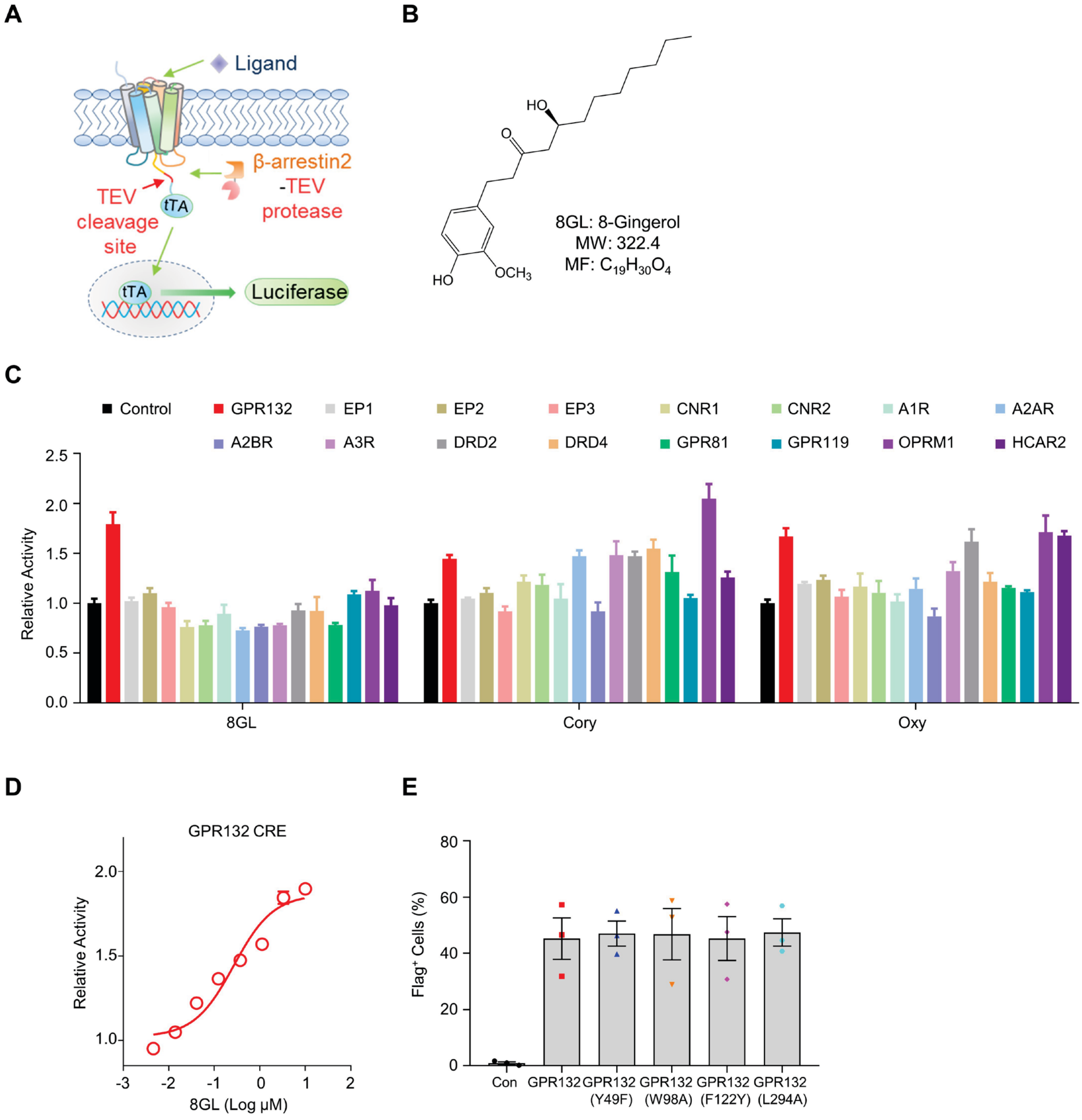
(N) Quantification of colony formation assay in Figure 2G. Data shown as mean ± SEM (n=3). Student’s t-tests were performed, *P < 0.05.

(O) Representative flow cytometric histogram of myeloid differentiation marker CD11b expression using AML cells (HL60 and MV4-11) with (OE) or without (Con) doxycycline treatment (1 μg/mL) for 72 h.

(P) Doxycycline (1 μg/mL, 48 h) do not affect CD11b expression in HL60 and MV4-11 as revealed by Flow-cytometry analysis. Data shown as mean ± SEM (n=3). Student’s t-tests were performed, N.S., non-significant.

(Q) Doxycycline (1 μg/mL) do not affect colony formation ability of AML cell lines (HL60 and MV4-11). Data shown as mean ± SEM (n=3). Student’s t-tests were performed, N.S., non-significant.

(R) Body weight of mice bearing xenografted tumor during 2-week treatment. Data shown as mean ± SEM (n=6).



Supplementary figure 3: related to Figure 3

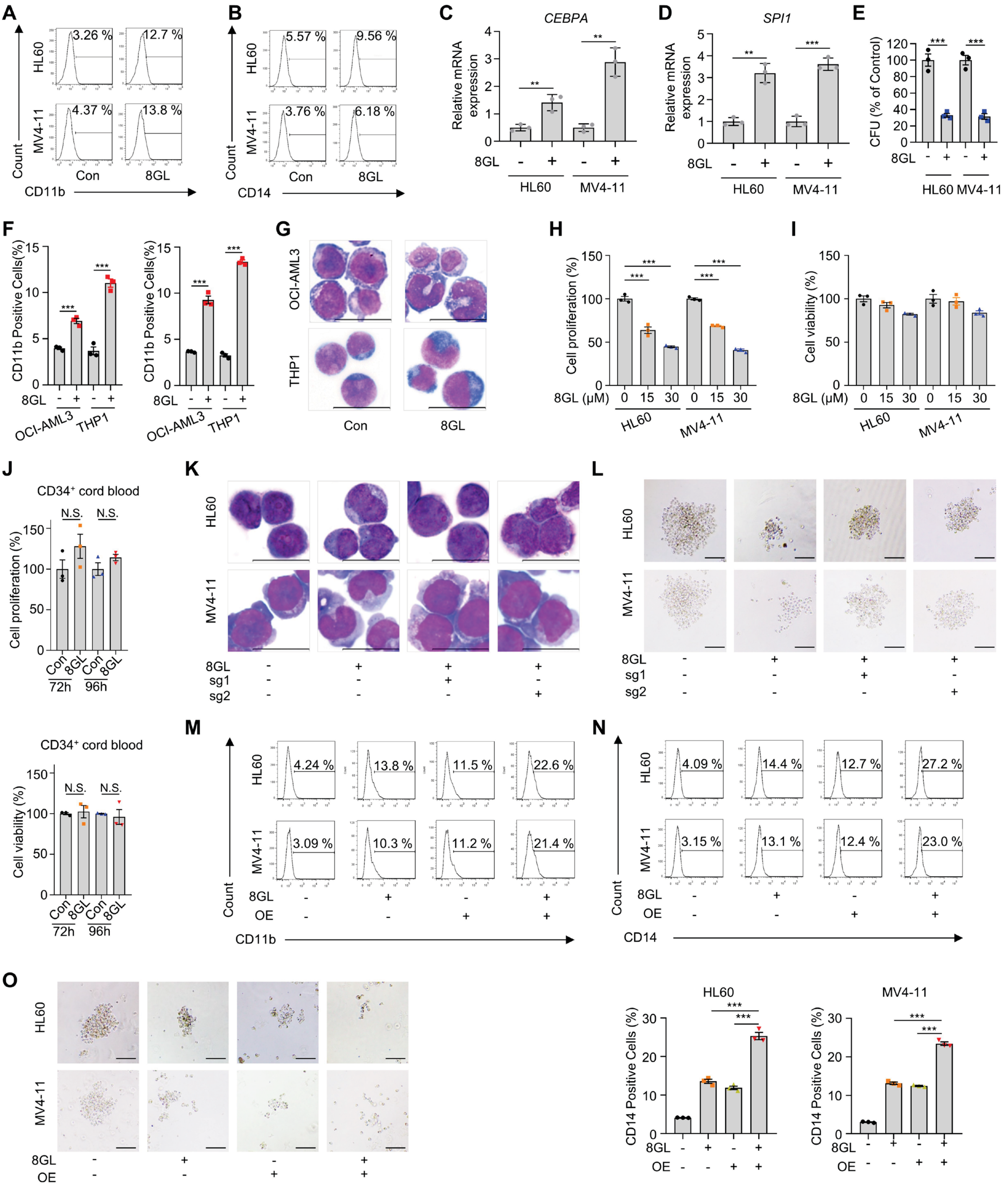
(A) Schematic illustration of the Tango assay. Ligand binding to the target receptor stimulates recruitment of the β-arrestin2-TEV protease fusion, triggering release of the tethered transcription factor tTA. The free tTA enters the nucleus and initiates expression of a reporter gene.

(B) Chemical structure of 8-Gingerol (8GL).

(C) Agonistic activity of 8-Gingerol (8GL), oxyresveratrol (Oxy) and corynoline (Cory) for GPCRs in Tango assay. Data was shown as mean ± SEM (n = 3).

(D) Dose-response curve of 8GL for GPR132 activation (EC50 = 0.44 μM) in CRE reporter-gene assays. Data are shown as means ± SEM (n=3).

(E) Flow-cytometry analysis of cell-surface expression of Flag-GPR132 (with or without mutation). CHO cells were transfected with Flag-GPR132 plasmids, and anti-Flag was used to determine cell-surface level of GPR132 after 24 h. Data was shown as mean ± SEM (n = 3).



Supplementary figure 4: related to Figure 4

(A-B) Representative flow cytometric histogram of the expression of cell surface markers CD11b (A) and CD14 (B) in HL60 and MV4-11 cells 72 h after 8GL treatment (30 μM).

(C-D) Boxplots of the mRNA expression of *CEBPA* (C) and *SPI1* (D) in AML cells (HL60 and MV4-11) treated with or without 30 μM 8GL for 12 h. One-way ANOVA with Tukey's multiple comparison tests were performed, **P < 0.01, ***P < 0.001.

(E) Quantification of colony formation at Day 9 in Figure 4E. Data was shown as mean ± SEM (n = 3). Unpaired Student's t-tests were performed, ***P < 0.001.

(F-G) OCI-AML3 and THP1 were incubated with 8GL (30 μM) for 72 h and cell differentiation were determined by Flow-cytometry analysis (F) and Wright-Giemsa staining (G). Data are presented as mean ± SEM (n = 3). Unpaired Student's t-tests were performed, ***P < 0.001. Scale bars represent 20 μm.

(H-I) Boxplots of proliferation (H) and viability (I) of HL60 and MV4-11 cells treated with indicated concentrations of 8GL for 72 h (n=3). One-way ANOVA with Tukey's multiple comparison tests were performed, ***P < 0.001.

(J) Cell proliferation (upper panel) and cell viability (lower panel) of $CD34^+$ human cord blood cells treated with 0 μM or 30 μM 8GL for 72 h or 96 h (n=3). Student's t-tests were performed. N.S., non-significant.

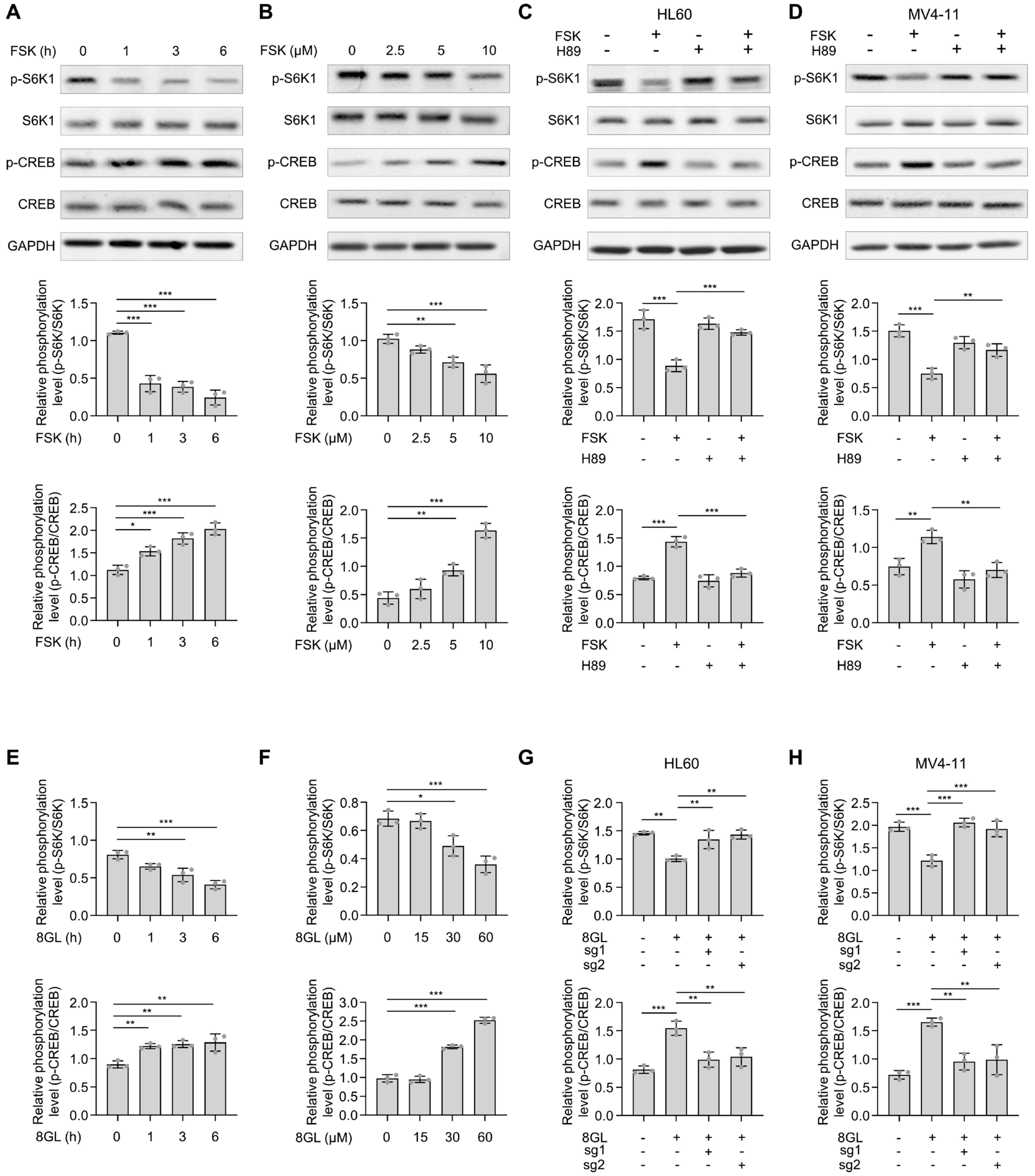
(K) Representative Wright-Giemsa staining results showing the mature myeloid cell morphology of *GPR132* wild-type (WT) and *GPR132* knockout (KO) AML cell lines. *GPR132*-WT and *GPR132*-KO cells were treated with 8GL with a concentration of 30 μM for 72 h. Scale bars represent 20 μm. Sg1 and sg2 represent two distinct sgRNAs for *GPR132*.

(L) Representative colony formation images of *GPR132*-WT and *GPR132*-KO AML cell lines treated with or without 8GL. 8GL treatment: 15 μM for 7 days. Colonies were photographed under a microscope on day 7. Scale bars represent 100 μm. Sg1 and sg2 represent two distinct sgRNAs targeting on *GPR132*.

(M) Representative flow cytometric histogram of the expression of cell surface markers CD11b in Tet-On AML cells treated with or without 8GL (30 μM for 72 h) in the presence or absence of doxycycline (1 μg/mL).

(N) Representative flow cytometric histogram (upper panel) and quantification (lower panel) of the expression of cell surface markers CD14 in Tet-On AML cells treated with or without 8GL (30 μM for 72 h) in the presence or absence of doxycycline (1 μg/mL). One-way ANOVA with Tukey's multiple comparison tests were performed (n = 3), ***P < 0.001.

(O) Representative colony formation images of Tet-On AML cells incubated with or without 8GL (15 μM for 7 days) in the presence or absence of doxycycline (1 μg/mL). Colonies were photographed under a microscope on day 7. Scale bars represent 100 μm.



Supplementary figure 5: related to Figure 5

(A) Western blotting (upper panel) and corresponding quantification (middle and lower panel) of p-S6K1 (Thr389) and p-CREB (Ser133) in HL60 cells treated with 10 μM FSK. Three independent experiments were performed. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05, ***P < 0.001.

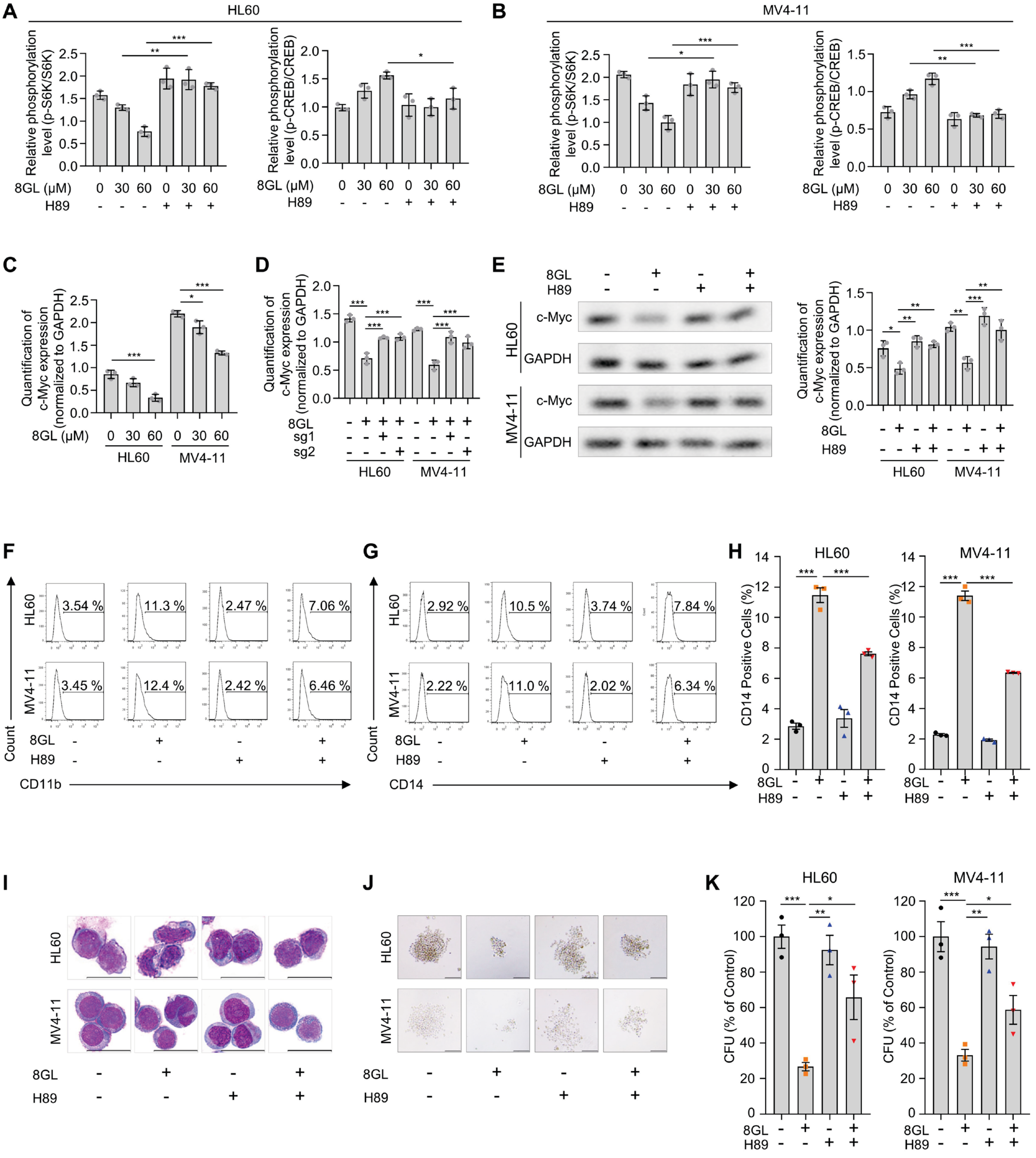
(B) Western blotting (upper panel) and corresponding quantification (middle and lower panel) of p-S6K1 (Thr389) and p-CREB (Ser133) in HL60 cells treated with indicating concentrations of FSK for 3 h. Three independent experiments were performed. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05, **P<0.01, ***P < 0.001.

(C-D) Western blotting (upper panel) and corresponding quantification (middle and lower panel) of p-S6K1 (Thr389) and p-CREB (Ser133) in HL60 cells (C) and MV4-11 cells (D) treated with 10 μM FSK and/or 1 μM FSK for 3 h. Three independent experiments were performed. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05, **P<0.01, ***P < 0.001.

(E) Quantification of western blotting of p-S6K1 (Thr389, upper panel) and p-CREB (Ser133, lower panel) in HL60 cells treated with 8GL (30 μM) for indicated times. Three independent experiments were performed. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05, **P<0.01, ***P < 0.001.

(F) Quantification of western blotting of p-S6K1 (Thr389, upper panel) and p-CREB (Ser133, lower panel) in HL60 cells treated with 8GL for indicated concentrations. Three independent experiments were performed. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05, **P<0.01, ***P < 0.001.

(G-H) Quantification of western blotting of p-S6K1 (Thr389, upper panel) and p-CREB (Ser133, lower panel) in 8GL-treated *GPR132* WT and *GPR132* KO HL60 cells (G) and MV4-11 cells (H). 8GL treatment: 30 μM for 3 h. Sg1 and sg2 represent two distinct sgRNAs targeting on *GPR132*. Three independent experiments were performed. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05, **P<0.01, ***P < 0.001.



Supplementary figure 6: related to Figure 5

(A-B) Quantification of western blotting of p-S6K1 (Thr389, upper panel) and p-CREB (Ser133, lower panel) in HL60 cells (A) and MV4-11 cells (B) incubated with 8GL (0 μM, 30 μM or 60 μM) and/or H89 (1 μM). Three independent experiments were performed. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05,

**P<0.01, ***P < 0.001.

(C) Quantification of western blotting of c-Myc in HL60 cells and MV4-11 cells incubated with 8GL (0 μM, 30 μM or 60 μM) for 48 h. Three independent experiments were performed. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05, **P<0.01, ***P < 0.001.

(D) Quantification of western blotting of c-Myc in *GPR132* WT and *GPR132* KO HL60 cells and MV4-11 cells incubated with 8GL (0 μM, 30 μM) for 48 h. Three independent experiments were performed. Sg1 and sg2 represent two distinct sgRNAs targeting on *GPR132*. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05, **P<0.01, ***P < 0.001.

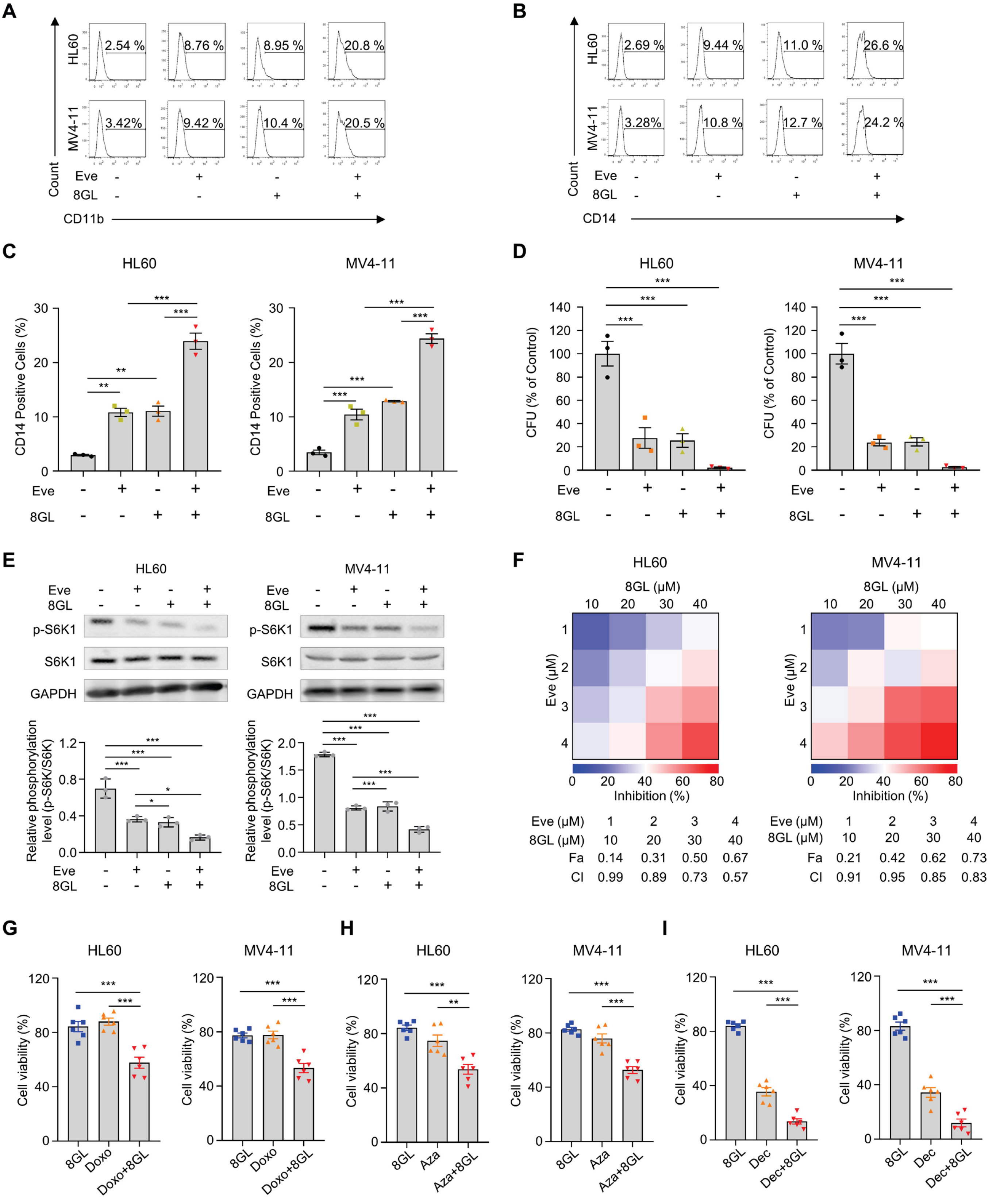
(E) Western blotting (left panel) and corresponding quantification (right panel) of c-Myc expression in 8GL (30 μM) and/or H89 (1 μM) treated HL60 cells and MV4-11 cells (48 h). Three independent experiments were performed. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05, **P<0.01, ***P < 0.001.

(F) Representative flow cytometric histogram of the expression of cell surface markers CD11b in AML cells treated with or without 30 μM 8GL and/or 1 μM H89 for 72 h.

(G-H) Representative flow cytometric histograms (G) and quantification (H) of CD14 expression in AML cells treated with or without 30 μM 8GL and/or 1 μM H89 for 72 h. Data are presented as mean ± SEM (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, ***P < 0.001.

(I) Representative Wright-Giemsa staining analysis of AML cells treated with or without 30 μM 8GL and/or 1 μM H89 for 72 h. Scale bars represent 20 μm.

(J-K) Representative colony formation images (J) and quantification (K) of HL60 and MV4-11 cells treated with or without 30 μM 8GL and/or 1 μM H89 for 7 Day. Scale bars represent 100 μm. Right: quantification of colony formation. Data are shown as mean ± SD (n = 3). Unpaired Student’s t-tests were performed, *P < 0.05, **P < 0.01, ***P < 0.001.



HL60

Eve (μM)	1	2	3	4
8GL (μM)	10	20	30	40
Fa	0.14	0.31	0.50	0.67
CI	0.99	0.89	0.73	0.57

MV4-11

Eve (μM)	1	2	3	4
8GL (μM)	10	20	30	40
Fa	0.21	0.42	0.62	0.73
CI	0.91	0.95	0.85	0.83

Supplementary figure 7: related to Figure 6

(A) Representative flow cytometric histograms of CD11b expression in AML cells treated with vehicle, 30 μM 8GL, 3 μM everolimus (Eve), or drug combination for 72 h.

(B-C) Representative flow cytometric histograms (B) and quantification (C) of CD14 expression in

HL60 and MV4-11 cells treated with vehicle, 8GL (30 μM) and/or Eve (3 μM) for 72 h. Data are presented as mean ± SEM (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, ***P < 0.001.

(D) Quantification of colony formation in Figure 6D. Data are shown as mean ± SEM (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, ***P < 0.001.

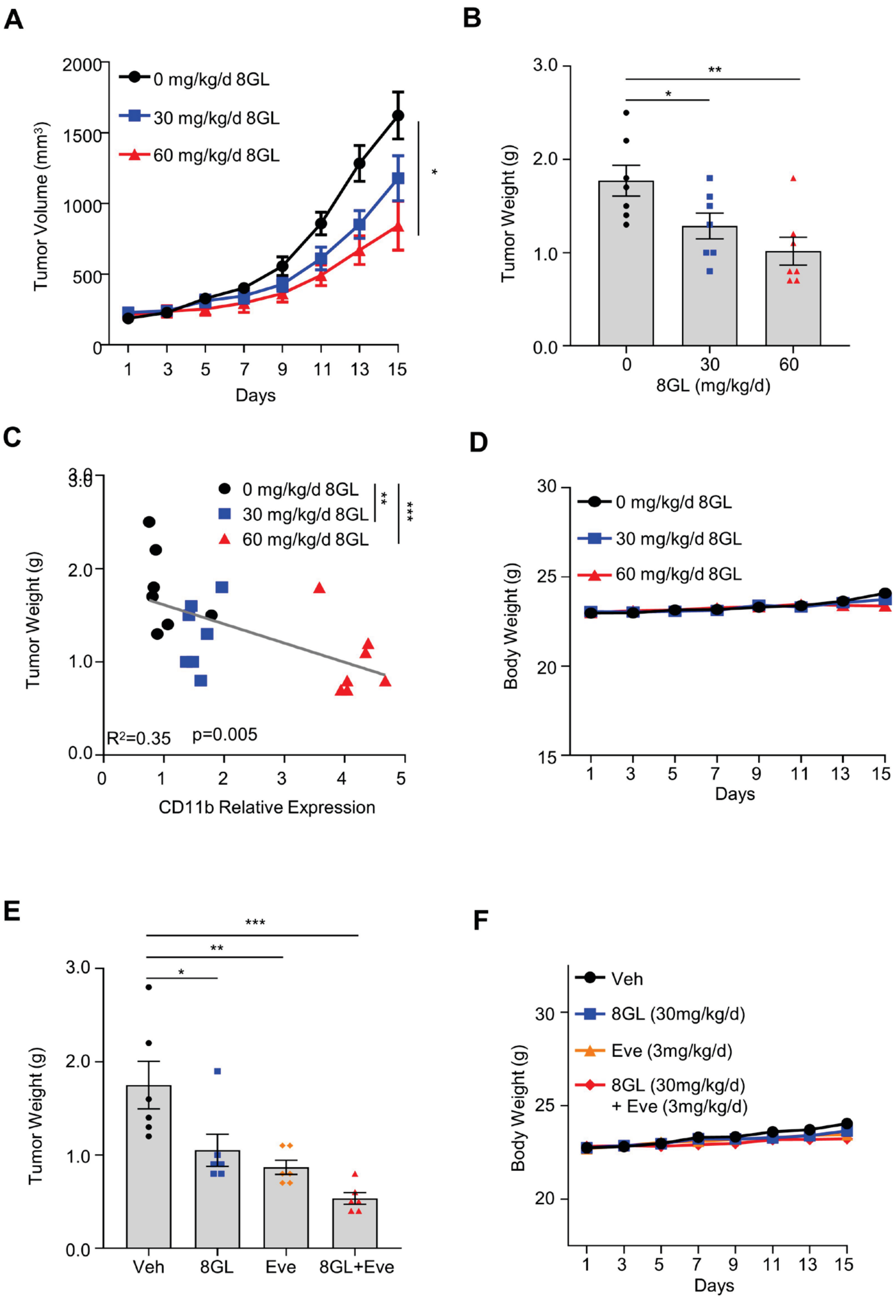
(E) Western blotting (upper panel) and corresponding quantification (lower panel) of p-S6K1 (Thr389) in HL60 cells and MV4-11 cells treated with vehicle, 8GL (30 μM) and/or Eve (3 μM). Three independent experiments were performed. Data are shown as mean ± SD (n = 3). One-way ANOVA with Tukey's multiple comparison tests were performed, *P<0.05, **P<0.01, ***P < 0.001.

(F) Heat map showing inhibition rate of combination between 8GL and Eve. Combination index (CI) were determined by CalcuSyn software (Version 2.1; Biosoft). CI value <1 indicates synergistic. HL60 and MV4-11 cells were treated with the indicated concentrations of 8GL, Eve, or 8GL plus Eve for 72 h and proliferation inhibition was measured using the MTS cell proliferation colorimetric Assay Kit.

(G) HL60 (left panel) and MV4-11 (right panel) cells were incubated with indicated single drug (8GL, 30 μM; doxorubicin, 0.05 μM) or their combination for 72 h, and cell viability was determined by MTS assay. Data are shown as mean ± SEM (n = 6). One-way ANOVA with Tukey's multiple comparison tests were performed, ***P < 0.001. DOXO, doxorubicin.

(H) HL60 (left panel) and MV4-11 (right panel) cells were incubated with indicated single drug (8GL, 30 μM; azacytidine, 1 μM) or their combination for 48 h, and cell viability was determined by MTS assay. Data are shown as mean ± SEM (n = 6). One-way ANOVA with Tukey's multiple comparison tests were performed, ***P < 0.001. Aza, azacytidine.

(I) HL60 (left panel) and MV4-11 (right panel) cells were incubated with indicated single drug (8GL, 30 μM; decitabine, 1 μM) or their combination for 72 h, and cell viability was determined by MTS assay. Data are shown as mean ± SEM (n = 6). One-way ANOVA with Tukey's multiple comparison tests were performed, ***P < 0.001. Dec, decitabine.



Supplementary figure 8: related to Figure 6

(A) 8GL delayed growth and promoted the differentiation of AML cells *in vivo*. HL60 cells were injected subcutaneously into the mid-right flank of female athymic nude mice. When tumor volumes reached almost 200 mm^3, the mice were treated with 8GL by intraperitoneal injection for 2 weeks. Data are presented as mean ± SEM (n = 7). One-way ANOVA with Tukey's multiple comparison tests were performed, *$P < 0.05$.

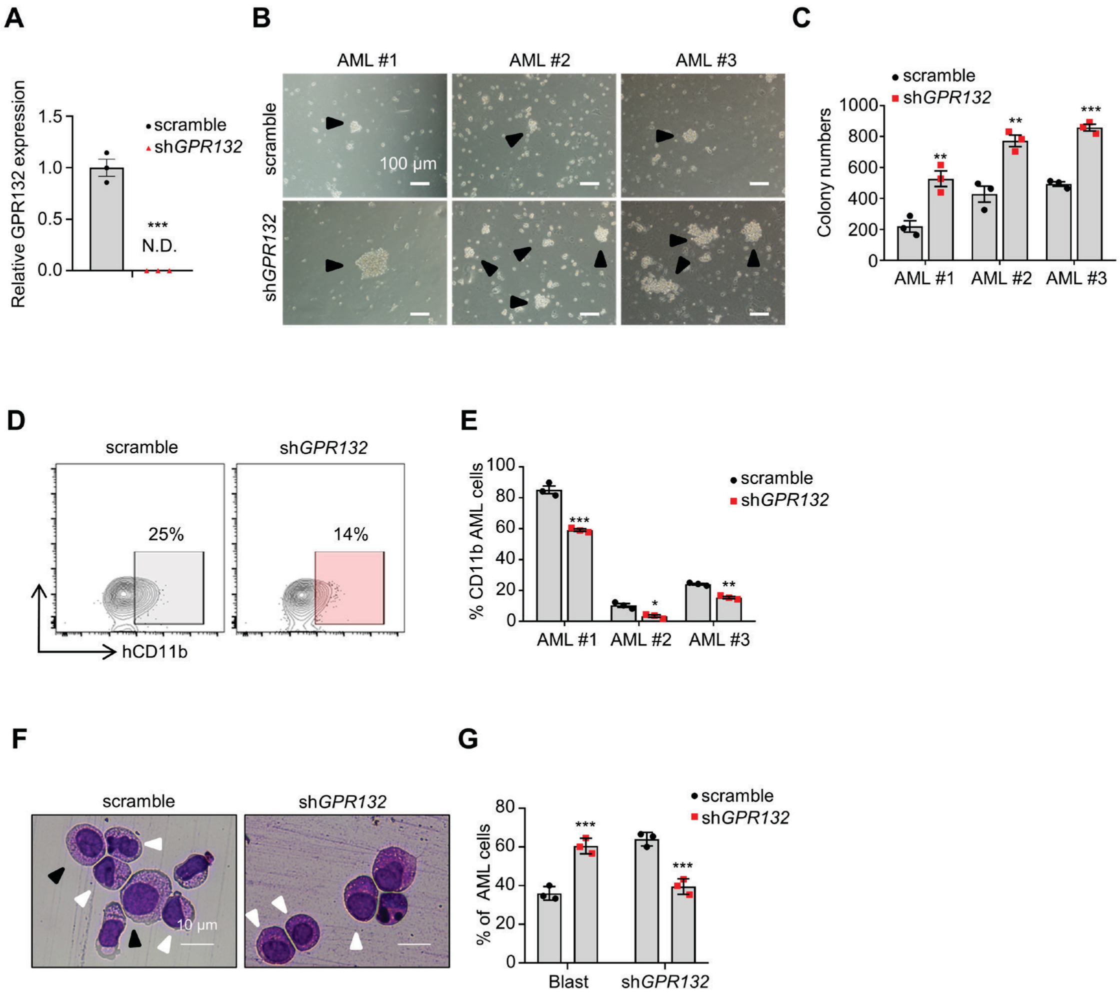
(B) Mean tumor weight of a subcutaneous HL60 xenograft model on day 15. Data are shown as mean ± SEM (n = 7). Student's t-tests were performed, *$P < 0.05$, **$P < 0.01$.

(C) Correlation analysis between tumor weight and *GPR132* expression detected using qPCR. Student's t-tests were performed (n = 6), **$P < 0.01$, ***$P < 0.001$.

(D) Body weight of HL60-xenografted mice during time in treatment. Data are shown as mean ± SEM (n = 7).

(E) Tumor weight of a subcutaneous HL60 xenograft model on day 15 treated as in Figure 6E. Data are shown as mean ± SEM (n = 6). One-way ANOVA with Tukey's multiple comparison tests were performed, *P < 0.05, **P < 0.01, ***P < 0.001.

(F) Body weight of HL60-xenografted mice during time in treatment. Data are shown as mean ± SEM (n = 6).



Supplementary figure 9: related to Figure 7

(A) Quantification of relative *GPR132* mRNA expression in U937 cells treated with sh*GPR132* or a scrambled control via quantitative RT-PCR. Data are shown as mean ± SEM (n = 3). Student's t-tests were performed, P*** < 0.001.N.D. represents not detected.

(B-C) Representative images (B) and quantitative data (C) for the colony numbers of *GPR132*-knockdown (sh*GPR132*) or control (scrambled) human primary AML cells. Data are shown as mean ± SEM (n = 3). Student's t-tests were performed, P** < 0.01, P*** < 0.001.

(D-E) Representative contour plots (D) and quantitative data (E) by flow cytometric analysis for the percentages of CD11b$^+$ cells in *GPR132*-knockdown (sh*GPR132*) or control (scrambled) human primary AML cells. Data are shown as mean ± SEM (n = 3). Student's t-tests were performed, *P<0.05, **P<0.01, ***P<0.001.

(F). Representative images of Wright-Giemsa staining of *GPR132*-knockdown (sh*GPR132*) and control (scrambled) human primary AML cells.

(G) Quantification data of the percentages of blast cells (black arrowhead) and differentiated cells (mature cells, white arrowheads) as shown in panel F. A total of 20-30 cells were counted for each section and 8-10 sections were evaluated. Data are shown as mean ± SEM ($n = 3$). Student’s t-tests were performed, P*** < 0.001.

Supplementary table 1: The list of orphan GPCRs (except olfactory receptors)

Orpha GPCRs							
Class A (Rhodopsin-like family)					Class B (Secretin/adhesion family)		Class C (Metabotropic family)
BRS3	GPR35	GPR87	GPR173	TAAR2	ADGRA1	ADGRF5	GPR156
GPR3	GPR37	GPR88	GPR174	TAAR3	ADGRA2	ADGRG1	GPR158
GPR4	GPR37L1	GPR101	GPR176	TAAR4P	ADGRA3	ADGRG2	GPR179
GPR6	GPR39	GPR119	GPR182	TAAR5	ADGRB1	ADGRG3	GPRC5A
GPR42	GPR45	GPR132	GPR183	TAAR6	ADGRB2	ADGRG4	GPRC5B
GPR12	GPR50	GPR135	LGR4	TAAR8	ADGRB3	ADGRG5	GPRC5C
GPR15	GPR52	GPR139	LGR5	TAAR9	CELSR1	ADGRG6	GPRC5D
GPR17	GPR55	GPR141	LGR6		CELSR2	ADGRG7	GPRC6A
GPR18	GPR61	GPR142	MAS1		CELSR3	ADGRL1	
GPR19	GPR62	GPR146	MAS1L		ADGRD1	ADGRL2	
GPR20	GPR63	GPR148	MRGPRD		ADGRD2	ADGRL3	
GPR21	GPR65	GPR149	MRGPRE		ADGRE1	ADGRL4	
GPR22	GPR68	GPR150	MRGPRF		ADGRE2	ADGRV1	
GPR25	GPR75	GPR151	MRGPRG		ADGRE3		
GPR26	GPR78	GPR152	MRGPRX1		ADGRE4P		
GPR27	GPR79	GPR153	MRGPRX2		ADGRE5		
GPR31	GPR82	GPR160	MRGPRX3		ADGRF1		
GPR32	GPR83	GPR161	MRGPRX4		ADGRF2		
GPR33	GPR84	GPR162	P2RY8		ADGRF3		
GPR34	GPR85	GPR171	P2RY10		ADGRF4		

Supplementary table 2: The Hazard Ratio of orphan GPCRs in AML

GSE12417-GPL570				
Gene	**Hazard Ratio (HR)**	**P-value**	**Log$_2$HR**	**- Log$_{10}$(P-value)**
LPHN3	3.1480	0.0005	1.6544	3.3010
CD97	2.5640	0.0006	1.3584	3.2218
GPR171	0.3004	0.0007	-1.7350	3.1549
GPR56	7.3060	0.0007	2.8691	3.1549
GPR114	4.7360	0.0016	2.2437	2.7959
GPCRC6A	6.7050	0.0018	2.7452	2.7447
GPR146	0.3981	0.0028	-1.3288	2.5528
P2RY10	0.4140	0.0030	-1.2723	2.5229
GPR37	0.2966	0.0035	-1.7534	2.4559
LGR6	0.4275	0.0041	-1.2260	2.3872
MAS1	0.4394	0.0054	-1.1864	2.2676
GPR123	2.2490	0.0065	1.1693	2.1871
GPR132	0.2236	0.0088	-2.1610	2.0555
GPR20	0.4588	0.0102	-1.1241	1.9914
GPR75	3.2840	0.0102	1.7155	1.9914
BAI2	0.2812	0.0157	-1.8303	1.8041
GPR32	0.4735	0.0167	-1.0786	1.7773
GPR6	2.3490	0.0194	1.2320	1.7122
LGR5	0.2596	0.0228	-1.9456	1.6421
GPR50	0.4841	0.0236	-1.0466	1.6271
ELTD1	0.4864	0.0247	-1.0398	1.6073
BRS3	2.2100	0.0250	1.1440	1.6021
GPR150	0.5083	0.0258	-0.9762	1.5884
GPR37L1	0.4834	0.0258	-1.0487	1.5884
GPR85	1.9410	0.0258	0.9568	1.5884
GPR162	4.2000	0.0263	2.0704	1.5800
BAI3	2.3060	0.0266	1.2054	1.5751
GPR31	0.3141	0.0292	-1.6707	1.5346
GPRC5D	0.5154	0.0334	-0.9562	1.4763
CELSR1	0.5329	0.0373	-0.9081	1.4283
GPR15	2.0440	0.0390	1.0314	1.4089
GPR173	0.5499	0.0425	-0.8628	1.3716
LGR4	2.2950	0.0431	1.1985	1.3655
LPHN2	0.5455	0.0461	-0.8743	1.3363
GPR63	2.7930	0.0469	1.4818	1.3288

GPRC5B	0.4852	0.0476	-1.0433	1.3224
GPR68	0.2978	0.0497	-1.7476	1.3036
EMR2	2.5380	0.0520	1.3437	1.2840
GPR97	1.7840	0.0549	0.8351	1.2604
GPR112	0.4598	0.0554	-1.1209	1.2565
GPR160	1.7810	0.0565	0.8327	1.2480
TAAR5	0.5106	0.0576	-0.9697	1.2396
GPR83	1.9870	0.0579	0.9906	1.2373
GPR35	0.5173	0.0637	-0.9509	1.1959
GPR25	0.4825	0.0665	-1.0514	1.1772
GPR17	0.3696	0.0682	-1.4360	1.1662
GPR19	2.0560	0.0712	1.0398	1.1475
GPR26	0.5109	0.0750	-0.9689	1.1249
GPR125	2.5360	0.0839	1.3426	1.0762
GPR126	0.6035	0.0891	-0.7286	1.0501
GPR52	0.4993	0.0902	-1.0020	1.0448
GPR110	0.5282	0.0924	-0.9208	1.0343
GPR18	0.3719	0.0927	-1.4270	1.0329
GPR113	1.8990	0.0931	0.9252	1.0311
GPR45	0.5487	0.0992	-0.8659	1.0035
GPR135	1.6940	0.1003	0.7604	0.9987
GPR174	1.6850	0.1041	0.7527	0.9825
GPR182	0.6240	0.1075	-0.6804	0.9686
GPR21	1.6840	0.1101	0.7519	0.9582
EMR1	0.5394	0.1114	-0.8906	0.9531
GPR128	2.1630	0.1125	1.1130	0.9488
GPRC5C	1.9340	0.1138	0.9516	0.9439
GPRC5A	1.6180	0.1145	0.6942	0.9412
GPR27	1.6100	0.1159	0.6871	0.9359
GPR161	0.6262	0.1193	-0.6753	0.9234
GPR55	1.8260	0.1226	0.8687	0.9115
GPR61	0.5985	0.1227	-0.7406	0.9112
GPR98	2.0330	0.1233	1.0236	0.9090
GPR156	0.6120	0.1385	-0.7084	0.8586
BAI1	2.1080	0.1407	1.0759	0.8517
GPR22	0.6221	0.1424	-0.6848	0.8465
GPR153	0.4494	0.1549	-1.1539	0.8099
GPR111	0.6644	0.1625	-0.5899	0.7891
GPR3	1.6520	0.1724	0.7242	0.7635

GPR124	1.5350	0.1791	0.6182	0.7469
GPR133	0.6764	0.1892	-0.5641	0.7231
GPR176	0.5806	0.1903	-0.7844	0.7206
GPR39	1.5350	0.1907	0.6182	0.7196
GPR64	1.4630	0.1943	0.5489	0.7115
GPR84	1.5670	0.1994	0.6480	0.7003
GPR42	1.5880	0.2053	0.6672	0.6876
GPR116	1.6610	0.2172	0.7321	0.6631
TAAR2	1.4640	0.2234	0.5499	0.6509
GPR183	0.5949	0.2532	-0.7493	0.5965
GPR4	0.7000	0.2533	-0.5146	0.5964
GPR34	0.6235	0.2609	-0.6815	0.5835
GPR115	1.7160	0.2670	0.7790	0.5735
CELSR2	0.6566	0.2696	-0.6069	0.5693
GPR87	1.3760	0.2791	0.4605	0.5542
MAS1L	1.3750	0.2990	0.4594	0.5243
GPR88	0.7454	0.3779	-0.4239	0.4226
GPR65	1.5720	0.4150	0.6526	0.3820
GPR12	1.4710	0.4397	0.5568	0.3568
LPHN1	1.2520	0.4695	0.3242	0.3284
CELSR3	1.2670	0.4799	0.3414	0.3188
EMR3	0.7533	0.5055	-0.4087	0.2963
GSE12417-GPL96				
Gene	**Hazard Ratio (HR)**	**P-value**	**Log$_2$HR**	**- Log$_{10}$(P-value)**
GPR114	2.0630	0.0011	1.0447	2.9586
GPR65	0.4899	0.0011	-1.0294	2.9586
GPR19	0.5276	0.0018	-0.9225	2.7447
GPR132	0.5524	0.0031	-0.8562	2.5086
TAAR5	2.4580	0.0032	1.2975	2.4949
GPR174	2.6580	0.0033	1.4103	2.4815
GPR12	1.7700	0.0041	0.8237	2.3872
GPR115	1.9500	0.0043	0.9635	2.3665
LPHN2	2.9210	0.0047	1.5465	2.3279
GPR150	1.8930	0.0056	0.9207	2.2518
GPR75	2.0500	0.0111	1.0356	1.9547
GPR156	1.7360	0.0114	0.7958	1.9431
GPR6	1.6710	0.0135	0.7407	1.8697
GPR56	1.6980	0.0140	0.7638	1.8539

GPR35	0.6075	0.0146	-0.7190	1.8356
GPR37	0.5550	0.0148	-0.8494	1.8297
GPR26	0.6024	0.0149	-0.7312	1.8268
GPR18	0.6157	0.0153	-0.6997	1.8153
GPR173	1.7680	0.0161	0.8221	1.7932
GPR113	1.8050	0.0174	0.8520	1.7595
GPR124	0.5413	0.0186	-0.8855	1.7305
GPR110	0.6033	0.0201	-0.7291	1.6968
GPR27	0.5770	0.0247	-0.7934	1.6073
GPR116	1.9120	0.0270	0.9351	1.5686
CELSR1	0.6484	0.0289	-0.6250	1.5391
GPR63	0.6437	0.0316	-0.6355	1.5003
GPR3	1.5240	0.0342	0.6079	1.4660
GPR183	0.6561	0.0350	-0.6080	1.4559
GPR52	1.6210	0.0433	0.6969	1.3635
ELTD1	0.6120	0.0460	-0.7084	1.3372
BAI1	0.5378	0.0528	-0.8949	1.2774
EMR3	0.6614	0.0529	-0.5964	1.2765
GPR87	1.5200	0.0538	0.6041	1.2692
GPRC5D	0.6669	0.0664	-0.5845	1.1778
GPR34	0.5944	0.0684	-0.7505	1.1649
GPR31	0.5944	0.0685	-0.7505	1.1643
CD97	1.4730	0.0712	0.5588	1.1475
LPHN1	1.4280	0.0737	0.5140	1.1325
GPR153	1.7390	0.0789	0.7983	1.1029
LGR4	0.6945	0.0875	-0.5260	1.0580
GPRC5C	1.4220	0.0886	0.5079	1.0526
EMR1	1.5660	0.0887	0.6471	1.0521
BAI2	0.6110	0.0888	-0.7108	1.0516
GPR50	0.6650	0.0914	-0.5886	1.0391
GPR135	1.4080	0.0915	0.4936	1.0386
GPR146	0.6506	0.0950	-0.6202	1.0223
GPR160	0.6848	0.0968	-0.5462	1.0141
GPR55	1.3920	0.1019	0.4772	0.9918
GPR161	1.4820	0.1047	0.5675	0.9801
GPR45	1.3900	0.1056	0.4751	0.9763
GPR98	1.3850	0.1078	0.4699	0.9674
P2RY10	0.7219	0.1081	-0.4701	0.9662
GPR20	0.7308	0.1145	-0.4525	0.9412

GPR176	1.3920	0.1172	0.4772	0.9311
GPR25	1.7630	0.1176	0.8180	0.9296
GPR162	1.5270	0.1258	0.6107	0.9003
GPR171	1.5140	0.1329	0.5984	0.8765
GPR123	0.6260	0.1389	-0.6758	0.8573
LGR5	1.5440	0.1474	0.6267	0.8315
GPR37L1	0.7250	0.1497	-0.4639	0.8248
LPHN3	0.6993	0.1641	-0.5160	0.7849
GPR21	1.6260	0.1649	0.7013	0.7828
GPR61	1.3980	0.1668	0.4834	0.7778
GPR32	1.4840	0.1683	0.5695	0.7739
LGR6	1.4040	0.1848	0.4895	0.7333
GPR4	0.7499	0.1997	-0.4152	0.6996
GPR17	0.7026	0.2023	-0.5092	0.6940
GPR68	1.3100	0.2095	0.3896	0.6788
GPR15	1.3190	0.2100	0.3994	0.6778
GPR85	0.7799	0.2277	-0.3586	0.6426
BAI3	1.3070	0.2521	0.3863	0.5984
MAS1	1.4080	0.2522	0.4936	0.5983
EMR2	1.4500	0.2550	0.5361	0.5935
GPR64	0.7906	0.2551	-0.3390	0.5933
GPR83	0.8080	0.2850	-0.3076	0.5452
GPRC5A	1.3750	0.2923	0.4594	0.5342
GPR133	0.7752	0.2937	-0.3674	0.5321
GPR88	0.7421	0.3079	-0.4303	0.5116
GPR22	1.2200	0.3183	0.2869	0.4972
GPRC5B	0.7331	0.3309	-0.4479	0.4803
MAS1L	1.2600	0.3313	0.3334	0.4798
GPR84	0.8279	0.3385	-0.2725	0.4704
GPR42	1.3080	0.3666	0.3874	0.4358
GPR39	0.8367	0.3935	-0.2572	0.4051
TAAR2	1.1850	0.4089	0.2449	0.3884
CELSR3	0.8110	0.4615	-0.3022	0.3358
GPR126	0.8230	0.4711	-0.2810	0.3269
GPR182	0.8298	0.5135	-0.2692	0.2895

CELSR2	0.8600	0.5486	-0.2176	0.2607
GSE8970				
Gene	**Hazard Ratio (HR)**	**P-value**	**Log_2HR**	**- Log_{10}(P-value)**
GPR25	0.0799	0.0005	-3.6455	3.3010
P2RY10	0.2624	0.0017	-1.9302	2.7696
ELTD1	0.0440	0.0024	-4.5070	2.6198
LPHN1	0.2137	0.0035	-2.2263	2.4559
GPR132	0.3420	0.0061	-1.5479	2.2147
GPR63	0.2405	0.0061	-2.0559	2.2147
GPR85	0.2465	0.0068	-2.0203	2.1675
GPR31	0.3257	0.0079	-1.6184	2.1024
GPR87	0.2144	0.0094	-2.2216	2.0269
MAS1	0.3593	0.0104	-1.4767	1.9830
GPR88	0.3364	0.0142	-1.5718	1.8477
GPR37	0.3039	0.0171	-1.7183	1.7670
GPR161	0.3015	0.0218	-1.7298	1.6615
GPR68	0.4076	0.0224	-1.2948	1.6498
GPR20	0.1392	0.0243	-2.8448	1.6144
GPR17	0.4094	0.0270	-1.2884	1.5686
GPR12	0.4086	0.0330	-1.2912	1.4815
GPR110	0.3621	0.0417	-1.4655	1.3799
EMR1	2.4160	0.0433	1.2726	1.3635
EMR3	5.3120	0.0441	2.4093	1.3556
GPR6	2.4920	0.0442	1.3173	1.3546
EMR2	2.8480	0.0485	1.5099	1.3143
GPR171	0.4289	0.0588	-1.2213	1.2306
GPR27	0.3816	0.0589	-1.3899	1.2299
GPR19	0.2750	0.0628	-1.8625	1.2020
GPR65	0.3516	0.0640	-1.5080	1.1938
GPR153	0.4190	0.0650	-1.2550	1.1871
GPR18	2.7970	0.0696	1.4839	1.1574
BRS3	0.4573	0.0778	-1.1288	1.1090
GPR64	2.8900	0.0810	1.5311	1.0915
TAAR2	0.5100	0.0838	-0.9714	1.0768

GPR162	0.4862	0.0864	-1.0404	1.0635
GPRC5C	0.5210	0.0888	-0.9406	1.0516
GPR4	2.4590	0.0962	1.2981	1.0168
GPR173	1.8760	0.0983	0.9077	1.0074
GPR3	2.1850	0.1062	1.1276	0.9739
GPR176	1.9090	0.1066	0.9328	0.9722
GPR35	0.4379	0.1072	-1.1913	0.9698
GPR182	0.4584	0.1111	-1.1253	0.9543
CD97	1.9840	0.1151	0.9884	0.9389
GPR52	2.0210	0.1176	1.0151	0.9296
GPR126	0.3237	0.1324	-1.6273	0.8781
BAI2	1.8220	0.1388	0.8655	0.8576
GPR124	3.0030	0.1392	1.5864	0.8564
GPR22	0.5620	0.1401	-0.8314	0.8536
LGR4	0.5556	0.1454	-0.8479	0.8374
GPR50	0.5321	0.1456	-0.9102	0.8368
BAI1	1.7450	0.1583	0.8032	0.8005
GPR98	0.5022	0.1636	-0.9937	0.7862
GPR32	0.4797	0.1646	-1.0598	0.7836
GPR135	0.5116	0.1678	-0.9669	0.7752
BAI3	2.0320	0.1764	1.0229	0.7535
GPR42	0.5346	0.1787	-0.9035	0.7479
GPRC5B	1.7250	0.1842	0.7866	0.7347
GPR183	1.7110	0.1873	0.7748	0.7275
GPR75	1.9330	0.2101	0.9508	0.6776
GPRC5D	1.6770	0.2128	0.7459	0.6720
LPHN2	0.5789	0.2171	-0.7886	0.6633
GPRC5A	0.5797	0.2180	-0.7866	0.6615
GPR45	0.4252	0.2219	-1.2338	0.6538
CELSR1	0.5351	0.2232	-0.9021	0.6513
GPR21	0.5586	0.2301	-0.8401	0.6381
TAAR5	1.7200	0.2351	0.7824	0.6287
GPR15	0.6425	0.2545	-0.6382	0.5943
GPR56	1.6700	0.2614	0.7398	0.5827
CELSR3	0.6514	0.2787	-0.6184	0.5549

GPR116	1.5200	0.2787	0.6041	0.5549
LGR5	1.5270	0.2900	0.6107	0.5376
GPR39	0.6045	0.2902	-0.7262	0.5373
GPR37L1	1.6490	0.3143	0.7216	0.5027
CELSR2	0.5957	0.3256	-0.7473	0.4873

Supplementary table 3. Patient information in GSE12417

Sample ID	age	Characteristics	OS days	Live status	GPR132 expression
GSM311695 CN_AML	40	FAB M1	33	1	9.1
GSM311716 CN_AML	67	FAB M4	114	0	8.8874
GSM311734 CN_AML	36	FAB M4	326	1	8.8597
GSM311601 CN_AML	66	FAB M4	280	0	8.8278
GSM311669 CN_AML	62	FAB M2	123	1	8.8151
GSM311668 CN_AML	80	FAB M4	27	1	8.7729
GSM311719 CN_AML	71	FAB M4	794	0	8.7548
GSM311713 CN_AML	75	FAB M1	13	1	8.7463
GSM311747 CN_AML	71	FAB M4	1176	0	8.744
GSM311720 CN_AML	83	FAB M2	127	1	8.7051
GSM311683 CN_AML	72	FAB M5	1176	0	8.705
GSM311752 CN_AML	59	FAB M1	1176	0	8.641
GSM311723 CN_AML	66	FAB M2	693	1	8.6353
GSM311757 CN_AML	56	FAB M5	676	0	8.627
GSM311646 CN_AML	19	FAB M2	826	0	8.6189
GSM311714 CN_AML	39	FAB M2	51	0	8.6068
GSM311633 CN_AML	62	FAB M2	842	0	8.6041
GSM311681 CN_AML	39	FAB M5	1176	0	8.5968
GSM311632 CN_AML	45	FAB M4	1176	0	8.5953
GSM311617 CN_AML	66	FAB M2	8	1	8.5912
GSM311598 CN_AML	62	FAB M4	4	1	8.5531
GSM311729 CN_AML	20	FAB M2	1176	0	8.5512
GSM311750 CN_AML	43	FAB M2	1176	0	8.5501
GSM311715 CN_AML	39	FAB M1	608	0	8.5465
GSM311697 CN_AML	44	FAB M4	251	1	8.5364
GSM311694 CN_AML	75	FAB M1	91	1	8.5321
GSM311620 CN_AML	64	FAB M1	223	1	8.5317
GSM311736 CN_AML	54	FAB M4	1176	0	8.527
GSM311688 CN_AML	47	FAB M1	416	1	8.5262
GSM311732 CN_AML	24	FAB M5	79	1	8.5243
GSM311629 CN_AML	63	FAB M1	18	1	8.5192
GSM311710 CN_AML	57	FAB M2	891	0	8.5172
GSM311659 CN_AML	48	FAB M4	31	1	8.5114
GSM311742 CN_AML	68	FAB M1	1113	0	8.5045
GSM311711 CN_AML	58	FAB M4	850	0	8.5011
GSM311628 CN_AML	78	FAB M2	4	1	8.4982
GSM311748 CN_AML	40	FAB M5	1176	0	8.4963
GSM311741 CN_AML	69	FAB M2	192	1	8.4958
GSM311627 CN_AML	54	FAB M1	75	1	8.4948
GSM311603 CN_AML	52	FAB M2	657	1	8.4945
GSM311602 CN_AML	61	MDS RAEB	275	0	8.4936
GSM311693 CN_AML	78	FAB M1	62	1	8.4886
GSM311615 CN_AML	26	FAB M1	317	0	8.487
GSM311728 CN_AML	65	FAB M4	1176	0	8.4867
GSM311745 CN_AML	67	FAB M1	1176	0	8.4861
GSM311634 CN_AML	28	FAB M1	425	0	8.4845
GSM311726 CN_AML	17	FAB M5	1176	0	8.484
GSM311619 CN_AML	61	FAB M1	860	0	8.4838
GSM311666 CN_AML	71	FAB M1	236	1	8.4836
GSM311604 CN_AML	66	FAB M1	427	1	8.4806

GSM311709 CN_AML	61	FAB M2	184	1	8.4736
GSM311712 CN_AML	57	FAB M4	575	0	8.4734
GSM311685 CN_AML	49	FAB M1	107	1	8.4629
GSM311687 CN_AML	40	FAB M5	250	1	8.4624
GSM311701 CN_AML	55	FAB M1	229	1	8.4556
GSM311640 CN_AML	33	FAB M2	293	1	8.4555
GSM311651 CN_AML	72	FAB M2	289	1	8.4533
GSM311649 CN_AML	59	FAB M4	1176	0	8.4511
GSM311631 CN_AML	41	FAB M4	1176	0	8.4506
GSM311708 CN_AML	38	FAB M1	581	0	8.4475
GSM311680 CN_AML	67	FAB M1	157	1	8.4441
GSM311754 CN_AML	61	FAB M4	1176	0	8.4383
GSM311718 CN_AML	49	FAB M4	840	0	8.4359
GSM311727 CN_AML	74	FAB M4	284	1	8.4337
GSM311677 CN_AML	75	FAB M1	50	1	8.4329
GSM311755 CN_AML	61	FAB M2	223	1	8.4227
GSM311600 CN_AML	66	FAB M2	432	1	8.4216
GSM311618 CN_AML	66	FAB M4	72	0	8.4192
GSM311698 CN_AML	53	FAB M4	314	1	8.4151
GSM311689 CN_AML	71	FAB M2	289	0	8.4144
GSM311758 CN_AML	53	FAB M4	1176	0	8.4143
GSM311630 CN_AML	55	FAB M6	1103	0	8.4139
GSM311621 CN_AML	62	FAB M4	214	1	8.4136
GSM311756 CN_AML	53	FAB M4	51	1	8.4131
GSM311642 CN_AML	46	FAB M4	105	1	8.4129
GSM311654 CN_AML	62	FAB M2	30	1	8.4104
GSM311700 CN_AML	44	FAB M0	741	1	8.4066
GSM311667 CN_AML	49	FAB M2	280	1	8.4042
GSM311730 CN_AML	70	FAB M1	19	1	8.403
GSM311724 CN_AML	59	FAB M1	31	1	8.4014
GSM311613 CN_AML	49	FAB M5	209	0	8.4006
GSM311722 CN_AML	44	FAB M4	486	0	8.3922
GSM311637 CN_AML	47	FAB M2	366	0	8.3896
GSM311643 CN_AML	43	FAB M2	119	1	8.3833
GSM311641 CN_AML	34	FAB M0	1176	0	8.3779
GSM311707 CN_AML	77	FAB M2	18	1	8.3776
GSM311725 CN_AML	65	FAB M2	148	1	8.3736
GSM311733 CN_AML	67	FAB M5	137	1	8.3735
GSM311699 CN_AML	72	FAB M1	176	1	8.3718
GSM311670 CN_AML	27	FAB M4	321	1	8.3689
GSM311661 CN_AML	46	FAB M2	1176	0	8.3614
GSM311662 CN_AML	81	FAB M1	41	1	8.3562
GSM311655 CN_AML	43	FAB M4	1176	0	8.3562
GSM311696 CN_AML	53	FAB M1	872	1	8.3525
GSM311622 CN_AML	61	FAB M1	33	1	8.3518
GSM311743 CN_AML	68	FAB M5	559	1	8.351
GSM311676 CN_AML	67	FAB M1	39	1	8.3487
GSM311652 CN_AML	66	FAB M5	113	1	8.3482
GSM311626 CN_AML	74	FAB M1	240	1	8.3477
GSM311658 CN_AML	26	FAB M2	44	1	8.346
GSM311660 CN_AML	69	FAB M2	86	1	8.345
GSM311691 CN_AML	20	FAB M4	340	1	8.3425
GSM311650 CN_AML	49	FAB M4	61	1	8.3369

GSM311616 CN_AML	25	FAB M2	190	1	8.3338
GSM311746 CN_AML	65	FAB M1	233	1	8.3327
GSM311749 CN_AML	38	FAB M1	1176	0	8.3261
GSM311648 CN_AML	52	FAB M2	283	1	8.3259
GSM311706 CN_AML	69	FAB M2	484	1	8.3244
GSM311692 CN_AML	60	FAB M2	452	0	8.3243
GSM311738 CN_AML	55	FAB M2	1176	0	8.3241
GSM311760 CN_AML	32	FAB M1	916	0	8.3189
GSM311703 CN_AML	56	FAB M1	4	1	8.3172
GSM311653 CN_AML	54	FAB M2	109	1	8.3149
GSM311739 CN_AML	75	FAB M4	41	1	8.3148
GSM311721 CN_AML	58	FAB M4	24	1	8.3136
GSM311610 CN_AML	64	FAB M0	761	1	8.3112
GSM311635 CN_AML	62	FAB M0	257	1	8.3111
GSM311664 CN_AML	76	FAB M2	1102	1	8.3104
GSM311645 CN_AML	73	FAB M2	260	1	8.3039
GSM311682 CN_AML	60	FAB M1	599	1	8.301
GSM311665 CN_AML	47	FAB M6	749	1	8.2867
GSM311656 CN_AML	40	FAB M2	205	1	8.2831
GSM311672 CN_AML	69	FAB M1	124	1	8.2829
GSM311657 CN_AML	70	FAB M1	252	1	8.281
GSM311684 CN_AML	45	FAB M1	238	1	8.277
GSM311636 CN_AML	73	FAB M4	1176	0	8.2759
GSM311690 CN_AML	77	FAB M1	28	1	8.271
GSM311606 CN_AML	48	FAB M1	41	1	8.2698
GSM311740 CN_AML	44	FAB M2	352	1	8.259
GSM311717 CN_AML	32	FAB M2	849	0	8.2557
GSM311644 CN_AML	65	FAB M5	47	1	8.2436
GSM311759 CN_AML	79	FAB M2	175	1	8.2423
GSM311679 CN_AML	58	FAB M4	77	1	8.2296
GSM311638 CN_AML	34	FAB M6	1176	0	8.2264
GSM311624 CN_AML	76	FAB M6	924	0	8.2261
GSM311753 CN_AML	29	FAB M1	1176	0	8.2229
GSM311673 CN_AML	60	FAB M2	256	1	8.2176
GSM311671 CN_AML	52	FAB M0	56	1	8.2128
GSM311678 CN_AML	46	FAB M1	17	1	8.2126
GSM311611 CN_AML	54	FAB M5	294	1	8.2126
GSM311647 CN_AML	63	FAB M5	461	1	8.2009
GSM311751 CN_AML	57	FAB M5	1176	0	8.2008
GSM311744 CN_AML	62	FAB M2	209	0	8.1971
GSM311686 CN_AML	53	FAB M6	175	1	8.1908
GSM311737 CN_AML	37	FAB M4	999	1	8.1897
GSM311704 CN_AML	47	FAB M4	1176	0	8.1869
GSM311674 CN_AML	54	FAB M4	442	1	8.1821
GSM311599 CN_AML	59	FAB M4	104	0	8.179
GSM311675 CN_AML	71	FAB M6	41	1	8.1782
GSM311735 CN_AML	66	FAB M2	304	1	8.1745
GSM311609 CN_AML	52	FAB M4	253	1	8.1734
GSM311625 CN_AML	76	FAB M2	1176	0	8.1688
GSM311612 CN_AML	48	FAB M5	719	0	8.1516
GSM311663 CN_AML	47	FAB M1	285	0	8.1445
GSM311705 CN_AML	38	FAB M4	271	1	8.1405
GSM311639 CN_AML	50	FAB M2	247	1	8.1385

GSM311614 CN_AML	48	FAB M5	190	1	8.1346
GSM311731 CN_AML	66	FAB M4	1176	0	8.1295
GSM311702 CN_AML	68	FAB M1	263	1	8.1015
GSM311608 CN_AML	55	FAB M4	51	1	8.0699
GSM311605 CN_AML	34	FAB M5	421	1	8.0665
GSM311623 CN_AML	72	FAB M1	3	1	8.02
GSM311607 CN_AML	56	FAB M5	1	1	7.9676

Supplementary table 4. List of primer sequences for quantitative qRT-PCR and shRNAs

qRT-PCR primers	Sequences (5’ - 3’)
Human *GPR132*-F	TGCTGCATCTCCTGCGATAG
Human *GPR132*-R	TCAAAATAGCTGTCCGGCGT
Human *CD11b*-F	GCCTTGACCTTATGTCATGGG
Human *CD11b*-R	CCTGTGCTGTAGTCGCACT
Human *CEBPA*-F	AGACGTCCATCGACATCAGC
Human *CEBPA*-R	AGGAACTCGTCGTTGAAGGC
Human *SPI1*-F	GCGACCATTACTGGGACTTCC
Human *SPI2*-R	GGGTATCGAGGACGTGCAT
shRNAs for *GPR132*	**Target sequences (5’ - 3’)**
Scrambled	CCTAAGGTTAAGTCGCCCTCG
Human sh*GPR132*	CTGGGTCATCTATATCCGCAA

Supplementary table 5 Infomations for AML patient samples

Sample	Gender	Age	Subtype	Survival	Cytogentics	Mutations
AML#1	Male	26	M5	6 months	46, XY	WT1
AML#2	Female	57	M2	Alive	46，X,X	None
AML#3	Male	49	M2	2 weeks	46，X,Y	None