Annexes

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Annexes

Annex I Additional information about the 11 candidate biomarkers in patients with AML-M1 categorized in the intermediate prognostic risk group. For each gene is represented the expression status related to the subgroup with better prognosis, the ratio calculated between the number of patients present in two subgroups, the foldchange, the t-test and Mann-Whitney test *p-value*, and the bibliographic searching.

gene	expression status	Ratio	foldchange	*p-value*	Bibliographic Analysis
TATDN3	low	1.44444	0.38293	0.04338	never cited
PBDC1	low	1.18182	0.39249	0.00885	non-leukemia cancer types
CLIC1	low	1.3	0.29932	0.04216	non-AML leukemia types
SNAP23	low	0.76923	0.32727	0.01879	cited in AML
NNMT	high	1.4	0.24789	0.00415	non-AML leukemia types
CLEC4G	high	0.84615	0.1776	0.00109	non-leukemia cancer types
ARHGAP23	high	0.84615	0.32331	0.04095	non-AML leukemia types
ABCC9	high	0.84615	-0.02822	0	non-leukemia cancer types
ZBED3	high	1.18182	0.36411	0.0352	non-leukemia cancer types
MCM4	high	0.76923	0.29567	0.02136	cited in AML
SLC10A4	high	0.76923	0.25972	0.00349	non-leukemia cancer types

Annex II List of the gene sets shared by the majority of the intermediate-poor AML-M1 that were differentially enriched in comparison with the intermediate-favorable subgroups. For each gene set is represented the number and the percentage of intermediate-poor subgroups that had the gene sets enriched (n and percentage), a representative *p-value* and the status (upregulated (up) or downregulated (down)).

Set	n	Percentage	p-value	status
GO:0045089 positive regulation of innate immune response	10	91	0.005	up
GO:0045088 regulation of innate immune response	10	91	0.005	up
GO:0002833 positive regulation of response to biotic stimulus	10	91	0.006	up
GO:0071800 podosome assembly	10	91	0.013	up
GO:0002715 regulation of natural killer cell mediated immunity	10	91	0.016	up
GO:0002228 natural killer cell mediated immunity	10	91	0.017	up
GO:0002831 regulation of response to biotic stimulus	10	91	0.017	up
GO:0071801 regulation of podosome assembly	10	91	0.025	up
GO:0002507 tolerance induction	10	91	0.027	up
GO:0044106 cellular amine metabolic process	10	91	0.032	up
GO:1903902 positive regulation of viral life cycle	10	91	0.042	up
GO:0042271 susceptibility to natural killer cell mediated cytotoxicity	10	91	0.044	up
GO:0042269 regulation of natural killer cell mediated cytotoxicity	10	91	0.046	up
GO:0015669 gas transport	11	100	0.003	down
GO:0001501 skeletal system development	11	100	0.006	down
GO:0035924 cellular response to vascular endothelial growth factor stimulus	11	100	0.007	down
GO:0042744 hydrogen peroxide catabolic process	11	100	0.008	down
GO:0038084 vascular endothelial growth factor signaling pathway	11	100	0.009	down
GO:0042476 odontogenesis	11	100	0.01	down
GO:0015671 oxygen transport	11	100	0.011	down
GO:0048593 camera-type eye morphogenesis	11	100	0.017	down
GO:0060042 retina morphogenesis in camera-type eye	11	100	0.018	down
GO:0060537 muscle tissue development	11	100	0.019	down
GO:0018149 peptide cross-linking	11	100	0.021	down
GO:0048762 mesenchymal cell differentiation	11	100	0.022	down
GO:0097090 presynaptic membrane organization	11	100	0.023	down
GO:0071772 response to BMP	11	100	0.023	down
GO:0071773 cellular response to BMP stimulus	11	100	0.023	down
GO:0030509 BMP signaling pathway	11	100	0.023	down
GO:0030199 collagen fibril organization	11	100	0.024	down
GO:0060485 mesenchyme development	11	100	0.024	down
GO:0043568 positive regulation of insulin-like growth factor receptor signaling pathway	11	100	0.027	down
GO:0044331 cell-cell adhesion mediated by cadherin	11	100	0.028	down
GO:0007494 midgut development	11	100	0.028	down
GO:0001958 endochondral ossification	11	100	0.028	down
GO:0036075 replacement ossification	11	100	0.028	down

Set	n	Percentage	p-value	status
GO:0048009 insulin-like growth factor receptor signaling pathway	11	100	0.029	down
GO:0070208 protein heterotrimerization	11	100	0.039	down
GO:0043567 regulation of insulin-like growth factor receptor signaling pathway	11	100	0.04	down
GO:0048863 stem cell differentiation	11	100	0.044	down
GO:0003407 neural retina development	11	100	0.044	down
GO:0060041 retina development in camera-type eye	11	100	0.045	down
GO:0070571 negative regulation of neuron projection regeneration	11	100	0.047	down
GO:0016339 calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	11	100	0.048	down
GO:0031111 negative regulation of microtubule polymerization or depolymerization	11	100	0.05	down
GO:0048592 eye morphogenesis	10	91	0.003	down
GO:0051216 cartilage development	10	91	0.008	down
GO:0001654 eye development	10	91	0.008	down
GO:0048705 skeletal system morphogenesis	10	91	0.013	down
GO:0010717 regulation of epithelial to mesenchymal transition	10	91	0.014	down
GO:0043010 camera-type eye development	10	91	0.016	down
GO:0007158 neuron cell-cell adhesion	10	91	0.019	down
GO:0150063 visual system development	10	91	0.02	down
GO:0001945 lymph vessel development	10	91	0.02	down
GO:0048880 sensory system development	10	91	0.02	down
GO:0061448 connective tissue development	10	91	0.022	down
GO:0030510 regulation of BMP signaling pathway	10	91	0.023	down
GO:0090596 sensory organ morphogenesis	10	91	0.023	down
GO:0048701 embryonic cranial skeleton morphogenesis	10	91	0.025	down
GO:0007423 sensory organ development	10	91	0.025	down
GO:0042475 odontogenesis of dentin-containing tooth	10	91	0.028	down
GO:0060393 regulation of pathway-restricted SMAD protein phosphorylation	10	91	0.031	down
GO:0048070 regulation of developmental pigmentation	10	91	0.031	down
GO:0048286 lung alveolus development	10	91	0.034	down
GO:0003283 atrial septum development	10	91	0.034	down
GO:0003180 aortic valve morphogenesis	10	91	0.035	down
GO:0002062 chondrocyte differentiation	10	91	0.036	down
GO:0044342 type B pancreatic cell proliferation	10	91	0.036	down
GO:0048048 embryonic eye morphogenesis	10	91	0.039	down
GO:0001946 lymphangiogenesis	10	91	0.040	down
GO:0060411 cardiac septum morphogenesis	10	91	0.040	down
GO:0003206 cardiac chamber morphogenesis	10	91	0.040	down
GO:0003179 heart valve morphogenesis	10	91	0.040	down

Set	n	Percentage	p-value	status
GO:0002063 chondrocyte development	10	91	0.040	down
GO:0042743 hydrogen peroxide metabolic process	10	91	0.042	down
GO:0198738 cell-cell signaling by wnt	10	91	0.042	down
GO:0016055 Wnt signaling pathway	10	91	0.043	down
GO:0001837 epithelial to mesenchymal transition	10	91	0.043	down
GO:0099068 postsynapse assembly	10	91	0.043	down
GO:0014033 neural crest cell differentiation	10	91	0.044	down
GO:0061298 retina vasculature development in camera-type eye	10	91	0.045	down
GO:0060349 bone morphogenesis	10	91	0.045	down
GO:0060389 pathway-restricted SMAD protein phosphorylation	10	91	0.046	down
GO:0010862 positive regulation of pathway-restricted SMAD protein phosphorylation	10	91	0.048	down
GO:0014706 striated muscle tissue development	10	91	0.048	down
GO:0010719 negative regulation of epithelial to mesenchymal transition	10	91	0.048	down
GO:0061383 trabecula morphogenesis	10	91	0.049	down
GO:0060840 artery development	10	91	0.049	down
GO:0060973 cell migration involved in heart development	10	91	0.035	down

Annex III The remaining 122 identified CpG sites whose DNA methylation were able to predict survival in patients with AML-M1 categorized in the intermediate prognostic risk group.

CpG sites	*p-value*	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (*p-value*)	Gene	HR
cg10965508	0.0187	0.3989	14	10	0.0947	*TTBK1*	4.8096
cg24729690	0.0068	0.2206	10	14	0.3481	*CPLX2*	4.8069
cg05277096	0.0161	0.4688	12	12	0.1054	*PDZRN3*	4.3179
cg20470136	0.0171	0.2702	14	10	0.1682	*MAGEC1*	4.2473
cg19784873	0.0251	0.9154	10	12	0.4479	*STOX2*	4.2361
cg15410411	0.0246	0.2963	12	11	0.5582	*HOXC9*	4.1089
cg19205023	0.0151	0.4179	10	14	0.5576	*DPYSL4*	4.0753
cg14663451	0.0180	0.5061	10	14	0.8603	*NRG1*	3.9259
cg10634568	0.0218	0.7492	12	12	0.1185	*ALK*	3.9188
cg08912317	0.0409	0.0967	14	10	0.1870	*SCIN*	3.8666
cg15574301	0.0364	0.5403	12	10	0.5747	*PDLIM4*	3.8156
cg11424776	0.0357	0.8303	12	12	0.3549	*IRX2*	3.7297
cg09498078	0.0362	0.5233	14	10	0.5381	*MYO10*	0.3257
cg19044630	0.0449	0.0961	11	13	0.1314	*PRUNE2*	0.3205
cg24199599	0.0333	0.3444	14	10	0.5775	*SOX18*	0.3154
cg18699242	0.0426	0.4518	14	10	0.2912	*USP18*	0.3130
cg22160300	0.0345	0.7079	13	11	0.5815	*TBL1XR1*	0.3113
cg05661282	0.0300	0.0902	14	10	0.0890	*ZNF154*	0.3089
cg16560209	0.0437	0.5582	12	11	0.1089	*SKI*	0.3080
cg00074365	0.0399	0.4328	13	11	0.9306	*UGP2*	0.3078
cg11432962	0.0254	0.1455	13	11	0.5046	*SOX21*	0.3075
cg11218954	0.0247	0.2899	14	10	0.4116	*SIX3*	0.3074
cg15176413	0.0405	0.4804	10	14	0.7470	*FOXK1*	0.3038
cg24255089	0.0373	0.1222	13	11	0.8618	*FEZF2*	0.3038
cg10447977	0.0336	0.5125	13	11	0.5424	*ADAMTS9*	0.2987
cg06616057	0.0494	0.4886	10	14	0.8603	*G0S2*	0.2971
cg09337254	0.0237	0.4117	14	10	0.1870	*CAPG*	0.2950
cg10963518	0.0196	0.3873	14	10	0.5001	*SIX3*	0.2908
cg02313495	0.0428	0.269	11	13	0.4683	*BMF*	0.2881
cg00853733	0.0356	0.1115	12	12	0.1254	*SETD1B*	0.2877
cg08440556	0.0256	0.2513	11	13	0.3099	*SCD5*	0.2834
cg12841020	0.0256	0.4653	12	12	0.4878	*PGF*	0.2819
cg16482474	0.0250	0.0504	12	11	0.0789	*WDR86*	0.2809
cg05259872	0.0367	0.5402	10	14	0.3634	*PALLD*	0.2760
cg05768983	0.0212	0.1014	14	10	0.6814	*HAUS3*	0.2719
cg04309234	0.0189	0.4608	13	11	0.6634	*PRDM1*	0.2713
cg02460419	0.0190	0.2436	12	12	0.8623	*ATP6V0A2*	0.2608
cg13930766	0.0257	0.4604	13	11	0.1551	*MIR147A*	0.2583
cg07787614	0.0219	0.5032	13	11	0.5815	*TNRC6C*	0.2556
cg13844899	0.0086	0.2417	14	10	0.0836	*EFCAB10*	0.2546

CpG sites	*p-value*	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (*p-value*)	Gene	HR
cg13406605	0.0159	0.7838	14	10	0.8834	*WDR43*	0.2538
cg26434090	0.0099	0.7677	14	10	0.6814	*DSCAML1*	0.2537
cg13422817	0.0166	0.4767	14	10	0.6814	*FGF6*	0.2501
cg15697476	0.0123	0.0427	14	10	0.4816	*TNXB*	0.2475
cg10966440	0.0133	0.5462	14	10	0.0890	*OPCML*	0.2436
cg08198176	0.0114	0.3667	12	12	0.7947	*ITGA9*	0.2422
cg14069287	0.0100	0.7564	13	11	0.1469	*PALLD*	0.2393
cg16993682	0.0204	0.7333	12	11	0.8292	*CD1C*	0.2381
cg23850277	0.0097	0.4696	13	11	0.2230	*MMP11*	0.2373
cg02473540	0.0176	0.2983	12	12	0.0778	*ZNF135*	0.2361
cg22888463	0.0178	0.5899	11	13	0.3239	*EIF4E3*	0.2348
cg11567001	0.0090	0.015	14	10	0.3332	*SMARCD3*	0.2347
cg09863950	0.0171	0.8218	11	13	0.7277	*HTR6*	0.2333
cg13454846	0.0413	0.7141	10	14	0.8603	*TMEM82*	0.2322
cg09652652	0.0090	0.0142	13	11	0.6425	*FAM43A*	0.2308
cg24845329	0.0412	0.7526	11	11	0.5542	*THEG*	0.2282
cg05643188	0.0076	0.4339	13	11	0.4507	*C1orf53*	0.2276
cg23865240	0.0180	0.8447	12	12	0.8623	*HOXA1*	0.2244
cg08901339	0.0094	0.6112	13	11	0.2122	*BLNK*	0.2217
cg12128164	0.0043	0.5706	14	10	0.0947	*LRFN3*	0.2195
cg19097500	0.0060	0.2859	13	11	0.0721	*NFIA*	0.2186
cg12059147	0.0078	0.2324	11	13	0.0817	*FAM183A*	0.2180
cg24109116	0.0122	0.2269	11	13	0.3841	*MBLAC1*	0.2179
cg17847344	0.0297	0.4583	9	14	0.2978	*EBF1*	0.2145
cg11923320	0.0047	0.5059	13	11	0.0924	*LINC00466*	0.2088
cg24764102	0.0228	0.6173	10	14	0.4635	*TCF3*	0.2023
cg14351425	0.0075	0.1359	13	11	0.5424	*GRK5*	0.2021
cg03942932	0.0064	0.4855	13	11	0.5233	*PRDM1*	0.2001
cg02960347	0.0081	0.5211	13	11	0.7061	*PTPRG*	0.1961
cg22675956	0.0042	0.4566	11	13	0.1637	*SH3PXD2B*	0.1960
cg11772661	0.0175	0.3004	11	13	0.9306	*SHTN1*	0.1951
cg16686175	0.0086	0.7369	11	13	0.1551	*DHX40*	0.1947
cg13456470	0.0183	0.5172	10	14	0.5381	*PTCH1*	0.1932
cg05264870	0.0034	0.3143	14	10	0.0606	*NRP2*	0.1918
cg01815626	0.0183	0.6091	10	13	0.5764	*KRT6A*	0.1889
cg16616386	0.0053	0.1146	12	12	0.5247	*TENT4B*	0.1850
cg09636245	0.0053	0.2728	13	11	0.4683	*CYB5R2*	0.1828
cg03048432	0.0140	0.4406	12	12	0.7505	*NIN*	0.1815
cg01268022	0.0143	0.6315	10	14	0.5381	*FKBP14*	0.1815
cg09857070	0.0050	0.6445	12	12	0.2847	*ACTRT2*	0.1805
cg06209897	0.0134	0.5729	11	13	0.8618	*PRKG1*	0.1793
cg19189201	0.0121	0.4762	10	14	0.1682	*FAM169B*	0.1776
cg02436098	0.0018	0.3836	14	10	0.2293	*TNFAIP8L1*	0.1746

CpG sites	*p-value*	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (*p-value*)	Gene	HR
cg03752138	0.0026	0.6808	13	11	0.0924	*SOCS3*	0.1723
cg01557754	0.0025	0.5579	13	10	0.1132	*FGF11*	0.1712
cg14003022	0.0094	0.494	11	13	0.0721	*HTT-AS*	0.1698
cg01423820	0.0047	0.1103	14	10	0.6182	*VASH1*	0.1698
cg19013753	0.0047	0.657	14	10	0.6182	*SNUPN*	0.1698
cg08084860	0.0041	0.1619	12	12	0.5061	*GBX2*	0.1687
cg11762213	0.0085	0.4997	10	14	0.5381	*LINGO3*	0.1653
cg07054253	0.0009	0.1328	14	10	0.0647	*MATK*	0.1617
cg25120210	0.0096	0.7703	9	13	0.9733	*DOK7*	0.1611
cg16904585	0.0022	0.1302	11	12	0.0789	*GRIN2A*	0.1580
cg04231888	0.0025	0.5938	13	10	0.5344	*NAV2*	0.1539
cg21171339	0.0054	0.698	11	12	0.2672	*VPS13A*	0.1531
cg22854078	0.0021	0.1486	12	12	0.0643	*CHIT1*	0.1529
cg03457195	0.0031	0.6267	13	11	0.3099	*TBR1*	0.1518
cg19933238	0.0051	0.6541	10	14	0.5189	*AP1AR*	0.1514
cg19334176	0.0047	0.3539	11	13	0.2831	*DIP2C*	0.1488
cg13097993	0.0015	0.561	13	11	0.1469	*ATL1*	0.1479
cg25143508	0.0016	0.4362	14	10	0.6601	*PRELP*	0.1474
cg10707081	0.0013	0.6332	11	13	0.0555	*PCDH9*	0.1451
cg14660726	0.0023	0.1256	12	12	0.4878	*HLX*	0.1332
cg25583983	0.0040	0.3381	13	11	0.0593	*MICA*	0.1303
cg11279838	0.0028	0.2111	11	13	0.1314	*IRX4*	0.1294
cg00653615	0.0007	0.389	13	10	0.1717	*CDC42SE1*	0.1264
cg16000360	0.0005	0.2596	14	10	0.2528	*GUK1*	0.1250
cg13176979	0.0023	0.566	10	14	0.6601	*HMGN3*	0.1250
cg26800803	0.0025	0.3975	12	12	0.2847	*FOXK1*	0.1241
cg27105990	0.0001	0.6998	13	9	0.1506	*SLC30A8*	0.1101
cg00044871	0.0007	0.5147	13	11	0.3239	*ATP8A2*	0.1045
cg19736179	0.0008	0.853	14	10	0.2181	*ARF6*	0.1039
cg19170156	0.0006	0.5414	12	12	0.2719	*GPATCH8*	0.0974
cg02748539	0.0005	0.2693	14	10	0.1273	*SLC9A3*	0.0959
cg25979108	0.0001	0.3175	14	10	0.1273	*REX1BD*	0.0840
cg12741639	0.0028	0.3065	9	14	0.3439	*CYTH4*	0.0830
cg13367169	0.0001	0.0983	14	10	0.0647	*EN1*	0.0801
cg12322146	0.0013	0.7377	11	13	0.3384	*RBMS3*	0.0743
cg19918549	0.0000	0.1466	12	11	0.2063	*EVL*	0.0000
cg03374729	0.0448	0.4797	13	11	0.7496	*MIR4493*	
cg06186790	0.0246	0.2652	11	13	0.0555	*PRSS22*	
cg04646186	0.0249	0.6721	10	14	0.1774	*GABRG3*	

Annex IV Additional information about the 137 identified CpG sites as candidate biomarkers of prognosis in patients with AML-M1 categorized in the intermediate prognostic risk group.

CpG site	Genomic location	status	Ratio	Delta beta	p-value	Gene	Bibliographic analysis
cg17410650	Distal Intergenic	low	1.18	-0.35	0.000001	*HOXC13*	AML
cg06577205	Promoter (<=1kb)	low	0.71	-0.34	0.000001	*FBXL7*	Cancer
cg12523924	Promoter (2-3kb)	low	0.85	-0.41	0.000001	*HTR1A*	leukemia
cg27344859	Promoter (1-2kb)	low	1.40	-0.28	0.000001	*MIR124-3*	cancer
cg21385821	Promoter (<=1kb)	low	1.18	-0.54	0.000001	*CA10*	cited in AML
cg00662963	Promoter (<=1kb)	low	1.00	-0.24	0.000001	*PRR23B*	never cited
cg00664792	Other Intron	low	1.18	-0.31	0.000000	*SMOC2*	non-leukemia cancer types
cg08692733	Promoter (<=1kb)	low	0.71	-0.35	0.000185	*RBM20*	non-leukemia cancer types
cg20708909	Promoter (<=1kb)	low	1.40	-0.31	0.000001	*OPCML*	non-leukemia cancer types
cg23385847	1st Intron	low	1.00	-0.23	0.000001	*CAMK4*	non-AML leukemia types
cg07674139	Promoter (<=1kb)	low	0.71	-0.55	0.000001	*NRK*	cited in AML
cg25406755	Promoter (<=1kb)	low	0.71	-0.35	0.000001	*TFIP11*	non-leukemia cancer types
cg23073879	Promoter (2-3kb)	low	1.40	-0.30	0.000001	*GALNT17*	cited in PubMed
cg25024717	Distal Intergenic	low	1.18	-0.37	0.000002	*HOXC13*	cited in AML
cg23876072	Promoter (<=1kb)	low	1.00	-0.21	0.000001	*ANO1*	non-AML leukemia types
cg10965508	Promoter (<=1kb)	low	1.40	-0.30	0.000001	*TTBK1*	non-leukemia cancer types
cg24729690	Promoter (1-2kb)	low	0.71	-0.40	0.000001	*CPLX2*	non-leukemia cancer types
cg06186790	3' UTR	low	0.85	-0.36	0.000000	*PRSS22*	non-leukemia cancer types
cg05277096	Promoter (1-2kb)	low	1.00	-0.33	0.000001	*PDZRN3*	non-leukemia cancer types
cg20470136	Other Exon	low	1.40	-0.24	0.000006	*MAGEC1*	non-AML leukemia types
cg19784873	1st Intron	low	0.83	-0.22	0.000003	*STOX2*	non-leukemia cancer types
cg15410411	Promoter (<=1kb)	low	1.09	-0.33	0.000003	*HOXC9*	cited in AML

CpG site	Genomic location	status	Ratio	Delta beta	p-value	Gene	Bibliographic analysis
cg19205023	Promoter (1-2kb)	low	0.71	-0.38	0.000001	*DPYSL4*	non-leukemia cancer types
cg04646186	Promoter (<=1kb)	low	0.71	-0.37	0.000001	*GABRG3*	non-leukemia cancer types
cg14663451	Promoter (<=1kb)	low	0.71	-0.28	0.000034	*NRG1*	cited in AML
cg10634568	Distal Intergenic	low	1.00	-0.27	0.000001	*ALK*	cited in AML
cg08912317	Promoter (<=1kb)	low	1.40	-0.33	0.000001	*SCIN*	cited in AML
cg15574301	Other Exon	low	1.20	-0.21	0.000003	*PDLIM4*	cited in AML
cg11424776	Distal Intergenic	low	1.00	-0.27	0.000001	*IRX2*	cited in AML
cg03374729	Distal Intergenic	low	1.18	-0.43	0.000001	*MIR4493*	non-leukemia cancer types
cg09498078	Promoter (1-2kb)	high	1.40	-0.46	0.000001	*MYO10*	non-AML leukemia types
cg19044630	Promoter (<=1kb)	high	0.85	-0.26	0.000001	*PRUNE2*	cited in AML
cg24199599	Promoter (<=1kb)	high	1.40	-0.49	0.000001	*SOX18*	cited in AML
cg18699242	Promoter (<=1kb)	high	1.40	-0.57	0.000000	*USP18*	cited in AML
cg22160300	1st Intron	high	1.18	-0.20	0.000001	*TBL1XR1*	cited in AML
cg05661282	Promoter (<=1kb)	high	1.40	-0.42	0.000001	*ZNF154*	non-leukemia cancer types
cg16560209	1st Intron	high	1.09	-0.23	0.000002	*SKI*	cited in AML
cg00074365	Other Intron	high	1.18	-0.49	0.000001	*UGP2*	cited in AML
cg11432962	Distal Intergenic	high	1.18	-0.28	0.000001	*SOX21*	non-leukemia cancer types
cg11218954	Distal Intergenic	high	1.40	-0.44	0.000001	*SIX3*	non-AML leukemia types
cg15176413	Other Intron	high	0.71	-0.48	0.000001	*FOXK1*	non-leukemia cancer types
cg24255089	Distal Intergenic	high	1.18	-0.22	0.000001	*FEZF2*	non-AML leukemia types
cg10447977	Other Intron	high	1.18	-0.42	0.000002	*ADAMTS9*	cited in AML
cg06616057	Promoter (<=1kb)	high	0.71	-0.33	0.000002	*G0S2*	cited in AML
cg09337254	Promoter (<=1kb)	high	1.40	-0.55	0.000001	*CAPG*	cited in AML
cg10963518	Distal Intergenic	high	1.40	-0.50	0.000000	*SIX3*	non-AML leukemia types

CpG site	Genomic location	status	Ratio	Delta beta	p-value	Gene	Bibliographic analysis
cg02313495	Promoter (<=1kb)	high	0.85	-0.35	0.000001	*BMF*	cited in AML
cg00853733	Promoter (1-2kb)	high	1.00	-0.43	0.000036	*SETD1B*	cited in AML
cg08440556	Promoter (1-2kb)	high	0.85	-0.36	0.000001	*SCD5*	non-AML leukemia types
cg12841020	Promoter (<=1kb)	high	1.00	-0.32	0.000003	*PGF*	cited in AML
cg16482474	Promoter (<=1kb)	high	1.09	-0.26	0.000002	*WDR86*	cited in PubMed
cg05259872	Promoter (<=1kb)	high	0.71	-0.38	0.000020	*PALLD*	cited in AML
cg05768983	Promoter (<=1kb)	high	1.40	-0.24	0.000001	*HAUS3*	non-leukemia cancer types
cg04309234	Distal Intergenic	high	1.18	-0.44	0.000000	*PRDM1*	cited in AML
cg02460419	Promoter (2-3kb)	high	1.00	-0.32	0.000001	*ATP6V0A2*	non-AML leukemia types
cg13930766	Distal Intergenic	high	1.18	-0.28	0.000001	*MIR147A*	never cited
cg07787614	Other Intron	high	1.18	-0.48	0.000001	*TNRC6C*	non-leukemia cancer types
cg13844899	Promoter (<=1kb)	high	1.40	-0.43	0.000000	*EFCAB10*	never cited
cg13406605	Promoter (2-3kb)	high	1.40	-0.25	0.000001	*WDR43*	cited in AML
cg26434090	Promoter (2-3kb)	high	1.40	-0.31	0.000001	*DSCAML1*	cited in AML
cg13422817	Other Intron	high	1.40	-0.30	0.000002	*FGF6*	cited in AML
cg15697476	Other Intron	high	1.40	-0.42	0.000001	*TNXB*	non-AML leukemia types
cg10966440	1st Intron	high	1.40	-0.37	0.000000	*OPCML*	non-leukemia cancer types
cg08198176	Promoter (<=1kb)	high	1.00	-0.41	0.000000	*ITGA9*	non-AML leukemia types
cg14069287	Other Intron	high	1.18	-0.22	0.000001	*PALLD*	cited in AML
cg16993682	Promoter (<=1kb)	high	1.09	-0.22	0.000002	*CD1C*	cited in AML
cg23850277	Promoter (<=1kb)	high	1.18	-0.38	0.000000	*MMP11*	non-leukemia cancer types
cg02473540	Promoter (<=1kb)	high	1.00	-0.42	0.000000	*ZNF135*	non-leukemia cancer types
cg22888463	Promoter (<=1kb)	high	0.85	-0.41	0.000001	*EIF4E3*	non-leukemia cancer types

CpG site	Genomic location	status	Ratio	Delta beta	p-value	Gene	Bibliographic analysis
cg11567001	Promoter (2-3kb)	high	1.40	-0.42	0.000047	*SMARCD3*	non-AML leukemia types
cg09863950	Promoter (1-2kb)	high	0.85	-0.27	0.000001	*HTR6*	non-leukemia cancer types
cg13454846	Promoter (<=1kb)	high	0.71	-0.26	0.000001	*TMEM82*	non-leukemia cancer types
cg09652652	Promoter (2-3kb)	high	1.18	-0.39	0.000039	*FAM43A*	non-leukemia cancer types
cg24845329	Promoter (<=1kb)	high	1.00	-0.30	0.000003	*THEG*	non-AML leukemia types
cg05643188	Promoter (1-2kb)	high	1.18	-0.38	0.000000	*C1orf53*	never cited
cg23865240	Promoter (1-2kb)	high	1.00	-0.26	0.000001	*HOXA1*	cited in AML
cg08901339	Promoter (<=1kb)	high	1.18	-0.52	0.000001	*BLNK*	cited in AML
cg12128164	Promoter (1-2kb)	high	1.40	-0.40	0.000001	*LRFN3*	non-leukemia cancer types
cg19097500	Promoter (<=1kb)	high	1.18	-0.42	0.000001	*NFIA*	cited in AML
cg12059147	Promoter (<=1kb)	high	0.85	-0.29	0.000001	*FAM183A*	cited in PubMed
cg24109116	Promoter (1-2kb)	high	0.85	-0.36	0.000001	*MBLAC1*	non-leukemia cancer types
cg17847344	Other Intron	high	0.64	-0.22	0.000003	*EBF1*	cited in AML
cg11923320	Promoter (1-2kb)	high	1.18	-0.35	0.000007	*LINC00466*	non-leukemia cancer types
cg24764102	Distal Intergenic	high	0.71	-0.34	0.000000	*TCF3*	cited in AML
cg14351425	Promoter (<=1kb)	high	1.18	-0.43	0.000001	*GRK5*	non-AML leukemia types
cg03942932	Distal Intergenic	high	1.18	-0.43	0.000000	*PRDM1*	cited in AML
cg02960347	1st Intron	high	1.18	-0.30	0.000001	*PTPRG*	cited in AML
cg22675956	Promoter (<=1kb)	high	0.85	-0.32	0.000003	*SH3PXD2B*	non-leukemia cancer types
cg11772661	Promoter (<=1kb)	high	0.85	-0.22	0.000001	*SHTN1*	non-leukemia cancer types
cg16686175	Promoter (<=1kb)	high	0.85	-0.39	0.000001	*DHX40*	non-leukemia cancer types
cg13456470	Promoter (2-3kb)	high	0.71	-0.34	0.000002	*PTCH1*	cited in AML
cg05264870	Other Intron	high	1.40	-0.24	0.000000	*NRP2*	non-AML leukemia types
cg01815626	Distal Intergenic	high	0.77	-0.24	0.000063	*KRT6A*	non-leukemia cancer types

CpG site	Genomic location	status	Ratio	Delta beta	p-value	Gene	Bibliographic analysis
cg16616386	Promoter (<=1kb)	high	1.00	-0.24	0.000001	*TENT4B*	non-leukemia cancer types
cg09636245	Distal Intergenic	high	1.18	-0.43	0.000001	*CYB5R2*	non-leukemia cancer types
cg03048432	Other Intron	high	1.00	-0.46	0.000000	*NIN*	cited in AML
cg01268022	Promoter (1-2kb)	high	0.71	-0.44	0.000001	*FKBP14*	non-leukemia cancer types
cg09857070	Distal Intergenic	high	1.00	-0.25	0.000001	*ACTRT2*	cited in PubMed
cg06209897	Other Intron	high	0.85	-0.31	0.000006	*PRKG1*	cited in AML
cg19189201	Distal Intergenic	high	0.71	-0.29	0.000025	*FAM169B*	never cited
cg02436098	Promoter (<=1kb)	high	1.40	-0.34	0.000001	*TNFAIP8L1*	non-AML leukemia types
cg03752138	Promoter (1-2kb)	high	1.18	-0.24	0.000001	*SOCS3*	cited in AML
cg01557754	Promoter (<=1kb)	high	1.30	-0.22	0.000002	*FGF11*	non-leukemia cancer types
cg14003022	Distal Intergenic	high	0.85	-0.42	0.000000	*HTT-AS*	cited in PubMed
cg01423820	Promoter (<=1kb)	high	1.40	-0.21	0.000001	*VASH1*	non-AML leukemia types
cg19013753	Promoter (<=1kb)	high	1.40	-0.35	0.000001	*SNUPN*	cited in AML
cg08084860	Distal Intergenic	high	1.00	-0.35	0.000001	*GBX2*	cited in AML
cg11762213	Promoter (<=1kb)	high	0.71	-0.36	0.000001	*LINGO3*	non-leukemia cancer types
cg07054253	Promoter (<=1kb)	high	1.40	-0.27	0.000001	*MATK*	non-AML leukemia types
cg25120210	Promoter (<=1kb)	high	0.69	-0.23	0.000004	*DOK7*	cited in AML
cg16904585	Promoter (<=1kb)	high	0.92	-0.23	0.000055	*GRIN2A*	non-leukemia cancer types
cg04231888	1st Intron	high	1.30	-0.29	0.000003	*NAV2*	non-leukemia cancer types
cg21171339	Promoter (1-2kb)	high	0.92	-0.36	0.000002	*VPS13A*	non-AML leukemia types
cg22854078	Promoter (<=1kb)	high	1.00	-0.31	0.000001	*CHIT1*	cited in AML
cg03457195	Distal Intergenic	high	1.18	-0.33	0.000004	*TBR1*	non-AML leukemia types
cg19933238	Promoter (1-2kb)	high	0.71	-0.38	0.000047	*AP1AR*	non-leukemia cancer types

CpG site	Genomic location	status	Ratio	Delta beta	p-value	Gene	Bibliographic analysis
cg19334176	Other Intron	high	0.85	-0.31	0.000045	*DIP2C*	non-leukemia cancer types
cg13097993	Promoter (<=1kb)	high	1.18	-0.42	0.000000	*ATL1*	non-leukemia cancer types
cg25143508	1st Intron	high	1.40	-0.23	0.000002	*PRELP*	non-AML leukemia types
cg10707081	Other Intron	high	0.85	-0.46	0.000001	*PCDH9*	cited in AML
cg14660726	Distal Intergenic	high	1.00	-0.23	0.000001	*HLX*	cited in AML
cg25583983	Promoter (<=1kb)	high	1.18	-0.53	0.000001	*MICA*	cited in AML
cg11279838	Promoter (1-2kb)	high	0.85	-0.41	0.000001	*IRX4*	non-leukemia cancer types
cg00653615	Promoter (2-3kb)	high	1.30	-0.26	0.000028	*CDC42SE1*	non-leukemia cancer types
cg16000360	Promoter (<=1kb)	high	1.40	-0.43	0.000001	*GUK1*	non-leukemia cancer types
cg13176979	Promoter (<=1kb)	high	0.71	-0.37	0.000001	*HMGN3*	non-leukemia cancer types
cg26800803	Other Intron	high	1.00	-0.39	0.000000	*FOXK1*	non-leukemia cancer types
cg27105990	Other Intron	high	1.44	-0.27	0.000004	*SLC30A8*	non-AML leukemia types
cg00044871	Promoter (<=1kb)	high	1.18	-0.35	0.000010	*ATP8A2*	non-leukemia cancer types
cg19736179	Distal Intergenic	high	1.40	-0.25	0.000001	*ARF6*	cited in AML
cg19170156	Promoter (1-2kb)	high	1.00	-0.40	0.000002	*GPATCH8*	non-leukemia cancer types
cg02748539	Promoter (<=1kb)	high	1.40	-0.24	0.000001	*SLC9A3*	non-leukemia cancer types
cg25979108	Promoter (1-2kb)	high	1.40	-0.37	0.000004	*REX1BD*	never cited
cg12741639	Promoter (<=1kb)	high	0.64	-0.29	0.000144	*CYTH4*	non-leukemia cancer types
cg13367169	Distal Intergenic	high	1.40	-0.29	0.000001	*EN1*	cited in AML
cg12322146	Distal Intergenic	high	0.85	-0.33	0.000001	*RBMS3*	non-leukemia cancer types
cg19918549	Promoter (<=1kb)	high	1.09	-0.20	0.000046	*EVL*	cited in AML

Annex V The remaining 43 genes whose expression was able to predict survival in patients with AML-M2 categorized in the intermediate prognostic risk group.

Gene	*p-value*	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (*p-value)*	HR
MRM3	0.02375	7.8114	11	7	0.44094	4.21824
CYBRD1	0.02929	11.2652	8	11	0.96704	0.25589
ZNF224	0.0133	9.0751	9	10	0.23603	0.24203
FAM20A	0.02328	4.3088	8	10	0.08285	0.24124
CLEC18B	0.01084	2.6684	9	10	0.16475	0.23357
ZNF684	0.0069	6.359	11	8	0.24726	0.23298
FAM126A	0.00979	9.4421	9	9	0.28882	0.21854
SNX16	0.00498	7.7374	11	8	0.64944	0.21561
SLA	0.00796	10.4127	9	10	0.32676	0.2134
ST6GALNAC3	0.00697	2.7741	9	10	0.43754	0.20956
C21orf91	0.00373	10.2372	10	9	0.06595	0.20251
KLHL13	0.00561	6.8216	9	10	0.23603	0.20233
EYA1	0.00561	2.5824	9	10	0.23603	0.20233
RGS5	0.00726	5.1358	8	10	0.26622	0.19748
RAB22A	0.00945	9.4165	9	8	0.73597	0.19501
SHROOM3	0.00656	1.2998	8	11	0.64944	0.18618
CACNA1D	0.00545	3.7138	8	11	0.23078	0.18088
C9orf84	0.00181	5.0632	11	7	0.11261	0.1805
MMAA	0.00161	7.4381	10	9	0.20527	0.17331
ZNF813	0.00227	8.1167	10	8	0.56317	0.17232
DDO	0.00194	6.4547	10	7	0.26116	0.16573
VWA5A	0.00356	7.9268	8	10	0.09104	0.16517
DPYD	0.0031	9.8943	11	7	0.89183	0.15982
CMTR2	0.00362	9.7721	10	7	0.80702	0.15787
ZNF732	0.00076	2.9797	10	9	0.23603	0.15306
OR13C8	0.0007	0	11	8	0.18606	0.15215
GORAB	0.00622	8.2834	7	11	0.36462	0.14778
AS3MT	0.00251	4.2256	11	8	0.53537	0.1475
LRIF1	0.00581	9.3435	7	10	0.10692	0.14218
ITGA1	0.00162	3.3232	11	8	0.43238	0.1397
PRTG	0.00232	1.4603	7	11	0.89183	0.11706
FLT1	0.00168	3.4566	9	10	0.90244	0.11355
PDE10A	0.00028	0	9	10	0.77486	0.08942
ABCB1	0.00016	7.8442	11	8	0.59114	0.08401
ANKRD20A4	0.00019	1.0214	10	9	0.19103	0.07699
SAMD9L	0.00289	11.0946	7	10	0.80702	
MINAR1	0.00004	5.5569	11	8	0.28265	0.06799
ARHGAP44	0.00076	3.848	9	7	0.87375	0.05893
PARP9	0.0004	10.2126	8	10	0.50472	0.05311

Gene	*p-value*	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (*p-value)*	HR
EPB41L1	0.00011	2.8691	9	10	0.26992	0.04358
KIAA1217	0.00011	3.8593	9	10	0.26992	0.04358
BHMT2	0.00004	0.7764	10	8	0.42366	0.04097
FAM234B	0.00011	8.4386	7	11	0.31864	0

Annex VI Additional information about the 58 candidate biomarkers of prognostic of gene expression in patients with AML-M2 categorized in the intermediate prognostic risk group.

Gene	status	Ratio	foldchange	*p-value*	Bibliographic analysis
OSM	low	0.90	0.4453	0.0343	cited in AML
MAP1LC3B2	low	1.43	0.3960	0.0164	non-leukemia cancer types
RNPEP	high	0.73	0.3461	0.0205	non-AML leukemia types
EIF1	low	1.25	0.2952	0.0010	non-leukemia cancer types
SPATA2L	low	1.43	0.4521	0.0164	never cited
SF1	low	1.11	0.2919	0.0001	cited in AML
DNAJC1	low	1.38	0.3675	0.0117	cited in AML
FOSL1	low	1.38	0.4838	0.0090	cited in AML
EXOSC6	low	1.11	0.3752	0.0155	non-AML leukemia types
MAFF	low	0.90	0.5095	0.0045	cited in AML
IL3RA	low	1.38	0.3992	0.0117	cited in AML
HSD11B1L	low	1.11	0.5827	0.0205	cited in PubMed
CYP27B1	low	0.90	0.6188	0.0003	cited in AML
DDX27	low	1.11	0.3350	0.0155	non-leukemia cancer types
NDUFS4	low	1.38	0.3725	0.0434	non-leukemia cancer types
MRM3	low	1.57	0.3943	0.0205	non-leukemia cancer types
CYBRD1	high	0.73	0.3006	0.0155	cited in AML
ZNF224	high	0.90	0.3371	0.0267	non-AML leukemia types
FAM20A	high	0.80	0.3910	0.0001	non-leukemia cancer types
CLEC18B	high	0.90	0.3562	0.0220	non-leukemia cancer types
ZNF684	high	1.38	0.3851	0.0014	never cited
FAM126A	high	1.00	0.3299	0.0343	non-leukemia cancer types
SNX16	low	1.38	0.3599	0.0014	non-leukemia cancer types
SLA	high	0.90	0.2984	0.0009	cited in AML
ST6GALNAC3	high	0.90	0.1649	0.0020	non-leukemia cancer types
C21orf91	high	1.11	0.2973	0.0086	non-leukemia cancer types
KLHL13	high	0.90	0.3225	0.0454	non-leukemia cancer types
EYA1	high	0.90	0.2484	0.0437	cited in AML
RGS5	high	0.80	0.4093	0.0330	cited in AML
RAB22A	high	1.13	0.3319	0.0007	non-AML leukemia types
SHROOM3	high	0.73	-0.2136	0.0254	non-leukemia cancer types
CACNA1D	high	0.73	0.3417	0.0228	non-AML leukemia types
C9orf84	low	1.57	0.3937	0.0464	non-leukemia cancer types
MMAA	high	1.11	0.3609	0.0002	non-leukemia cancer types
ZNF813	high	1.25	0.3566	0.0360	non-leukemia cancer types
DDO	high	1.43	0.3628	0.0281	cited in AML
VWA5A	high	0.80	0.3563	0.0360	non-leukemia cancer types
DPYD	high	1.57	0.3186	0.0111	cited in AML
CMTR2	high	1.43	0.3291	0.0499	cited in PubMed
ZNF732	high	1.11	0.2918	0.0005	never cited

Gene	status	Ratio	foldchange	*p-value*	Bibliographic analysis
OR13C8	high	1.38	-0.5242	0.0153	non-leukemia cancer types
GORAB	high	0.64	0.3577	0.0055	non-leukemia cancer types
AS3MT	low	1.38	0.3864	0.0436	cited in AML
LRIF1	high	0.70	0.3312	0.0052	non-leukemia cancer types
ITGA1	high	1.38	0.3197	0.0099	non-AML leukemia types
PRTG	high	0.64	-0.1882	0.0066	non-leukemia cancer types
FLT1	high	0.90	0.3799	0.0307	cited in AML
PDE10A	high	0.90	-1.0800	0.0090	non-AML leukemia types
ABCB1	high	1.38	0.3015	0.0445	cited in AML
ANKRD20A4	high	1.11	0.0047	0.0349	never cited
SAMD9L	high	0.70	0.3029	0.0079	cited in AML
MINAR1	high	1.38	0.3720	0.0006	non-leukemia cancer types
ARHGAP44	high	1.29	0.4251	0.0256	non-leukemia cancer types
PARP9	high	0.80	0.3157	0.0250	cited in AML
EPB41L1	high	0.90	0.2740	0.0381	cited in AML
KIAA1217	high	0.90	0.2268	0.0121	non-leukemia cancer types
BHMT2	high	1.25	-0.5441	0.0044	non-leukemia cancer types
FAM234B	high	0.64	0.3470	0.0360	cited in PubMed

Annex VII List of the gene sets shared by the majority of the intermediate-poor AML-M2 that are differentially enriched in comparison with the intermediate-favorable subgroups. For each gene set is represented the number and the percentage of intermediate-poor subgroups that have the gene sets enriched (n and percentage), a representative *p-value* and the status (upregulated (up) or downregulated (down)).

Set	n	Percentage	*p-value*	status
GO:0045333 cellular respiration	54	95	0.002	up
GO:0022904 respiratory electron transport chain	54	95	0.003	up
GO:0015985 energy coupled proton transport, down electrochemical gradient	54	95	0.003	up
GO:0015986 ATP synthesis coupled proton transport	54	95	0.003	up
GO:0007005 mitochondrion organization	54	95	0.003	up
GO:0022613 ribonucleoprotein complex biogenesis	54	95	0.003	up
GO:0009145 purine nucleoside triphosphate biosynthetic process	54	95	0.003	up
GO:0009206 purine ribonucleoside triphosphate biosynthetic process	54	95	0.004	up
GO:0009201 ribonucleoside triphosphate biosynthetic process	54	95	0.004	up
GO:0006119 oxidative phosphorylation	54	95	0.004	up
GO:0070469 respirasome	54	95	0.004	up
GO:0006754 ATP biosynthetic process	54	95	0.005	up
GO:0009144 purine nucleoside triphosphate metabolic process	54	95	0.005	up
GO:0005746 mitochondrial respirasome	54	95	0.006	up
GO:0009205 purine ribonucleoside triphosphate metabolic process	54	95	0.006	up
GO:0042254 ribosome biogenesis	54	95	0.007	up
GO:0009199 ribonucleoside triphosphate metabolic process	54	95	0.007	up
GO:0090150 establishment of protein localization to membrane	54	95	0.010	up
GO:0009142 nucleoside triphosphate biosynthetic process	54	95	0.010	up
GO:0033108 mitochondrial respiratory chain complex assembly	54	95	0.010	up
GO:0007006 mitochondrial membrane organization	54	95	0.014	up
GO:0006364 rRNA processing	54	95	0.014	up
GO:0042773 ATP synthesis coupled electron transport	54	95	0.015	up
GO:0042775 mitochondrial ATP synthesis coupled electron transport	54	95	0.016	up
GO:0009141 nucleoside triphosphate metabolic process	54	95	0.016	up
GO:0016072 rRNA metabolic process	54	95	0.020	up
GO:0022900 electron transport chain	54	95	0.022	up
GO:0006605 protein targeting	54	95	0.022	up
GO:0006839 mitochondrial transport	54	95	0.023	up
GO:0034470 ncRNA processing	54	95	0.024	up
GO:1902600 proton transmembrane transport	54	95	0.024	up

Set	n	Percentage	*p-value*	status
GO:0006120 mitochondrial electron transport, NADH to ubiquinone	54	95	0.026	up
GO:0010257 NADH dehydrogenase complex assembly	54	95	0.026	up
GO:0032981 mitochondrial respiratory chain complex I assembly	54	95	0.026	up
GO:0015980 energy derivation by oxidation of organic compounds	54	95	0.029	up
GO:0006402 mRNA catabolic process	54	95	0.031	up
GO:0046034 ATP metabolic process	54	95	0.041	up
GO:0006457 protein folding	54	95	0.042	up
GO:0006401 RNA catabolic process	54	95	0.046	up
GO:0070126 mitochondrial translational termination	53	93	0.027	up
GO:0006415 translational termination	53	93	0.028	up
GO:0140053 mitochondrial gene expression	53	93	0.028	up
GO:0070125 mitochondrial translational elongation	53	93	0.028	up
GO:0032543 mitochondrial translation	53	93	0.040	up
GO:0006403 RNA localization	53	93	0.044	up
GO:0042273 ribosomal large subunit biogenesis	53	93	0.044	up
GO:0022618 ribonucleoprotein complex assembly	53	93	0.045	up
GO:0071826 ribonucleoprotein complex subunit organization	53	93	0.045	up
GO:0008380 RNA splicing	53	93	0.049	up
GO:0050657 nucleic acid transport	52	91	0.028	up
GO:0050658 RNA transport	52	91	0.028	up
GO:0051236 establishment of RNA localization	52	91	0.028	up
GO:0046902 regulation of mitochondrial membrane permeability	52	91	0.031	up
GO:0006612 protein targeting to membrane	52	91	0.038	up
GO:0045727 positive regulation of translation	52	91	0.040	up
GO:0019080 viral gene expression	52	91	0.041	up
GO:0051028 mRNA transport	52	91	0.046	up
GO:0006353 DNA-templated transcription, termination	52	91	0.049	up
GO:0002181 cytoplasmic translation	52	91	0.049	up
GO:0006767 water-soluble vitamin metabolic process	52	91	0.049	up
GO:0035023 regulation of Rho protein signal transduction	54	95	0.006	down
GO:0007266 Rho protein signal transduction	54	95	0.017	down
GO:1902904 negative regulation of supramolecular fiber organization	54	95	0.026	down
GO:0007626 locomotory behavior	54	95	0.027	down
GO:0002040 sprouting angiogenesis	54	95	0.027	down
GO:0010766 negative regulation of sodium ion transport	54	95	0.037	down
GO:0008344 adult locomotory behavior	54	95	0.038	down
GO:0042472 inner ear morphogenesis	54	95	0.041	down
GO:0030534 adult behavior	54	95	0.042	down

Set	n	Percentage	*p-value*	status
GO:0051056 regulation of small GTPase mediated signal transduction	54	95	0.043	down
GO:0072089 stem cell proliferation	54	95	0.047	down
GO:0006813 potassium ion transport	54	95	0.048	down
GO:0071805 potassium ion transmembrane transport	54	95	0.049	down
GO:0044331 cell-cell adhesion mediated by cadherin	53	93	0.029	down
GO:0051494 negative regulation of cytoskeleton organization	53	93	0.030	down
GO:0048839 inner ear development	53	93	0.030	down
GO:0046578 regulation of Ras protein signal transduction	53	93	0.030	down
GO:0060841 venous blood vessel development	53	93	0.036	down
GO:1904738 vascular associated smooth muscle cell migration	53	93	0.036	down
GO:1904752 regulation of vascular associated smooth muscle cell migration	53	93	0.036	down
GO:0030318 melanocyte differentiation	53	93	0.042	down
GO:0055078 sodium ion homeostasis	53	93	0.042	down
GO:2001028 positive regulation of endothelial cell chemotaxis	53	93	0.045	down
GO:0090596 sensory organ morphogenesis	53	93	0.046	down
GO:0003071 renal system process involved in regulation of systemic arterial blood pressure	53	93	0.047	down
GO:0003401 axis elongation	53	93	0.049	down
GO:0001508 action potential	53	93	0.049	down
GO:0006874 cellular calcium ion homeostasis	52	91	0.014	down
GO:0055074 calcium ion homeostasis	52	91	0.021	down
GO:0007204 positive regulation of cytosolic calcium ion concentration	52	91	0.034	down
GO:0034329 cell junction assembly	52	91	0.035	down
GO:0021954 central nervous system neuron development	52	91	0.036	down
GO:0021953 central nervous system neuron differentiation	52	91	0.039	down
GO:0001977 renal system process involved in regulation of blood volume	52	91	0.042	down
GO:0060560 developmental growth involved in morphogenesis	52	91	0.042	down
GO:0035627 ceramide transport	52	91	0.045	down
GO:0051952 regulation of amine transport	52	91	0.045	down
GO:0042471 ear morphogenesis	52	91	0.045	down
GO:0098802 plasma membrane signaling receptor complex	52	91	0.048	down
GO:0048854 brain morphogenesis	52	91	0.049	down

Annex VIII The remaining 676 identified CpG sites whose DNA methylation were able to predict survival in patients with AML-M2 categorized in the intermediate prognostic risk group.

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg18867923	0.00009	0.3572	9	10	0.90244	22.10625	*TBX1*
cg22595391	0.00015	0.1701	9	9	0.37673	21.92512	*CYBC1*
cg07691306	0.00026	0.0815	10	8	0.16801	20.27607	*ARID3A*
cg25832925	0.0002	0.3477	10	9	0.96741	19.88858	*ARX*
cg08076437	0.00051	0.3483	11	8	0.90134	18.24669	*IRX3*
cg00741986	0.00051	0.4486	11	8	0.90134	18.24669	*TNIP2*
cg00306721	0.00104	0.0785	9	8	1	15.96265	*BSCL2*
cg01496199	0.0009	0.6579	10	7	0.80702	15.12847	*IFNL2*
cg07820189	0.00024	0.505	8	11	0.82921	12.34639	*LAMC2*
cg07991621	0.00016	0.0968	8	11	0.59114	11.90304	*SH3BP2*
cg06588645	0.00016	0.6311	8	11	0.59114	11.90304	*TNS3*
cg22738642	0.00016	0.7844	8	11	0.59114	11.90304	*PRICKLE1*
cg27123691	0.00016	0.414	8	11	0.59114	11.90304	*CSPG4*
cg17858880	0.00016	0.6794	8	11	0.59114	11.90304	*TNS3*
cg11223365	0.00016	0.6106	8	11	0.59114	11.90304	*WNT9A*
cg10734665	0.00016	0.516	8	11	0.59114	11.90304	*ATP10A*
cg25151498	0.00016	0.0802	8	11	0.59114	11.90304	*ETV5*
cg10542562	0.00016	0.6523	8	11	0.59114	11.90304	*FLI1*
cg10745272	0.00016	0.3636	8	11	0.59114	11.90304	*SH3BP2*
cg15630950	0.00016	0.8979	8	11	0.59114	11.90304	*HLA-DOA*
cg27635394	0.0002	0.1016	7	11	0.61822	11.71134	*HIST1H2BB*
cg24943609	0.00025	0.2604	11	8	0.38552	11.5108	*ZNF652*
cg02639366	0.00041	0.698	8	11	0.91416	10.93459	*AGO4*
cg18252102	0.00041	0.9014	8	11	0.91416	10.93459	*FARP1*
cg02198513	0.00053	0.322	11	8	0.3419	10.69393	*TMEM156*
cg04359840	0.00053	0.4261	11	8	0.3419	10.69393	*XYLT1*
cg13225413	0.00045	0.1458	10	9	1	10.66517	*ZNF232*
cg08668790	0.00045	0.5831	10	9	1	10.66517	*ZNF154*
cg12407791	0.00045	0.4975	10	9	1	10.66517	*UNC13D*
cg20392842	0.00062	0.1747	9	10	0.43754	10.46969	*HLA-DMB*
cg08515841	0.00062	0.0649	9	10	0.43754	10.46969	*KLF7*
cg21429394	0.00062	0.5165	9	10	0.43754	10.46969	*SLC17A8*
cg16236263	0.00062	0.088	9	10	0.43754	10.46969	*HLA-DMB*
cg16430854	0.00062	0.261	9	10	0.43754	10.46969	*SDK2*
cg02627403	0.00062	0.5024	9	10	0.43754	10.46969	*UNC13D*
cg01951879	0.00062	0.3053	9	10	0.43754	10.46969	*IRX3*
cg10792987	0.00062	0.7098	9	10	0.43754	10.46969	*ELL*
cg13320436	0.00062	0.7586	9	10	0.43754	10.46969	*MRPL15*
cg03015498	0.0007	0.7299	11	8	0.59114	10.28675	*SFMBT2*
cg01467100	0.00061	0.6937	8	11	0.94843	10.2529	*PFKFB3*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg03187301	0.00078	0.2279	9	10	0.32676	10.22436	*MCRS1*
cg22074576	0.0008	0.5082	10	9	0.86302	10.09594	*OSBPL5*
cg15594585	0.00075	0.5642	8	11	0.77238	9.87486	*ZNF678*
cg10002133	0.00106	0.1168	11	8	0.83631	9.82462	*NTRK3*
cg07010633	0.00106	0.4312	11	8	0.83631	9.82462	*UNC13D*
cg08347500	0.00106	0.0237	11	8	0.83631	9.82462	*IRX3*
cg14905657	0.00106	0.686	11	8	0.83631	9.82462	*LMO3*
cg21747330	0.00122	0.5347	11	8	0.67944	9.67995	*GRIA3*
cg16207110	0.00091	0.8308	8	11	0.59114	9.67781	*TRNA*
cg08369368	0.00091	0.8241	8	11	0.59114	9.67781	*NSD1*
cg06400704	0.00155	0.3498	11	8	0.93638	9.45053	*FMN2*
cg24924577	0.00077	0.2737	11	8	0.30158	9.37756	*SEMA4B*
cg05818394	0.00153	0.1791	7	10	0.73024	9.15505	*HMGB1*
cg24387864	0.00096	0.2027	11	8	0.53537	9.12368	*CCND1*
cg18176723	0.00145	0.3495	10	8	0.72201	8.99401	*PPCDC*
cg03599590	0.00189	0.1492	10	8	1	8.73616	*SLC35A5*
cg07967918	0.00158	0.2937	11	8	0.48238	8.17529	*SOBP*
cg06975048	0.00158	0.1203	11	8	0.48238	8.17529	*KCNAB3*
cg06427054	0.00248	0.0924	11	8	0.56292	7.70834	*GSX2*
cg05649922	0.0006	0.3783	10	9	0.20527	7.70506	*ARID1A*
cg12573289	0.0006	0.4822	10	9	0.20527	7.70506	*CCM2*
cg17103217	0.0006	0.5589	10	9	0.20527	7.70506	*B3GALT4*
cg09584521	0.0006	0.0667	10	9	0.20527	7.70506	*CD58*
cg13707025	0.00306	0.5205	11	8	1	7.50442	*KCNK10*
cg21518432	0.00334	0.1394	11	8	0.97877	7.42078	*SHC4*
cg12258811	0.00334	0.6557	11	8	0.97877	7.42078	*PER3*
cg23681664	0.00099	0.3434	9	10	0.71306	7.25055	*CPNE9*
cg22371591	0.00162	0.445	8	11	0.43238	7.15824	*MSX1*
cg27175287	0.00162	0.6519	8	11	0.43238	7.15824	*FOXE3*
cg03247049	0.0012	0.3948	10	9	0.59529	7.11753	*AXL*
cg19037007	0.0012	0.6648	10	9	0.59529	7.11753	*SLC52A3*
cg12571423	0.0014	0.2295	11	8	0.12628	7.10914	*CCNA1*
cg20589883	0.0014	0.4865	11	8	0.12628	7.10914	*ELOVL6*
cg21618521	0.0014	0.6277	11	8	0.12628	7.10914	*B3GALT4*
cg21611682	0.0014	0.7785	11	8	0.12628	7.10914	*LRP5*
cg04313565	0.0014	0.4158	11	8	0.12628	7.10914	*XYLT1*
cg16300030	0.0014	0.197	11	8	0.12628	7.10914	*HLA-DMB*
cg16794579	0.0014	0.4959	11	8	0.12628	7.10914	*XYLT1*
cg17901382	0.0014	0.6384	11	8	0.12628	7.10914	*TSEN54*
cg12135856	0.0013	0.4042	9	10	1	6.99765	*DSCAM*
cg07071609	0.00184	0.042	9	10	0.98166	6.78331	*PLIN5*
cg17239923	0.00259	0.2728	11	8	0.43238	6.56017	*FLI1*
cg07834682	0.00259	0.2256	11	8	0.43238	6.56017	*SIX2*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg04779860	0.00654	0.1837	11	8	0.56292	6.53922	*EBF3*
cg27346806	0.00238	0.3166	9	10	0.87217	6.53506	*VENTX*
cg23357130	0.00238	0.7852	9	10	0.87217	6.53506	*OSBPL5*
cg24640390	0.00272	0.4716	9	10	0.65309	6.39782	*NEUROG3*
cg09005679	0.00311	0.3316	9	10	0.48729	6.29664	*EDN3*
cg08883485	0.00311	0.6893	9	10	0.48729	6.29664	*NAV1*
cg24217984	0.00097	0.3789	8	11	0.06904	6.27113	*RGMA*
cg08001559	0.00147	0.3052	10	9	0.06595	6.23938	*GNG2*
cg18342462	0.0035	0.7651	9	10	0.73024	6.20998	*C11orf88*
cg03655371	0.0035	0.1735	9	10	0.73024	6.20998	*TIFAB*
cg05836145	0.00581	0.6094	8	11	0.94843	5.9466	*SP8*
cg07681748	0.00443	0.7032	9	10	0.65309	5.89502	*CD200*
cg04365202	0.00442	0.5044	8	11	0.43238	5.84824	*LHX9*
cg05257898	0.01493	0.6369	11	7	0.93075	5.82792	*NKAP*
cg26487031	0.0054	0.3074	7	11	0.71399	5.78903	*MPZL2*
cg00779638	0.00161	0.8381	9	10	0.20527	5.7699	*AGTPBP1*
cg17156534	0.00631	0.6103	10	9	0.65739	5.76096	*TOP1*
cg14422240	0.00346	0.7104	10	9	0.26992	5.68723	*CMTR1*
cg02876258	0.00795	0.2579	11	8	0.86872	5.58201	*FGF5*
cg07928083	0.00545	0.3915	11	8	0.96704	5.52843	*FOXB1*
cg09757109	0.0025	0.7213	9	10	0.34732	5.44607	*DIXDC1*
cg25042430	0.00485	0.1557	10	9	0.43754	5.40502	*KIAA1217*
cg21068610	0.00295	0.1412	9	10	0.25258	5.33656	*CHD3*
cg14371590	0.00583	0.3628	10	9	0.71306	5.25486	*SLC26A10*
cg07220903	0.00385	0.3457	10	9	0.13057	5.2257	*CCDC12*
cg24994127	0.00689	0.0903	11	8	0.17268	5.1727	*RALGAPA2*
cg07941108	0.00689	0.4091	11	8	0.17268	5.1727	*PSMC1*
cg24250393	0.00225	0.373	8	11	0.2002	5.14653	*PRKCB*
cg04918402	0.02242	0.0609	11	7	0.85612	5.13963	*LIMD2*
cg27257822	0.00822	0.7718	9	10	0.90244	5.12833	*EPHB3*
cg20276630	0.00467	0.5384	8	11	0.9828	5.08608	*PDLIM1*
cg04420723	0.00461	0.2922	8	11	0.80419	5.05131	*ZNF184*
cg05551825	0.00275	0.2138	8	11	0.13685	5.02535	*RNF216*
cg20421446	0.01447	0.7554	10	8	0.76977	4.96965	*NRN1*
cg18073471	0.00561	0.5211	10	9	0.23603	4.94251	*PRDM8*
cg13276502	0.00561	0.6534	10	9	0.23603	4.94251	*SOX4*
cg23045908	0.00373	0.3492	9	10	0.06595	4.93797	*PDE4B*
cg08667275	0.00897	0.3568	10	9	0.98034	4.93107	*RNF26*
cg05327596	0.00303	0.6993	8	11	0.38552	4.9275	*COL11A2*
cg14762436	0.00929	0.487	11	8	0.30158	4.92254	*OSBPL3*
cg05071046	0.00929	0.2484	11	8	0.30158	4.92254	*IRX3*
cg15683295	0.00586	0.2588	8	11	0.93413	4.87704	*HOTTIP*
cg18653350	0.01278	0.1233	11	8	0.47252	4.85896	*SACS*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg19839325	0.00332	0.5809	8	11	0.11636	4.79908	*KLHL26*
cg27396824	0.00809	0.4542	7	10	0.35328	4.78441	*ZAN*
cg22996489	0.00702	0.5376	8	11	0.91416	4.77457	*OXGR1*
cg06638433	0.00683	0.6003	8	11	0.64944	4.76916	*IGF2BP1*
cg26111030	0.01176	0.0963	10	9	0.90192	4.71842	*ERBB2*
cg22902505	0.00806	0.5824	10	9	0.63958	4.71808	*PRDM8*
cg14892768	0.00759	0.6387	9	10	0.98166	4.70051	*AXL*
cg08586366	0.00759	0.5095	9	10	0.98166	4.70051	*FLI1*
cg03465652	0.0078	0.521	8	11	0.48238	4.68015	*GLI2*
cg10334354	0.00637	0.3956	8	11	0.2151	4.67935	*EPHA5*
cg17691657	0.01272	0.1361	11	8	1	4.66183	*SLC4A4*
cg07275218	0.0133	0.558	9	9	1	4.6518	*BRD2*
cg19471574	0.00833	0.1943	10	9	0.59529	4.64428	*TMEM161B*
cg13409248	0.00878	0.3804	8	11	0.7464	4.60468	*ENTPD3*
cg19175386	0.00878	0.2224	8	11	0.7464	4.60468	*TBX3*
cg27077033	0.00878	0.2871	8	11	0.7464	4.60468	*CEP170B*
cg12220058	0.00438	0.9443	8	11	0.24726	4.59604	*NMB*
cg21760990	0.00908	0.7335	8	11	0.61999	4.575	*TBC1D32*
cg25313172	0.01378	0.2479	10	9	0.87017	4.56545	*KRT7*
cg02390329	0.01378	0.5304	10	9	0.87017	4.56545	*ZIC4*
cg26955132	0.00845	0.6996	10	9	0.09388	4.44137	*FAM234B*
cg18305855	0.00845	0.7495	10	9	0.09388	4.44137	*BMT2*
cg05395947	0.01117	0.6638	8	11	0.76266	4.4325	*SASH1*
cg20645065	0.00582	0.428	8	11	0.3419	4.399	*ALPL*
cg20910202	0.00582	0.5359	8	11	0.3419	4.399	*KBTBD11*
cg09436375	0.00582	0.6828	8	11	0.3419	4.399	*GNMT*
cg01606885	0.01286	0.7794	10	9	0.60475	4.36926	*HSPB3*
cg02457623	0.0202	0.0254	11	7	0.44094	4.3608	*ATP2B4*
cg11175192	0.01265	0.4237	8	11	0.66616	4.34588	*WNT6*
cg18495563	0.01399	0.1158	8	10	0.96331	4.32258	*TCP11L1*
cg05923595	0.02031	0.2546	11	8	1	4.31315	*AZIN2*
cg01597891	0.00813	0.2382	7	11	0.18865	4.27102	*INA*
cg14640670	0.0158	0.4511	11	8	0.77238	4.23702	*PURA*
cg07557423	0.0158	0.3851	11	8	0.77238	4.23702	*ATP8A1*
cg17345569	0.0201	0.3752	11	8	0.90134	4.22375	*GNMT*
cg27439456	0.02231	0.4953	10	9	0.55428	4.17672	*OSCP1*
cg10592171	0.01003	0.4634	8	11	0.40855	4.05428	*DLX4*
cg06248480	0.02617	0.1339	10	9	0.28806	4.04427	*LAMB1*
cg19211800	0.01941	0.3197	8	10	0.62471	3.93445	*MARCKS*
cg15246619	0.01299	0.6012	8	11	0.83631	3.90174	*FGF17*
cg09681675	0.03308	0.631	11	8	0.28265	3.77546	*ZNF597*
cg04995300	0.01923	0.3852	9	10	0.77486	3.77501	*KBTBD8*
cg24378136	0.03455	0.5045	11	8	0.86872	3.75007	*RNF39*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg03469082	0.03632	0.4306	11	8	1	3.71243	*GABRG1*
cg23196346	0.04141	0.2472	9	10	0.46204	3.2734	*KIAA1217*
cg23119487	0.03609	0.6869	8	11	0.43238	3.24685	*TMED3*
cg05977462	0.03569	0.8558	8	11	0.50851	3.13776	*CUX2*
cg26508928	0.04323	0.6204	11	8	0.28265	0.33258	*ZNF519*
cg01408845	0.03751	0.6919	9	10	0.96741	0.30411	*SARM1*
cg19628739	0.03751	0.6581	9	10	0.96741	0.30411	*PNPLA3*
cg16151494	0.03751	0.4326	9	10	0.96741	0.30411	*GPBP1*
cg01931994	0.02683	0.3641	11	8	0.18606	0.3027	*BRINP2*
cg00639635	0.03221	0.6437	10	9	0.30701	0.29871	*FUCA2*
cg06578276	0.03217	0.1106	11	8	0.61999	0.29494	*BAIAP2*
cg09083945	0.03217	0.0869	11	8	0.61999	0.29494	*BAIAP2*
cg08147563	0.03051	0.7359	9	10	0.36869	0.29322	*ROBO1*
cg23973972	0.03051	0.5789	9	10	0.96741	0.29322	*CNDP2*
cg00059161	0.03051	0.6613	9	10	0.96741	0.29322	*SLITRK3*
cg22333471	0.03105	0.5636	9	10	0.36869	0.28824	*SDHAF1*
cg01116873	0.02234	0.5139	11	8	0.56292	0.28777	*RN7SK*
cg22366943	0.03141	0.7671	8	11	0.90134	0.28076	*NKAIN2*
cg00036408	0.03689	0.0682	10	9	0.56729	0.2792	*TMEM105*
cg19404979	0.01592	0.4822	10	9	0.09388	0.26382	*ELSPBP1*
cg14150727	0.0163	0.7347	10	9	0.48729	0.26213	*LGR6*
cg18766685	0.019	0.7814	9	10	0.41381	0.26035	*SHH*
cg25050975	0.02109	0.8281	8	11	0.56292	0.25638	*NXN*
cg08988179	0.01223	0.1485	10	9	0.08613	0.25527	*C1QL1*
cg24336447	0.01151	0.4745	11	8	0.64944	0.25182	*GALP*
cg06322601	0.01451	0.0141	11	8	0.11636	0.25175	*RASA4*
cg02952295	0.02058	0.5722	11	8	0.59114	0.25054	*TRPM8*
cg17398252	0.0242	0.0418	8	10	0.35035	0.24991	*BVES*
cg05184519	0.00979	0.476	11	8	0.2002	0.24552	*NTM*
cg02198701	0.01601	0.1473	8	11	0.3633	0.24425	*IRX6*
cg16599143	0.02506	0.7212	8	11	1	0.24367	*FMO3*
cg11633310	0.01941	0.7054	8	11	0.74096	0.2436	*MS4A10*
cg12650635	0.01762	0.7509	8	11	0.48238	0.24001	*AQP2*
cg13691209	0.00799	0.5527	11	8	0.43238	0.23774	*PLEKHG4B*
cg08432013	0.01643	0.4912	9	10	0.87017	0.23716	*DLG2*
cg13223682	0.01643	0.2362	9	10	0.87017	0.23716	*SP3*
cg26578156	0.01643	0.5904	9	10	0.87017	0.23716	*ZNF423*
cg13052638	0.0158	0.6639	8	11	0.77238	0.23602	*RASSF5*
cg02385848	0.0158	0.7978	8	11	0.61999	0.23602	*LINC00473*
cg06333800	0.0158	0.5656	8	11	0.77238	0.23602	*PRKAG2*
cg06499030	0.0158	0.5517	8	11	0.61999	0.23602	*HLA-DQB2*
cg11019923	0.00782	0.494	10	9	0.16475	0.22889	*DNAJA4*
cg25744552	0.0121	0.1818	10	9	0.90244	0.2267	*CD2*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg15396204	0.0121	0.5604	10	9	0.90244	0.2267	*PRMT6*
cg22830507	0.01557	0.5306	8	11	1	0.22175	*TBX3*
cg18998321	0.01557	0.5392	8	11	0.70997	0.22175	*LAMA1*
cg13968218	0.01794	0.1932	9	10	0.53994	0.22009	*ADGRD2*
cg27297993	0.00944	0.7711	10	8	0.75557	0.21972	*GABBR1*
cg23575349	0.00542	0.7491	11	8	0.23078	0.21893	*GRM5*
cg06001524	0.01163	0.6955	11	8	0.96704	0.218	*STX8*
cg22220986	0.00955	0.7631	10	9	0.83812	0.21695	*TTC29*
cg22142922	0.0152	0.4695	9	9	0.92956	0.21111	*ANO1*
cg23057870	0.0057	0.2006	11	8	0.77238	0.20398	*HEY1*
cg05543593	0.00561	0.6922	9	10	0.23603	0.20233	*APOB*
cg25962699	0.00561	0.3697	9	10	0.23603	0.20233	*SLC7A14*
cg08166767	0.00561	0.692	9	10	0.23603	0.20233	*LCE2A*
cg13441112	0.00561	0.5996	9	10	0.23603	0.20233	*CFHR4*
cg01253818	0.01078	0.3371	8	11	0.93413	0.20068	*PPP2R2C*
cg24296920	0.01604	0.7742	10	7	1	0.20027	*ARMS2*
cg22234930	0.01294	0.367	9	10	0.59529	0.19871	*PKM*
cg00736104	0.01294	0.6099	9	10	0.59529	0.19871	*SUDS3*
cg07202214	0.01294	0.1484	9	10	0.59529	0.19871	*LRRC32*
cg13026772	0.00478	0.8474	9	10	0.32676	0.19808	*PKNOX2*
cg07302934	0.00544	0.6208	11	8	0.17268	0.19501	*GLIS2*
cg21756194	0.00822	0.0977	10	9	0.90244	0.195	*CALCR*
cg27590787	0.00872	0.4601	8	11	0.30158	0.19437	*PNCK*
cg02999224	0.01	0.591	9	10	0.48729	0.19084	*SLC7A7*
cg10558233	0.01	0.5328	9	10	0.48729	0.19084	*MIR378D2*
cg13541713	0.01	0.6256	9	10	0.48729	0.19084	*SYNPO2*
cg02147126	0.01	0.2621	9	10	0.48729	0.19084	*AZU1*
cg05641048	0.01048	0.5299	11	8	0.91527	0.18937	*GCNT3*
cg06427176	0.00762	0.7376	8	10	0.30638	0.18913	*ADAMTS2*
cg15843496	0.00299	0.4757	11	8	0.56292	0.18621	*OR11H12*
cg21122370	0.00656	0.2007	8	11	0.74096	0.18618	*SLIT3*
cg03495053	0.00969	0.771	10	8	0.65652	0.18605	*THBS2*
cg12910797	0.00826	0.4464	10	9	0.80633	0.18581	*HOXB3*
cg22053945	0.00826	0.6732	10	9	0.80633	0.18581	*HOXB3*
cg26342141	0.00796	0.745	8	9	0.14867	0.18566	*MIR2113*
cg19052164	0.00624	0.6086	8	11	0.3419	0.18437	*PLEKHG4B*
cg26256521	0.00812	0.2985	10	8	0.89386	0.18392	*MIR4710*
cg05905844	0.0025	0.3472	10	9	0.34732	0.18362	*CHRM2*
cg00306893	0.00763	0.7616	11	7	0.68329	0.18322	*MECOM*
cg08548882	0.00716	0.7074	10	9	0.96741	0.18197	*PLEKHG1*
cg23908019	0.00716	0.7519	10	9	0.96741	0.18197	*OCA2*
cg13139361	0.00658	0.5185	11	8	0.67042	0.18136	*C1D*
cg26492744	0.00545	0.4268	8	11	0.23078	0.18088	*EFNB1*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg14408356	0.00906	0.7941	11	7	0.92776	0.17849	*DTX1*
cg22152605	0.00621	0.5619	10	9	0.68283	0.1782	*FPR1*
cg26681975	0.00697	0.441	11	8	0.93413	0.17649	*PNPLA1*
cg00683788	0.00524	0.173	10	9	0.51326	0.17387	*PDYN*
cg21943117	0.01382	0.453	8	11	0.77238	0.1734	*ACTRT2*
cg07147383	0.00709	0.5999	11	8	0.97877	0.17314	*FSCN2*
cg17819250	0.00709	0.255	11	8	0.97877	0.17314	*RN7SK*
cg12512337	0.00709	0.3881	11	8	0.97877	0.17314	*GSX1*
cg08577913	0.00471	0.1391	11	8	0.96704	0.1726	*TRIM21*
cg12630277	0.00453	0.3749	11	8	0.74096	0.17168	*GJD4*
cg26090020	0.00659	0.8482	7	11	0.29714	0.17103	*C17orf102*
cg20043105	0.00659	0.2109	7	11	0.29714	0.17103	*LINC01551*
cg14663914	0.00443	0.1832	10	9	0.65309	0.16963	*AZU1*
cg12249234	0.00443	0.1769	10	9	0.65309	0.16963	*KSR1*
cg15697257	0.00443	0.1521	10	9	0.65309	0.16963	*SYNPO*
cg05876069	0.00443	0.271	10	9	0.65309	0.16963	*SYNPO*
cg16643542	0.00443	0.3588	10	9	0.65309	0.16963	*AZU1*
cg15610437	0.00443	0.3109	10	9	0.65309	0.16963	*AZU1*
cg11119767	0.00443	0.1948	10	9	0.65309	0.16963	*MAP3K20*
cg00426709	0.0036	0.8176	8	11	0.13685	0.16926	*PRDM13*
cg24693341	0.00266	0.191	11	8	0.32133	0.16836	*PHOX2B*
cg16708938	0.00518	0.317	11	8	0.61999	0.16586	*SIK1*
cg01446692	0.00505	0.5139	11	8	0.96704	0.16516	*CER1*
cg17504164	0.00505	0.5482	11	8	0.96704	0.16516	*ADGRL4*
cg11560431	0.00505	0.4465	11	8	0.96704	0.16516	*SLC22A23*
cg20776947	0.00505	0.6251	11	8	0.96704	0.16516	*P2RX2*
cg24004178	0.00326	0.7799	8	11	0.50851	0.16482	*TRNA*
cg23122650	0.00343	0.4922	11	8	0.70997	0.16436	*COBL*
cg26765567	0.00388	0.3087	9	10	0.48729	0.16302	*FGF4*
cg07637239	0.00312	0.4801	11	8	0.83631	0.16256	*KCNK18*
cg09406107	0.0043	0.4985	11	8	0.77238	0.16171	*AGAP1*
cg14539466	0.0043	0.668	11	8	0.77238	0.16171	*MPDZ*
cg07336872	0.0043	0.2221	11	8	0.77238	0.16171	*ULBP3*
cg03145200	0.0043	0.3358	11	8	0.77238	0.16171	*IL21R*
cg14750475	0.0043	0.5349	11	8	0.77238	0.16171	*RRAS*
cg04940329	0.0043	0.256	11	8	0.77238	0.16171	*KRT23*
cg24720967	0.0043	0.7138	11	8	0.77238	0.16171	*RHOT1*
cg27260684	0.0043	0.6319	11	8	0.77238	0.16171	*KIAA0513*
cg04118102	0.0043	0.6823	11	8	0.77238	0.16171	*ADORA2B*
cg04571189	0.0043	0.4386	11	8	0.77238	0.16171	*ODC1*
cg18915156	0.0043	0.5177	11	8	0.77238	0.16171	*LRRC75A*
cg15690511	0.0043	0.4296	11	8	0.77238	0.16171	*OR4C12*
cg18236066	0.0043	0.2654	11	8	0.77238	0.16171	*RPH3A*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg12380764	0.0043	0.3743	11	8	0.77238	0.16171	*IL19*
cg23866916	0.0043	0.5156	11	8	0.77238	0.16171	*SBNO2*
cg27541604	0.0043	0.3416	11	8	0.77238	0.16171	*AIM2*
cg06244240	0.0043	0.2077	11	8	0.77238	0.16171	*METRNL*
cg21083556	0.0043	0.7029	11	8	0.77238	0.16171	*ADSSL1*
cg03625911	0.0043	0.3176	11	8	0.77238	0.16171	*CHI3L1*
cg12458039	0.0043	0.957	11	8	0.77238	0.16171	*FAM20C*
cg17085688	0.0043	0.2018	11	8	0.77238	0.16171	*GNGT1*
cg18022554	0.0043	0.702	11	8	0.77238	0.16171	*HCN4*
cg11145776	0.0043	0.4186	11	8	0.77238	0.16171	*SLC6A12*
cg11806633	0.0043	0.3528	11	8	0.77238	0.16171	*ARHGEF10L*
cg27119904	0.0043	0.174	11	8	0.77238	0.16171	*RASA3*
cg03774957	0.0043	0.4477	11	8	0.77238	0.16171	*PCDH1*
cg21856784	0.0043	0.2631	11	8	0.77238	0.16171	*TRIM15*
cg15978561	0.0043	0.107	11	8	0.77238	0.16171	*HDAC4*
cg23313963	0.0043	0.8215	11	8	0.77238	0.16171	*TNXB*
cg15102179	0.0043	0.3607	11	8	0.77238	0.16171	*NAP1L4*
cg00411072	0.0043	0.69	11	8	0.77238	0.16171	*HOXB3*
cg21551253	0.0043	0.5238	11	8	0.77238	0.16171	*ADGRD1*
cg03833794	0.0043	0.579	11	8	0.77238	0.16171	*SGSH*
cg16522250	0.0043	0.8636	11	8	0.77238	0.16171	*CNTN6*
cg12806681	0.0043	0.6871	11	8	0.77238	0.16171	*AHRR*
cg07127883	0.0043	0.7867	11	8	0.77238	0.16171	*SHQ1*
cg02226672	0.0043	0.5987	11	8	0.77238	0.16171	*SMPD3*
cg01058360	0.0043	0.4969	11	8	0.77238	0.16171	*PRKAG2*
cg24490227	0.0043	0.1747	11	8	0.77238	0.16171	*JAM3*
cg00114012	0.0043	0.6006	11	8	0.77238	0.16171	*SLC2A8*
cg00864684	0.0043	0.5517	11	8	0.77238	0.16171	*CHST15*
cg25011257	0.0043	0.4431	11	8	0.77238	0.16171	*TH*
cg00697095	0.0043	0.643	11	8	0.77238	0.16171	*GRB7*
cg17400947	0.0043	0.6015	11	8	0.77238	0.16171	*GALNT18*
cg23312375	0.0043	0.5877	11	8	0.77238	0.16171	*RASA3*
cg03991871	0.0043	0.5705	11	8	0.77238	0.16171	*AHRR*
cg08136806	0.0043	0.3945	11	8	0.77238	0.16171	*KRT6C*
cg08105471	0.0043	0.7274	11	8	0.77238	0.16171	*CNTN3*
cg04637264	0.0043	0.4636	11	8	0.77238	0.16171	*WISP3*
cg15646543	0.0043	0.3789	11	8	0.77238	0.16171	*PCDH1*
cg05178291	0.0043	0.1724	11	8	0.77238	0.16171	*SAA1*
cg00667298	0.0043	0.3057	11	8	0.77238	0.16171	*GABBR1*
cg15072976	0.0043	0.5928	11	8	0.77238	0.16171	*GAL3ST2*
cg00540067	0.0043	0.6539	11	8	0.77238	0.16171	*KLF15*
cg04843555	0.0043	0.9189	11	8	0.77238	0.16171	*RN7SK*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg07409200	0.0043	0.6076	11	8	0.77238	0.16171	*FAM216B*
cg22425467	0.0043	0.2421	11	8	0.77238	0.16171	*TRIM15*
cg08735550	0.0043	0.5194	11	8	0.77238	0.16171	*RGS11*
cg26857521	0.0043	0.6951	11	8	0.77238	0.16171	*PEX10*
cg16704797	0.0043	0.7324	11	8	0.77238	0.16171	*KLHL29*
cg08980014	0.0043	0.5822	11	8	0.77238	0.16171	*ARHGEF10*
cg00720829	0.0043	0.2891	11	8	0.77238	0.16171	*TRIM15*
cg22779896	0.0043	0.5677	11	8	0.77238	0.16171	*KIAA0232*
cg05701418	0.0043	0.1767	11	8	0.77238	0.16171	*TRIM15*
cg14039246	0.0043	0.3281	11	8	0.77238	0.16171	*ECHDC2*
cg01604946	0.0043	0.2778	11	8	0.77238	0.16171	*SH3TC2*
cg05870586	0.0043	0.2179	11	8	0.77238	0.16171	*HDAC4*
cg08190125	0.0043	0.4935	11	8	0.77238	0.16171	*IGHG1*
cg02570920	0.0043	0.6208	11	8	0.77238	0.16171	*RN7SK*
cg17023856	0.0043	0.4789	11	8	0.77238	0.16171	*PRKCZ*
cg11691844	0.0043	0.2473	11	8	0.77238	0.16171	*SYTL2*
cg03608093	0.0043	0.5248	11	8	0.77238	0.16171	*DEAF1*
cg16603012	0.0043	0.669	11	8	0.77238	0.16171	*APRT*
cg27152299	0.0043	0.3751	11	8	0.77238	0.16171	*KRTAP5-7*
cg08422803	0.0043	0.3369	11	8	0.77238	0.16171	*ITGB2*
cg25627098	0.0043	0.1326	11	8	0.77238	0.16171	*SPEM2*
cg23726831	0.0043	0.728	11	8	0.77238	0.16171	*SLC4A4*
cg10135708	0.0043	0.5836	11	8	0.77238	0.16171	*UCN2*
cg16928335	0.0043	0.5806	11	8	0.77238	0.16171	*SH2D1A*
cg08936645	0.0043	0.8783	11	8	0.77238	0.16171	*TBC1D1*
cg26120971	0.0043	0.7191	11	8	0.77238	0.16171	*MED30*
cg11800608	0.0043	0.4108	11	8	0.77238	0.16171	*C20orf85*
cg16596317	0.0043	0.4637	11	8	0.77238	0.16171	*BCL10*
cg13557773	0.0043	0.5165	11	8	0.77238	0.16171	*RASA3*
cg22733910	0.00294	0.1637	11	8	0.90134	0.16114	*PDE4B*
cg13525397	0.00294	0.5613	11	8	0.90134	0.16114	*HCG22*
cg19972648	0.00294	0.541	11	8	0.90134	0.16114	*KCNMA1*
cg03604424	0.00294	0.3182	11	8	0.90134	0.16114	*TRIO*
cg08549011	0.00294	0.6287	11	8	0.90134	0.16114	*FSTL4*
cg12690978	0.01301	0.6238	7	11	0.68329	0.16067	*MFAP5*
cg00017842	0.00329	0.4966	9	10	0.65309	0.15771	*EN1*
cg14660328	0.00329	0.7103	9	10	0.65309	0.15771	*TENM4*
cg03564793	0.00357	0.1031	11	8	0.50851	0.15767	*COL12A1*
cg22778788	0.00357	0.1354	11	8	0.50851	0.15767	*NKX2-3*
cg07798610	0.00331	0.4362	8	11	0.53537	0.15671	*PRSS21*
cg05303280	0.0037	0.7094	10	9	1	0.15481	*GLDN*
cg08814947	0.00213	0.6275	11	8	0.70997	0.15404	*KLK11*
cg03233426	0.00284	0.3673	11	8	0.13685	0.15286	*TMEM100*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg22129183	0.00246	0.204	9	10	0.53994	0.15245	*EVA1A*
cg10909152	0.00246	0.4217	9	10	0.53994	0.15245	*SIVA1*
cg23026228	0.00259	0.3201	8	11	0.43238	0.15244	*FNDC1*
cg04285362	0.00259	0.6152	8	11	0.43238	0.15244	*SNORA63*
cg02558625	0.00259	0.1805	8	11	0.43238	0.15244	*COL4A1*
cg21006686	0.00203	0.6581	10	9	0.32676	0.14940	*NOS1*
cg02855850	0.00227	0.5139	11	8	0.2002	0.14819	*IVL*
cg00870837	0.00227	0.7534	11	8	0.2002	0.14819	*C1QTNF8*
cg09418852	0.00227	0.6756	11	8	0.2002	0.14819	*SQOR*
cg13805537	0.00227	0.0406	11	8	0.2002	0.14819	*FAM102A*
cg23121615	0.00274	0.5468	10	9	0.96741	0.14761	*C8orf31*
cg19743254	0.00251	0.1595	11	8	0.53537	0.1475	*OPCML*
cg23304023	0.00205	0.2771	11	8	0.32133	0.14399	*TACC2*
cg24768113	0.0014	0.6313	10	9	0.83812	0.14338	*FIBIN*
cg23345292	0.0014	0.548	8	11	0.12628	0.14066	*LOXHD1*
cg06728135	0.0014	0.4206	8	11	0.12628	0.14066	*IRX2*
cg25242423	0.00536	0.6435	8	11	0.83631	0.13996	*RTBDN*
cg16451324	0.00138	0.4283	11	8	0.83631	0.13807	*PDE1A*
cg08661007	0.00138	0.2824	11	8	0.83631	0.13807	*ROBO1*
cg15534052	0.00254	0.8367	10	7	0.20428	0.13782	*MC2R*
cg17524162	0.00423	0.1312	8	11	0.50851	0.13533	*HLA-DQA2*
cg20016673	0.00538	0.0792	7	11	0.36462	0.13499	*NTNG1*
cg11747462	0.00113	0.7661	11	8	0.97877	0.13367	*OPCML*
cg25784280	0.00459	0.4383	8	11	0.77238	0.12958	*DTNA*
cg23670353	0.00459	0.3761	8	11	0.77238	0.12958	*FGGY*
cg13196652	0.00092	0.1079	10	9	0.26992	0.12805	*ADCY8*
cg18746826	0.00092	0.5495	10	9	0.26992	0.12805	*SCARA5*
cg10085326	0.00291	0.7595	8	11	0.70997	0.12781	*MMP13*
cg08036172	0.00332	0.3204	9	10	0.77486	0.12434	*MGLL*
cg07345515	0.00332	0.4744	9	10	0.77486	0.12434	*TNXB*
cg21335375	0.00332	0.1944	9	10	0.77486	0.12434	*CCL3*
cg12707346	0.00332	0.5058	9	10	0.77486	0.12434	*RASSF3*
cg07470708	0.00332	0.3125	9	10	0.77486	0.12434	*NTF4*
cg04348689	0.00332	0.3853	9	10	0.77486	0.12434	*BTBD7*
cg00275828	0.00332	0.4927	9	10	0.77486	0.12434	*KRTAP2-4*
cg04751839	0.00284	0.5414	9	10	0.65309	0.12179	*GRTP1*
cg16287284	0.00267	0.5552	10	7	0.76956	0.12083	*SLC5A8*
cg08616516	0.00284	0.4086	9	9	0.85968	0.12058	*GRM5*
cg17878899	0.00247	0.7454	9	10	0.41381	0.11967	*KIAA1210*
cg02709924	0.00247	0.3903	9	10	0.41381	0.11967	*NRG1*
cg00573887	0.00174	0.6139	8	11	0.90134	0.11739	*RN7SK*
cg05807489	0.00174	0.4673	8	11	0.90134	0.11739	*SOX8*
cg18052106	0.00246	0.6802	8	11	0.30158	0.11712	*EPHA7*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg27535687	0.00246	0.722	8	11	0.30158	0.11712	*CPLX4*
cg01982835	0.00246	0.5762	8	11	0.30158	0.11712	*DLGAP4*
cg25673598	0.00262	0.7197	10	9	0.93487	0.11706	*EPN2*
cg14387312	0.00221	0.5285	10	9	0.96741	0.11462	*RASL11B*
cg07015886	0.00221	0.4418	10	9	0.96741	0.11462	*TLR5*
cg08027265	0.00221	0.6876	10	9	0.96741	0.11462	*NUDT1*
cg12935818	0.00221	0.3388	10	9	0.96741	0.11462	*RAB17*
cg09578829	0.00221	0.7693	10	9	0.96741	0.11462	*TBC1D1*
cg07236190	0.00221	0.7203	10	9	0.96741	0.11462	*AMDHD1*
cg10769201	0.00221	0.5725	10	9	0.96741	0.11462	*VWA3B*
cg24997585	0.00221	0.8025	10	9	0.96741	0.11462	*GABRB3*
cg23030159	0.00221	0.8235	10	9	0.96741	0.11462	*UNCX*
cg10142837	0.00168	0.5999	9	10	0.90244	0.11355	*PITX2*
cg18432441	0.00175	0.5716	9	10	0.71306	0.11277	*TUB*
cg10320783	0.00175	0.7569	9	10	0.71306	0.11277	*CADM1*
cg21318380	0.00175	0.1962	9	10	0.71306	0.11277	*KCNG1*
cg26346796	0.00175	0.5242	9	10	0.71306	0.11277	*TNXB*
cg09490523	0.00186	0.6362	10	9	0.80633	0.11219	*BCAR1*
cg08525713	0.00143	0.3736	10	9	0.59529	0.11209	*DNAH5*
cg24102792	0.00143	0.9018	10	9	0.59529	0.11209	*TEX29*
cg01181681	0.00143	0.1611	10	9	0.59529	0.11209	*TLR5*
cg23244948	0.00143	0.8445	10	9	0.59529	0.11209	*RPL10L*
cg27183007	0.00143	0.5497	10	9	0.59529	0.11209	*ZPBP*
cg17413460	0.00143	0.673	10	9	0.59529	0.11209	*HAL*
cg13720705	0.00151	0.7486	9	10	0.46204	0.11093	*MTRNR2L7*
cg10888138	0.00121	0.4629	10	9	0.87017	0.10984	*SHISA2*
cg18194850	0.00127	0.8493	9	10	0.59529	0.10878	*SUCLG2*
cg17242362	0.00127	0.6248	9	10	0.59529	0.10878	*ATXN7L1*
cg23878404	0.00127	0.6053	9	10	0.59529	0.10878	*KRTAP1-5*
cg09268963	0.00127	0.6557	9	10	0.59529	0.10878	*SYNE2*
cg01252455	0.00127	0.5573	9	10	0.59529	0.10878	*CPLX2*
cg25060339	0.00168	0.7001	11	8	0.83631	0.10821	*MIR203B*
cg23696618	0.00168	0.7518	11	8	0.83631	0.10821	*SERPINB10*
cg26914334	0.00168	0.6620	11	8	0.83631	0.10821	*GRIK4*
cg03229996	0.00173	0.6076	8	10	0.50494	0.10803	*ZNF469*
cg16179969	0.00097	0.3707	9	9	0.47947	0.10712	*ACAN*
cg07175433	0.00155	0.5629	8	11	0.94843	0.10581	*KCNIP4*
cg07940804	0.00139	0.5196	8	11	0.96704	0.10463	*ACTRT1*
cg15731296	0.00139	0.5094	8	11	0.96704	0.10463	*PRRG3*
cg09718371	0.00091	0.7411	11	8	0.59114	0.10333	*JAKMIP3*
cg22027471	0.00112	0.084	10	8	0.62471	0.10213	*SLC5A4*
cg10451200	0.00112	0.7098	10	8	0.68897	0.10213	*GRM5*
cg19526076	0.00112	0.6926	10	8	0.68897	0.10213	*KLF12*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg15050865	0.00091	0.777	10	9	0.71306	0.10206	*CDH18*
cg15379170	0.00103	0.7144	11	8	0.16003	0.10185	*EFHD1*
cg03099780	0.00106	0.5415	8	11	0.83631	0.10179	*MBNL2*
cg08674227	0.00075	0.4698	11	8	0.77238	0.10127	*XKRX*
cg01126560	0.00075	0.1289	11	8	0.77238	0.10127	*PAXX*
cg00497905	0.00075	0.1443	11	8	0.77238	0.10127	*MYO7A*
cg20959965	0.00075	0.4067	11	8	0.77238	0.10127	*CYBB*
cg14410557	0.00075	0.5356	11	8	0.77238	0.10127	*C9orf62*
cg26651775	0.00075	0.2822	11	8	0.77238	0.10127	*METRN*
cg24860560	0.00075	0.6941	11	8	0.77238	0.10127	*MIR4472-1*
cg24852442	0.00075	0.1635	11	8	0.77238	0.10127	*MYO7A*
cg20860188	0.00075	0.2732	11	8	0.77238	0.10127	*KLHL29*
cg10040821	0.00095	0.4445	10	9	0.53994	0.09971	*ANKS1B*
cg03544781	0.00095	0.669	10	9	0.53994	0.09971	*PDP1*
cg25880242	0.00095	0.8111	10	9	0.53994	0.09971	*ACTRT2*
cg00840694	0.00095	0.6633	10	9	0.53994	0.09971	*MYOM2*
cg20152871	0.00095	0.633	10	9	0.53994	0.09971	*MIR1208*
cg02585931	0.00095	0.7145	10	9	0.53994	0.09971	*GALR3*
cg21549497	0.00095	0.617	10	9	0.53994	0.09971	*CRYAA*
cg11068289	0.00095	0.5057	10	9	0.53994	0.09971	*CHMP6*
cg19091930	0.00095	0.7087	10	9	0.53994	0.09971	*LRRC14B*
cg13010014	0.00095	0.2945	10	9	0.53994	0.09971	*ROBO3*
cg06291334	0.00095	0.0782	10	9	0.53994	0.09971	*SPOP*
cg22101045	0.00095	0.3735	10	9	0.53994	0.09971	*NUP160*
cg18559799	0.00095	0.551	10	9	0.53994	0.09971	*PPY*
cg21564495	0.00095	0.4624	10	9	0.53994	0.09971	*FAM19A5*
cg18778097	0.00095	0.6214	10	9	0.53994	0.09971	*NLRP7*
cg23057567	0.00095	0.391	10	9	0.53994	0.09971	*PNMA8B*
cg10287786	0.00095	0.6589	10	9	0.53994	0.09971	*DSCAML1*
cg26677288	0.00095	0.6044	10	9	0.53994	0.09971	*KIF26B*
cg12838168	0.00095	0.4293	10	9	0.53994	0.09971	*LRRC15*
cg02886188	0.00095	0.2837	10	9	0.53994	0.09971	*DCTD*
cg14432251	0.00095	0.7468	10	9	0.53994	0.09971	*DNAJB6*
cg03333699	0.00095	0.6317	10	9	0.53994	0.09971	*ADAP1*
cg19794207	0.00095	0.3521	10	9	0.53994	0.09971	*GRIN1*
cg26865084	0.00095	0.5346	10	9	0.53994	0.09971	*SMOC2*
cg16726532	0.00095	0.6012	10	9	0.53994	0.09971	*AEBP2*
cg11211263	0.00095	0.6233	10	9	0.53994	0.09971	*STUM*
cg09696747	0.00095	0.7028	10	9	0.53994	0.09971	*TEX29*
cg16257533	0.00095	0.6861	10	9	0.53994	0.09971	*NTM*
cg00234046	0.00095	0.7051	10	9	0.53994	0.09971	*CDH23*
cg00588517	0.00095	0.6509	10	9	0.53994	0.09971	*C2*
cg13491662	0.00095	0.6353	10	9	0.53994	0.09971	*C2orf27B*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg00396699	0.00095	0.6897	10	9	0.53994	0.09971	*CACNA1H*
cg15715746	0.00061	0.9452	11	8	1	0.09879	*MAGEB2*
cg08706312	0.00061	0.8313	11	8	1	0.09879	*MAGEB1*
cg13183298	0.00078	0.566	10	9	0.32676	0.09781	*PLCH2*
cg02143487	0.00078	0.0462	10	9	0.32676	0.09781	*TMEM105*
cg14095048	0.00046	0.1111	10	9	0.77486	0.09776	*TMEM211*
cg19250417	0.00046	0.7096	10	9	0.77486	0.09776	*CRMP1*
cg00139681	0.00062	0.2176	10	9	0.43754	0.09551	*CCDC71L*
cg05046377	0.00062	0.7021	10	9	0.43754	0.09551	*OR51A7*
cg17742099	0.00062	0.5526	10	9	0.43754	0.09551	*GABBR1*
cg10819238	0.00062	0.1908	10	9	0.43754	0.09551	*SBNO2*
cg09284275	0.00062	0.3432	10	9	0.43754	0.09551	*MYH11*
cg10818566	0.00062	0.5818	10	9	0.43754	0.09551	*TTC7A*
cg20063450	0.00062	0.4013	10	9	0.43754	0.09551	*KRT32*
cg15230985	0.00062	0.8494	10	9	0.43754	0.09551	*RPTOR*
cg27310092	0.00062	0.1779	10	9	0.43754	0.09551	*S100A10*
cg26928972	0.00062	0.3466	10	9	0.43754	0.09551	*CSTA*
cg11939346	0.00062	0.8668	10	9	0.43754	0.09551	*KALRN*
cg06586713	0.00062	0.7013	10	9	0.43754	0.09551	*PCLO*
cg26925644	0.00062	0.3798	10	9	0.43754	0.09551	*PHLDB1*
cg23083774	0.00062	0.3935	10	9	0.43754	0.09551	*PLPPR3*
cg01883046	0.00062	0.7095	10	9	0.43754	0.09551	*SP3*
cg14161165	0.00062	0.7987	10	9	0.43754	0.09551	*ASTN2*
cg14187687	0.00062	0.1918	10	9	0.43754	0.09551	*SAMD4A*
cg04949225	0.00062	0.5063	10	9	0.43754	0.09551	*DLEU1*
cg16452651	0.00062	0.3708	10	9	0.43754	0.09551	*ITSN1*
cg02258846	0.00062	0.4423	10	9	0.43754	0.09551	*SCML4*
cg12866960	0.00062	0.4611	10	9	0.43754	0.09551	*IRAK3*
cg24341657	0.00062	0.5979	10	9	0.43754	0.09551	*DOK7*
cg22009908	0.00062	0.1438	10	9	0.43754	0.09551	*EFNA5*
cg00078513	0.00062	0.4067	10	9	0.43754	0.09551	*SNORD115-40*
cg14457875	0.00062	0.5716	10	9	0.43754	0.09551	*MUC21*
cg14462670	0.00062	0.171	10	9	0.43754	0.09551	*CRK*
cg21243944	0.00062	0.5936	10	9	0.43754	0.09551	*RNU6ATAC*
cg02098075	0.00062	0.546	10	9	0.43754	0.09551	*EFCAB1*
cg19984911	0.00062	0.2693	10	9	0.43754	0.09551	*SYNPO*
cg07549474	0.00062	0.4889	10	9	0.43754	0.09551	*MAGEC2*
cg06172871	0.00062	0.2834	10	9	0.43754	0.09551	*HP*
cg00987534	0.00062	0.4476	10	9	0.43754	0.09551	*CLDN3*
cg14022913	0.00062	0.394	10	9	0.43754	0.09551	*NEIL3*
cg15167202	0.00062	0.6919	10	9	0.43754	0.09551	*SYNPO*
cg09824603	0.00062	0.3941	10	9	0.43754	0.09551	*IGFBP3*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg27268708	0.00062	0.6608	10	9	0.43754	0.09551	*HS3ST1*
cg01579636	0.00062	0.4498	10	9	0.43754	0.09551	*IL17B*
cg12738008	0.00062	0.859	10	9	0.43754	0.09551	*MYOM2*
cg24955682	0.00062	0.1483	10	9	0.43754	0.09551	*HLA-G*
cg06578434	0.00062	0.3089	10	9	0.43754	0.09551	*SBNO2*
cg25941151	0.00062	0.4543	10	9	0.43754	0.09551	*TYR*
cg09648454	0.00062	0.5148	10	9	0.43754	0.09551	*ABCC12*
cg13575139	0.00062	0.1119	10	9	0.43754	0.09551	*KCTD6*
cg17631184	0.00062	0.7184	10	9	0.43754	0.09551	*CTTN*
cg17943672	0.00062	0.3481	10	9	0.43754	0.09551	*TCAIM*
cg26657086	0.00062	0.5049	10	9	0.43754	0.09551	*BTNL2*
cg03579045	0.00062	0.603	10	9	0.43754	0.09551	*GATA4*
cg21448927	0.00062	0.4998	10	9	0.43754	0.09551	*FNDC1*
cg23482746	0.00062	0.5897	10	9	0.43754	0.09551	*TMEM266*
cg02961101	0.00062	0.1485	10	9	0.43754	0.09551	*SIAH1*
cg13694680	0.00062	0.4974	10	9	0.43754	0.09551	*FIBIN*
cg26415633	0.00062	0.7187	10	9	0.43754	0.09551	*KLK1*
cg02809611	0.00062	0.3341	10	9	0.43754	0.09551	*OR1F1*
cg19027636	0.00062	0.8043	10	9	0.43754	0.09551	*NSD1*
cg25113360	0.00053	0.2603	8	11	0.3419	0.09351	*GRIK4*
cg05556461	0.00053	0.6092	8	11	0.3419	0.09351	*CARTPT*
cg19139729	0.00036	0.5603	11	8	0.53537	0.09288	*SULT2A1*
cg24822127	0.00048	0.4112	10	9	0.11103	0.09265	*FATE1*
cg07776049	0.00034	0.4089	11	8	0.90134	0.09007	*SNTG2*
cg24640101	0.00034	0.1073	11	8	0.90134	0.09007	*SNORD115-37*
cg26958838	0.0003	0.7912	11	7	0.38909	0.08909	*IRX2*
cg12669395	0.00027	0.3945	11	8	0.70997	0.08845	*DDR1*
cg00583426	0.00027	0.1515	11	8	0.70997	0.08845	*CACNA1H*
cg19175742	0.00027	0.3542	11	8	0.70997	0.08845	*AP3B2*
cg08747676	0.00059	0.4768	10	9	0.41381	0.08785	*C1QTNF8*
cg16966496	0.00021	0.5065	11	8	0.457	0.08649	*TBX3*
cg01998808	0.00021	0.5453	11	8	0.457	0.08649	*LMF1*
cg16034268	0.00021	0.25	11	8	0.457	0.08649	*SFRP1*
cg10052840	0.00054	0.4552	11	8	0.3419	0.08542	*SEMA6B*
cg15597096	0.00054	0.5181	11	8	0.3419	0.08542	*CSF3R*
cg24323597	0.00054	0.8157	11	8	0.3419	0.08542	*KALRN*
cg00074348	0.00016	0.3931	11	8	0.59114	0.08401	*APLNR*
cg21591938	0.00016	0.6461	11	8	0.59114	0.08401	*FAR2*
cg17823175	0.00016	0.2411	11	8	0.59114	0.08401	*AZU1*
cg22620071	0.00016	0.6982	11	8	0.59114	0.08401	*YTHDC2*
cg24517501	0.00016	0.2411	11	8	0.59114	0.08401	*GFI1*
cg08625482	0.00016	0.3715	11	8	0.59114	0.08401	*NEFL*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg05294112	0.00016	0.1785	11	8	0.59114	0.08401	*SOX1*
cg09674502	0.00016	0.7046	11	8	0.59114	0.08401	*GFI1*
cg16631083	0.00016	0.4827	11	8	0.59114	0.08401	*HUNK*
cg02987482	0.00016	0.1434	11	8	0.59114	0.08401	*MLLT1*
cg01766941	0.00016	0.5479	11	8	0.59114	0.08401	*GFI1*
cg20689476	0.00016	0.4021	11	8	0.59114	0.08401	*PPP2R2C*
cg18004847	0.00016	0.2749	11	8	0.59114	0.08401	*SBNO2*
cg04777348	0.00016	0.5611	11	8	0.59114	0.08401	*GFI1*
cg07717083	0.00016	0.6494	11	8	0.59114	0.08401	*TNXB*
cg18618429	0.00016	0.142	11	8	0.59114	0.08401	*CSTA*
cg09488090	0.00031	0.5882	11	8	0.26455	0.08091	*PMFBP1*
cg26394380	0.00031	0.6128	11	8	0.26455	0.08091	*SFTPB*
cg16544010	0.00031	0.7266	11	8	0.26455	0.08091	*DLK1*
cg13250566	0.00031	0.5158	11	8	0.26455	0.08091	*TUBG2*
cg15060366	0.00022	0.1775	9	10	0.23603	0.08	*PCSK2*
cg14561934	0.0001	0.5273	10	9	0.59529	0.07704	*FAM171A1*
cg00947324	0.00026	0.8096	10	8	0.16801	0.07562	*AK7*
cg26123605	0.00008	0.1344	10	7	0.26116	0.07049	*ZIC1*
cg14431020	0.00082	0.3698	8	9	0.88509	0.06106	*ELMO1*
cg23749637	0.00098	0.1166	8	10	0.89386	0.05915	*NXN*
cg07812957	0.00069	0.5273	8	11	1	0.0564	*KLF2*
cg14544831	0.00069	0.195	8	11	1	0.0564	*BCL2*
cg23009780	0.00069	0.6074	8	11	1	0.0564	*ADRA2B*
cg26201596	0.0006	0.4575	8	11	0.74096	0.05566	*DIP2C*
cg03706086	0.00051	0.4413	8	11	0.90134	0.0548	*NCOA2*
cg01293740	0.00051	0.3207	8	11	0.90134	0.0548	*CACNG8*
cg09842053	0.00051	0.7695	8	11	0.90134	0.0548	*XDH*
cg24764810	0.00051	0.5592	8	11	0.90134	0.0548	*HCG22*
cg11228126	0.00055	0.2631	9	9	0.40106	0.05399	*NEUROG3*
cg17919471	0.00033	0.6935	8	11	0.64944	0.05215	*XAGE3*
cg06729381	0.00029	0.6602	9	10	0.83812	0.0520	*SYT7*
cg21878759	0.00029	0.5101	9	10	0.83812	0.0520	*LOXHD1*
cg14765834	0.00043	0.5971	9	10	0.83812	0.05189	*YBX2*
cg20951266	0.00043	0.4929	9	10	0.83812	0.05189	*SMCP*
cg16591659	0.00043	0.7846	9	10	0.83812	0.05189	*NPTX1*
cg14962049	0.00043	0.8189	9	10	0.83812	0.05189	*PRELID2*
cg26331243	0.00025	0.6428	9	10	0.93487	0.05121	*CCDC33*
cg14520512	0.00036	0.6286	9	10	0.56729	0.05109	*MBNL3*
cg24508310	0.00036	0.5879	9	10	0.56729	0.05109	*BCOR*
cg25927227	0.00036	0.5727	9	10	0.56729	0.05109	*SFRP1*
cg11229415	0.00029	0.5424	9	10	0.71306	0.05015	*PLCH2*
cg11612905	0.00029	0.8075	9	10	0.71306	0.05015	*DGKD*
cg01759110	0.00029	0.6416	9	10	0.71306	0.05015	*ADAMDEC1*

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	HR	Gene
cg00328597	0.00029	0.6838	9	10	0.71306	0.05015	*ACTN2*
cg19145082	0.00029	0.4592	9	10	0.71306	0.05015	*CHST2*
cg20048109	0.00029	0.5326	9	10	0.71306	0.05015	*MAGI2*
cg05573626	0.00029	0.3643	9	10	0.71306	0.05015	*ZNF423*
cg17086773	0.00029	0.6137	9	10	0.71306	0.05015	*CD200R1L*
cg16375358	0.00029	0.5481	9	10	0.71306	0.05015	*CACNG5*
cg04755857	0.00024	0.6854	8	11	0.38552	0.04991	*EVC*
cg08313382	0.00024	0.5539	8	11	0.38552	0.04991	*MIR4278*
cg01206723	0.00024	0.5947	8	11	0.38552	0.04991	*RNU4-1*
cg16491739	0.00014	0.4567	10	9	1	0.04713	*C14orf180*
cg14737125	0.00019	0.8232	10	9	0.48729	0.04700	*GBX2*
cg06079509	0.00016	0.6766	9	10	0.48729	0.04684	*WFS1*
cg10331779	0.00024	0.3407	7	11	0.46828	0.04612	*CTNND2*
cg17588373	0.00014	0.5269	10	9	0.13057	0.04552	*GPM6B*
cg27426921	0.00009	0.7377	10	9	0.90244	0.04524	*PFKP*
cg12580770	0.00007	0.5010	10	8	0.22985	0.04387	*HTR5A*
cg08318283	0.00011	0.1952	9	10	0.26992	0.04358	*HCN4*
cg05035315	0.00011	0.4064	9	10	0.26992	0.04358	*OPCML*
cg04697056	0.00011	0.4756	9	10	0.26992	0.04358	*FAT1*
cg04086012	0.00011	0.6792	9	10	0.26992	0.04358	*TRIML1*
cg05576949	0.00011	0.3892	9	10	0.26992	0.04358	*IGF2BP2*
cg11873482	0.00006	0.2734	11	8	0.50851	0.04249	*TAC1*
cg04139223	0.00006	0.4809	11	8	0.50851	0.04249	*SLC9A3*
cg14206523	0.00004	0.6480	10	9	0.65309	0.04215	*GJD2*
cg11889730	0.00006	0.3548	9	10	0.19103	0.03748	*MTRNR2L7*
cg14737484	0.00975	0.0411	11	8	0.44036		*TNXB*
cg04318657	0.0002	0.3044	9	10	0.94502		*PRKX*
cg11638347	0.0002	0.5405	9	10	0.94502		*HLCS*
cg18142353	0.0002	0.2310	9	10	0.94502		*LRP6*
cg11678461	0.0002	0.4534	9	10	0.94502		*OSBPL5*
cg22202121	0.00012	0.2889	8	11	0.94843		*ZNF292*
cg05255275	0.00981	0.1323	9	9	0.28907		*C14orf39*
cg01377936	0.00253	0.5973	9	10	0.36869		*DMD*
cg16101493	0.00253	0.1580	9	10	0.36869		*POU4F3*
cg10815229	0.00253	0.1535	9	10	0.17753		*HELT*
cg06532574	0.00107	0.8731	8	11	0.81254		*ELL2*
cg18568145	0.00107	0.3519	8	11	0.81254		*FAM189B*

Annex IX Additional information about the 691 candidate biomarkers of prognostic of DNA methylation in patients with AML-M2 categorized in the intermediate prognostic risk group.

CpG sites	location	status	ratio	delta beta	*p-value*	Gene	Bibliographic analysis	cluster
cg00645383	Distal Intergenic	low	1.11	-0.28	7.91E-08	SPACA7	non-leukemia cancer types	
cg12899423	1st Intron	low	1.11	-0.29	1.63E-05	ALX4	cited in AML	
cg02939781	3' UTR	low	0.90	-0.29	9.67E-08	KLHL6	cited in AML	
cg23357198	Promoter (1-2kb)	low	1.38	-0.34	7.78E-07	PTPRT	cited in AML	49
cg17264618	Promoter (<=1kb)	low	1.38	-0.33	1.13E-04	ENTPD3	non-leukemia cancer types	49
cg25824217	Promoter (<=1kb)	low	1.11	-0.54	2.17E-05	HLA-DPA1	cited in AML	12
cg14178336	Promoter (1-2kb)	low	1.11	-0.39	7.79E-07	CALN1	non-leukemia cancer types	12
cg00622702	3' UTR	low	1.11	-0.45	1.11E-06	IFR1	cited in AML	12
cg06321596	Promoter (1-2kb)	low	1.11	-0.49	2.17E-05	XYLT1	non-leukemia cancer types	12
cg08708961	Other Intron	low	1.11	-0.65	2.17E-05	PSEN2	cited in AML	12
cg12224030	Promoter (1-2kb)	low	1.11	-0.29	2.17E-05	DLX4	cited in AML	12
cg14396892	Distal Intergenic	low	0.73	-0.41	3.26E-04	MIR4291	never cited	
cg08198176	Promoter (<=1kb)	low	0.90	-0.34	2.25E-05	ITGA9	non-AML leukemia types	75
cg03572859	Promoter (<=1kb)	low	0.90	-0.49	1.91E-06	SORBS3	non-leukemia cancer types	75
cg17142470	Promoter (<=1kb)	low	0.90	-0.51	9.40E-06	SORBS3	non-leukemia cancer types	75
cg18867923	Other Intron	low	0.90	-0.43	8.11E-08	TBX1	non-AML leukemia types	75
cg22595391	Promoter (<=1kb)	low	1.00	-0.22	2.04E-04	CYBC1	cited in PubMed	
cg07691306	Other Intron	low	1.25	-0.23	4.57E-05	ARID3A	cited in AML	
cg25832925	Downstream (<=300)	low	1.11	-0.43	1.19E-05	ARX	cited in AML	
cg08076437	Downstream (<=300)	low	1.38	-0.46	2.72E-06	IRX3	cited in AML	111
cg00741986	Other Intron	low	1.38	-0.25	2.40E-05	TNIP2	non-AML leukemia types	111
cg00306721	Promoter (<=1kb)	low	1.13	-0.21	8.23E-05	BSCL2	non-AML leukemia types	
cg01496199	Distal Intergenic	low	1.43	-0.25	8.55E-04	IFNL2	non-AML leukemia types	
cg07820189	Distal Intergenic	low	0.73	-0.31	2.58E-04	LAMC2	non-AML leukemia types	

cg07991621	Promoter (<=1kb)	low	0.73	-0.52	2.65E-05	SH3BP2	non-AML leukemia types	32
cg06588645	Promoter (2-3kb)	low	0.73	-0.55	2.65E-05	TNS3	non-leukemia cancer types	32
cg22738642	Distal Intergenic	low	0.73	-0.31	2.65E-05	PRICKLE1	non-AML leukemia types	32
cg27123691	Promoter (<=1kb)	low	0.73	-0.41	1.18E-05	CSPG4	cited in AML	32
cg17858880	Promoter (2-3kb)	low	0.73	-0.32	1.66E-05	TNS3	non-leukemia cancer types	32
cg11223365	Distal Intergenic	low	0.73	-0.50	2.65E-05	WNT9A	cited in AML	32
cg10734665	Promoter (<=1kb)	low	0.73	-0.52	2.65E-05	ATP10A	non-AML leukemia types	32
cg25151498	Other Intron	low	0.73	-0.54	2.65E-05	ETV5	non-AML leukemia types	32
cg10542562	Promoter (<=1kb)	low	0.73	-0.41	2.65E-05	FLI1	cited in AML	32
cg10745272	Promoter (<=1kb)	low	0.73	-0.38	3.34E-06	SH3BP2	non-AML leukemia types	32
cg15630950	Promoter (<=1kb)	low	0.73	-0.37	2.65E-05	HLA-DOA	cited in AML	32
cg27635394	Promoter (<=1kb)	low	0.64	-0.30	6.28E-05	HIST1H2BB	non-leukemia cancer types	
cg24943609	Promoter (1-2kb)	low	1.38	-0.23	1.04E-04	ZNF652	cited in AML	
cg02639366	Promoter (1-2kb)	low	0.73	-0.22	2.03E-05	AGO4	non-leukemia cancer types	302
cg18252102	Promoter (1-2kb)	low	0.73	-0.21	2.65E-05	FARP1	non-leukemia cancer types	302
cg02198513	Other Intron	low	1.38	-0.65	2.65E-05	TMEM156	non-leukemia cancer types	221
cg04359840	Promoter (1-2kb)	low	1.38	-0.48	8.77E-07	XYLT1	non-leukemia cancer types	221
cg13225413	Promoter (<=1kb)	low	1.11	-0.30	2.17E-05	ZNF232	non-leukemia cancer types	156
cg08668790	Promoter (<=1kb)	low	1.11	-0.50	5.17E-05	ZNF154	non-leukemia cancer types	156
cg12407791	Other Intron	low	1.11	-0.38	5.11E-06	UNC13D	cited in AML	156
cg20392842	Promoter (<=1kb)	low	0.90	-0.51	2.17E-05	HLA-DMB	cited in AML	60
cg08515841	Promoter (<=1kb)	low	0.90	-0.62	2.17E-05	KLF7	cited in AML	60
cg21429394	Promoter (<=1kb)	low	0.90	-0.37	2.08E-05	SLC17A8	non-leukemia cancer types	60
cg16236263	Promoter (<=1kb)	low	0.90	-0.45	2.17E-05	HLA-DMB	cited in AML	60
cg16430854	Promoter (<=1kb)	low	0.90	-0.24	4.85E-06	SDK2	non-leukemia cancer types	60
cg02627403	3' UTR	low	0.90	-0.31	4.23E-05	UNC13D	cited in AML	60
cg01951879	Downstream (<=300)	low	0.90	-0.54	2.17E-05	IRX3	cited in AML	60

cg10792987	Other Intron	low	0.90	-0.57	2.17E-05	ELL	cited in AML	60
cg13320436	Distal Intergenic	low	0.90	-0.25	1.12E-04	MRPL15	non-leukemia cancer types	60
cg03015498	Distal Intergenic	low	1.38	-0.30	2.65E-05	SFMBT2	cited in AML	
cg01467100	Promoter (1-2kb)	low	0.73	-0.24	1.16E-06	PFKFB3	cited in AML	
cg03187301	Promoter (1-2kb)	low	0.90	-0.25	5.51E-06	MCRS1	non-AML leukemia types	
cg22074576	1st Intron	low	1.11	-0.59	5.65E-07	OSBPL5	non-leukemia cancer types	
cg15594585	Distal Intergenic	low	0.73	-0.26	1.27E-06	ZNF678	never cited	
cg10002133	Promoter (<=1kb)	low	1.38	-0.20	2.65E-05	NTRK3	cited in AML	20
cg07010633	Other Intron	low	1.38	-0.45	2.65E-05	UNC13D	cited in AML	20
cg08347500	Downstream (<=300)	low	1.38	-0.47	2.65E-05	IRX3	cited in AML	20
cg14905657	Promoter (<=1kb)	low	1.38	-0.21	2.65E-05	LMO3	non-AML leukemia types	20
cg21747330	Promoter (<=1kb)	low	1.38	-0.55	2.65E-05	GRIA3	non-leukemia cancer types	
cg16207110	Promoter (1-2kb)	low	0.73	-0.49	2.65E-05	TR	cited in AML	122
cg08369368	Promoter (<=1kb)	low	0.73	-0.43	2.65E-05	NSD1	cited in AML	122
cg06400704	Promoter (1-2kb)	low	1.38	-0.45	5.91E-06	FMN2	non-AML leukemia types	
cg24924577	1st Intron	low	1.38	-0.36	8.66E-05	SEMA4B	non-AML leukemia types	
cg05818394	Promoter (1-2kb)	low	0.70	-0.20	2.90E-05	HMGB1	cited in AML	
cg24387864	Promoter (1-2kb)	low	1.38	-0.51	2.65E-05	CCND1	cited in AML	
cg18176723	Other Intron	low	1.25	-0.24	4.57E-05	PPCDC	non-leukemia cancer types	
cg03599590	Promoter (1-2kb)	low	1.25	-0.36	4.57E-05	SLC35A5	non-leukemia cancer types	
cg07967918	Promoter (1-2kb)	low	1.38	-0.29	3.04E-05	SOBP	non-AML leukemia types	105
cg06975048	3' UTR	low	1.38	-0.24	2.65E-05	KCB3	non-leukemia cancer types	105
cg06427054	Other Intron	low	1.38	-0.40	2.65E-05	GSX2	cited in AML	
cg05649922	1st Intron	low	1.11	-0.33	4.53E-06	ARID1A	cited in AML	67
cg12573289	1st Intron	low	1.11	-0.25	2.33E-06	CCM2	non-leukemia cancer types	67
cg17103217	Promoter (<=1kb)	low	1.11	-0.24	6.21E-06	B3GALT4	non-leukemia cancer types	67
cg09584521	Promoter (<=1kb)	low	1.11	-0.36	2.17E-05	CD58	cited in AML	67

cg13707025	Promoter (<=1kb)	low	1.38	-0.32	1.11E-05	KCNK10	non-leukemia cancer types	
cg21518432	Promoter (<=1kb)	low	1.38	-0.20	6.07E-05	SHC4	non-leukemia cancer types	280
cg12258811	Promoter (<=1kb)	low	1.38	-0.26	2.65E-05	PER3	cited in AML	280
cg23681664	Promoter (1-2kb)	low	0.90	-0.57	2.17E-05	CPNE9	never cited	
cg22371591	Promoter (<=1kb)	low	0.73	-0.62	2.65E-05	MSX1	cited in AML	48
cg27175287	Promoter (1-2kb)	low	0.73	-0.32	3.65E-05	FOXE3	non-AML leukemia types	48
cg03247049	Promoter (<=1kb)	low	1.11	-0.38	4.22E-05	AXL	cited in AML	149
cg19037007	3' UTR	low	1.11	-0.27	2.09E-05	SLC52A3	non-leukemia cancer types	149
cg12571423	Promoter (<=1kb)	low	1.38	-0.28	1.30E-04	CC1	cited in AML	6
cg20589883	Other Intron	low	1.38	-0.42	2.65E-05	ELOVL6	cited in AML	6
cg21618521	Promoter (<=1kb)	low	1.38	-0.31	1.50E-04	B3GALT4	non-leukemia cancer types	6
cg21611682	Other Intron	low	1.38	-0.26	2.65E-05	LRP5	cited in AML	6
cg04313565	Promoter (2-3kb)	low	1.38	-0.30	5.31E-06	XYLT1	non-leukemia cancer types	6
cg16300030	Promoter (<=1kb)	low	1.38	-0.50	1.05E-06	HLA-DMB	cited in AML	6
cg16794579	Promoter (2-3kb)	low	1.38	-0.51	2.65E-05	XYLT1	non-leukemia cancer types	6
cg17901382	Promoter (2-3kb)	low	1.38	-0.40	2.65E-05	TSEN54	non-leukemia cancer types	6
cg12135856	Promoter (<=1kb)	low	0.90	-0.39	2.17E-05	DSCAM	non-AML leukemia types	
cg07071609	Promoter (<=1kb)	low	0.90	-0.48	2.17E-05	PLIN5	non-leukemia cancer types	
cg17239923	Promoter (<=1kb)	low	1.38	-0.67	2.65E-05	FLI1	cited in AML	85
cg07834682	3' UTR	low	1.38	-0.23	3.04E-07	SIX2	non-AML leukemia types	85
cg04779860	Promoter (1-2kb)	low	1.38	-0.36	2.09E-06	EBF3	cited in AML	
cg27346806	Promoter (<=1kb)	low	0.90	-0.61	2.17E-05	VENTX	cited in AML	295
cg23357130	1st Intron	low	0.90	-0.54	2.17E-05	OSBPL5	non-leukemia cancer types	295
cg24640390	Distal Intergenic	low	0.90	-0.34	2.37E-05	NEUROG3	non-AML leukemia types	
cg09005679	Promoter (<=1kb)	low	0.90	-0.28	1.59E-05	EDN3	non-leukemia cancer types	146
cg08883485	Promoter (2-3kb)	low	0.90	-0.35	2.17E-05	V1	cited in AML	146
cg24217984	Promoter (<=1kb)	low	0.73	-0.37	1.20E-06	RGMA	non-AML leukemia types	

cg08001559	Promoter (<=1kb)	low	1.11	-0.38	3.55E-05	GNG2	non-AML leukemia types	
cg18342462	Promoter (<=1kb)	low	0.90	-0.51	2.17E-05	C11orf88	never cited	276
cg03655371	Distal Intergenic	low	0.90	-0.68	2.17E-05	TIFAB	cited in AML	276
cg05836145	Promoter (<=1kb)	low	0.73	-0.29	2.26E-06	SP8	non-AML leukemia types	
cg07681748	Promoter (1-2kb)	low	0.90	-0.59	2.17E-05	CD200	cited in AML	
cg04365202	Promoter (2-3kb)	low	0.73	-0.40	2.65E-05	LHX9	non-leukemia cancer types	
cg05257898	Promoter (<=1kb)	low	1.57	-0.22	1.14E-06	NKAP	non-AML leukemia types	
cg26487031	Promoter (<=1kb)	low	0.64	-0.35	7.72E-06	MPZL2	non-leukemia cancer types	
cg00779638	Promoter (1-2kb)	low	0.90	-0.41	2.17E-05	AGTPBP1	non-leukemia cancer types	
cg17156534	Promoter (1-2kb)	low	1.11	-0.43	5.43E-05	TOP1	cited in AML	
cg14422240	Other Intron	low	1.11	-0.39	2.17E-05	CMTR1	non-leukemia cancer types	
cg02876258	Promoter (2-3kb)	low	1.38	-0.50	5.05E-07	FGF5	non-AML leukemia types	
cg07928083	Promoter (1-2kb)	low	1.38	-0.36	8.04E-05	FOXB1	non-leukemia cancer types	
cg09757109	Promoter (<=1kb)	low	0.90	-0.51	2.17E-05	DIXDC1	cited in AML	
cg25042430	Promoter (1-2kb)	low	1.11	-0.37	2.17E-05	KIAA1217	non-leukemia cancer types	
cg21068610	Promoter (1-2kb)	low	0.90	-0.22	2.17E-05	CHD3	cited in AML	
cg14371590	Promoter (<=1kb)	low	1.11	-0.42	4.37E-06	SLC26A10	cited in PubMed	
cg07220903	Other Intron	low	1.11	-0.49	1.26E-07	CCDC12	cited in AML	
cg24994127	Other Intron	low	1.38	-0.38	2.65E-05	RALGAPA2	non-leukemia cancer types	178
cg07941108	Downstream (<=300)	low	1.38	-0.37	3.88E-05	PSMC1	non-leukemia cancer types	178
cg24250393	Promoter (<=1kb)	low	0.73	-0.29	5.90E-07	PRKCB	cited in AML	
cg04918402	Promoter (<=1kb)	low	1.57	-0.25	6.28E-05	LIMD2	non-leukemia cancer types	
cg27257822	Other Intron	low	0.90	-0.20	3.93E-06	EPHB3	non-AML leukemia types	
cg20276630	Distal Intergenic	low	0.73	-0.41	7.14E-05	PDLIM1	cited in AML	
cg04420723	Promoter (<=1kb)	low	0.73	-0.67	2.65E-05	ZNF184	non-leukemia cancer types	
cg05551825	Other Intron	low	0.73	-0.43	2.65E-05	RNF216	non-AML leukemia types	
cg20421446	Distal Intergenic	low	1.25	-0.31	4.57E-05	NRN1	non-leukemia cancer types	

cg18073471	Promoter (<=1kb)	low	1.11	-0.54	2.17E-05	PRDM8	non-leukemia cancer types	165
cg13276502	Distal Intergenic	low	1.11	-0.48	2.17E-05	SOX4	cited in AML	165
cg23045908	Promoter (1-2kb)	low	0.90	-0.58	2.17E-05	PDE4B	non-AML leukemia types	
cg08667275	Downstream (<=300)	low	1.11	-0.30	8.58E-05	RNF26	non-AML leukemia types	
cg05327596	Downstream (<=300)	low	0.73	-0.26	1.06E-06	COL11A2	cited in AML	
cg14762436	1st Intron	low	1.38	-0.52	1.03E-07	OSBPL3	non-AML leukemia types	195
cg05071046	Distal Intergenic	low	1.38	-0.40	1.25E-05	IRX3	cited in AML	195
cg15683295	Other Exon	low	0.73	-0.34	2.65E-05	HOTTIP	cited in AML	
cg18653350	Promoter (<=1kb)	low	1.38	-0.42	2.65E-05	SACS	cited in AML	
cg19839325	1st Intron	low	0.73	-0.35	2.72E-05	KLHL26	non-leukemia cancer types	
cg27396824	Other Exon	low	0.70	-0.21	0.001052	ZAN	non-AML leukemia types	
cg22996489	Promoter (<=1kb)	low	0.73	-0.52	1.16E-06	OXGR1	non-leukemia cancer types	
cg06638433	Promoter (<=1kb)	low	0.73	-0.45	3.88E-06	IGF2BP1	cited in AML	
cg26111030	Promoter (<=1kb)	low	1.11	-0.49	2.78E-04	ERBB2	cited in AML	
cg22902505	Promoter (<=1kb)	low	1.11	-0.53	2.17E-05	PRDM8	non-leukemia cancer types	
cg14892768	Promoter (<=1kb)	low	0.90	-0.35	8.86E-05	AXL	cited in AML	278
cg08586366	Promoter (1-2kb)	low	0.90	-0.48	5.36E-06	FLI1	cited in AML	278
cg03465652	Other Intron	low	0.73	-0.39	1.11E-05	GLI2	cited in AML	
cg10334354	Promoter (<=1kb)	low	0.73	-0.33	4.94E-06	EPHA5	non-AML leukemia types	
cg17691657	Promoter (<=1kb)	low	1.38	-0.20	1.48E-05	SLC4A4	non-AML leukemia types	
cg07275218	Promoter (1-2kb)	low	1.00	-0.27	6.41E-05	BRD2	cited in AML	
cg19471574	Distal Intergenic	low	1.11	-0.30	2.17E-05	TMEM161B	non-leukemia cancer types	
cg13409248	Promoter (<=1kb)	low	0.73	-0.62	2.65E-05	ENTPD3	non-leukemia cancer types	273
cg19175386	Distal Intergenic	low	0.73	-0.44	2.65E-05	TBX3	non-AML leukemia types	273
cg27077033	Distal Intergenic	low	0.73	-0.24	2.30E-07	CEP170B	never cited	273
cg12220058	Promoter (1-2kb)	low	0.73	-0.57	2.65E-05	NMB	cited in AML	
cg21760990	Promoter (<=1kb)	low	0.73	-0.35	1.23E-05	TBC1D32	cited in PubMed	

cg25313172	Promoter (<=1kb)	low	1.11	-0.39	2.13E-04	KRT7	non-AML leukemia types	78
cg02390329	Promoter (1-2kb)	low	1.11	-0.43	2.72E-05	ZIC4	cited in AML	78
cg26955132	Other Intron	low	1.11	-0.29	8.35E-05	FAM234B	cited in PubMed	113
cg18305855	Other Intron	low	1.11	-0.45	2.17E-05	BMT2	cited in AML	113
cg05395947	Distal Intergenic	low	0.73	-0.33	2.65E-05	SASH1	non-leukemia cancer types	
cg20645065	Promoter (<=1kb)	low	0.73	-0.29	1.46E-05	ALPL	cited in AML	35
cg20910202	Promoter (<=1kb)	low	0.73	-0.40	1.91E-06	KBTBD11	non-AML leukemia types	35
cg09436375	Promoter (<=1kb)	low	0.73	-0.38	6.98E-05	GNMT	cited in AML	35
cg01606885	Distal Intergenic	low	1.11	-0.25	2.17E-05	HSPB3	non-leukemia cancer types	
cg02457623	1st Intron	low	1.57	-0.23	6.28E-05	ATP2B4	non-AML leukemia types	
cg11175192	Promoter (<=1kb)	low	0.73	-0.35	1.61E-05	WNT6	non-AML leukemia types	
cg18495563	Promoter (<=1kb)	low	0.80	-0.23	4.57E-05	TCP11L1	cited in PubMed	
cg05923595	Promoter (<=1kb)	low	1.38	-0.32	7.26E-06	AZIN2	non-leukemia cancer types	
cg01597891	Promoter (<=1kb)	low	0.64	-0.23	1.27E-07	I	cited in AML	
cg14640670	Promoter (1-2kb)	low	1.38	-0.21	7.55E-05	PURA	cited in AML	103
cg07557423	Promoter (1-2kb)	low	1.38	-0.51	2.65E-05	ATP8A1	non-leukemia cancer types	103
cg17345569	Promoter (<=1kb)	low	1.38	-0.46	1.91E-06	GNMT	cited in AML	
cg27439456	Promoter (<=1kb)	low	1.11	-0.67	2.17E-05	OSCP1	cited in AML	
cg10592171	Promoter (2-3kb)	low	0.73	-0.39	8.56E-06	DLX4	cited in AML	
cg06248480	Promoter (<=1kb)	low	1.11	-0.27	2.17E-05	LAMB1	cited in AML	
cg19211800	Promoter (<=1kb)	low	0.80	-0.22	3.36E-06	MARCKS	cited in AML	
cg15246619	Other Intron	low	0.73	-0.31	1.84E-05	FGF17	non-AML leukemia types	
cg09681675	Distal Intergenic	low	1.38	-0.40	2.65E-05	ZNF597	non-leukemia cancer types	
cg04995300	Distal Intergenic	low	0.90	-0.29	3.41E-06	KBTBD8	cited in PubMed	
cg24378136	Promoter (1-2kb)	low	1.38	-0.35	2.06E-06	RNF39	non-leukemia cancer types	
cg03469082	Promoter (<=1kb)	low	1.38	-0.45	1.71E-05	GABRG1	non-AML leukemia types	
cg23196346	Other Intron	low	0.90	-0.42	2.17E-05	KIAA1217	non-leukemia cancer types	

cg23119487	Distal Intergenic	low	0.73	-0.33	7.59E-06	TMED3	non-leukemia cancer types	
cg05977462	1st Intron	low	0.73	-0.25	2.65E-05	CUX2	non-AML leukemia types	
cg26508928	Distal Intergenic	high	1.38	-0.26	1.66E-06	ZNF519	cited in PubMed	
cg01408845	Other Intron	high	0.90	-0.40	7.90E-06	SARM1	non-leukemia cancer types	5
cg19628739	Promoter (2-3kb)	high	0.90	-0.43	2.17E-05	PNPLA3	non-AML leukemia types	5
cg16151494	Distal Intergenic	high	0.90	-0.51	2.65E-06	GPBP1	non-leukemia cancer types	5
cg01931994	Promoter (<=1kb)	high	1.38	-0.39	2.55E-05	BRINP2	cited in PubMed	
cg00639635	Distal Intergenic	high	1.11	-0.24	5.52E-05	FUCA2	non-leukemia cancer types	
cg06578276	Other Intron	high	1.38	-0.46	2.65E-05	BAIAP2	non-leukemia cancer types	190
cg09083945	Promoter (2-3kb)	high	1.38	-0.40	3.26E-04	BAIAP2	non-leukemia cancer types	190
cg08147563	1st Intron	high	0.90	-0.30	5.10E-04	ROBO1	cited in AML	
cg23973972	Distal Intergenic	high	0.90	-0.46	2.32E-05	CNDP2	non-leukemia cancer types	191
cg00059161	Other Exon	high	0.90	-0.36	1.69E-05	SLITRK3	non-leukemia cancer types	191
cg22333471	Distal Intergenic	high	0.90	-0.26	4.61E-05	SDHAF1	non-leukemia cancer types	
cg01116873	Distal Intergenic	high	1.38	-0.43	3.59E-05	RN7SK	non-leukemia cancer types	
cg22366943	Other Intron	high	0.73	-0.40	2.65E-05	NKAIN2	non-AML leukemia types	
cg00036408	Distal Intergenic	high	1.11	-0.42	2.17E-05	TMEM105	cited in PubMed	
cg19404979	Promoter (<=1kb)	high	1.11	-0.28	3.31E-04	ELSPBP1	cited in PubMed	
cg14150727	Promoter (<=1kb)	high	1.11	-0.20	4.24E-05	LGR6	non-leukemia cancer types	
cg18766685	Distal Intergenic	high	0.90	-0.23	2.17E-05	SHH	cited in AML	
cg25050975	Other Intron	high	0.73	-0.29	2.65E-05	NXN	non-leukemia cancer types	
cg08988179	Promoter (<=1kb)	high	1.11	-0.23	2.17E-05	C1QL1	non-leukemia cancer types	
cg24336447	Distal Intergenic	high	1.38	-0.50	2.65E-05	GALP	non-AML leukemia types	
cg06322601	Other Intron	high	1.38	-0.23	3.26E-04	RASA4	non-AML leukemia types	
cg02952295	Other Intron	high	1.38	-0.56	3.26E-04	TRPM8	non-AML leukemia types	
cg17398252	Promoter (<=1kb)	high	0.80	-0.31	4.57E-05	BVES	non-leukemia cancer types	
cg05184519	Other Intron	high	1.38	-0.49	4.55E-05	NTM	cited in AML	

cg02198701	3' UTR	high	0.73	-0.37	2.65E-05	IRX6	non-leukemia cancer types	
cg16599143	Promoter (1-2kb)	high	0.73	-0.36	4.47E-04	FMO3	non-AML leukemia types	
cg11633310	Promoter (<=1kb)	high	0.73	-0.23	9.04E-05	MS4A10	non-leukemia cancer types	
cg12650635	Promoter (<=1kb)	high	0.73	-0.23	2.98E-05	AQP2	cited in AML	
cg13691209	Distal Intergenic	high	1.38	-0.42	4.05E-04	PLEKHG4B	cited in PubMed	
cg08432013	Promoter (<=1kb)	high	0.90	-0.36	3.70E-06	DLG2	non-AML leukemia types	86
cg13223682	Distal Intergenic	high	0.90	-0.61	2.17E-05	SP3	cited in AML	86
cg26578156	1st Intron	high	0.90	-0.44	2.17E-05	ZNF423	cited in AML	86
cg13052638	Distal Intergenic	high	0.73	-0.49	2.65E-05	RASSF5	non-AML leukemia types	61
cg02385848	Distal Intergenic	high	0.73	-0.23	2.65E-05	LINC00473	non-leukemia cancer types	174
cg06333800	Other Intron	high	0.73	-0.45	1.02E-06	PRKAG2	non-leukemia cancer types	61
cg06499030	Promoter (1-2kb)	high	0.73	-0.28	9.14E-05	HLA-DQB2	non-leukemia cancer types	174
cg11019923	Promoter (<=1kb)	high	1.11	-0.31	6.91E-05	DJA4	non-leukemia cancer types	
cg25744552	Distal Intergenic	high	1.11	-0.42	2.17E-05	CD2	cited in AML	19
cg15396204	Distal Intergenic	high	1.11	-0.33	1.66E-04	PRMT6	cited in AML	19
cg22830507	Distal Intergenic	high	0.73	-0.30	1.35E-05	TBX3	non-AML leukemia types	
cg18998321	5' UTR	high	0.73	-0.51	2.93E-06	LAMA1	non-AML leukemia types	
cg13968218	Promoter (<=1kb)	high	0.90	-0.28	2.17E-05	ADGRD2	non-leukemia cancer types	
cg27297993	Other Exon	high	1.25	-0.23	4.57E-05	GABBR1	non-leukemia cancer types	
cg23575349	Promoter (1-2kb)	high	1.38	-0.30	2.65E-05	GRM5	non-leukemia cancer types	
cg06001524	Other Intron	high	1.38	-0.25	5.80E-06	STX8	non-leukemia cancer types	
cg22220986	Other Intron	high	1.11	-0.27	2.17E-05	TTC29	non-leukemia cancer types	
cg22142922	Other Intron	high	1.00	-0.26	4.24E-04	ANO1	non-AML leukemia types	
cg23057870	Promoter (<=1kb)	high	1.38	-0.46	2.65E-05	HEY1	cited in AML	
cg05543593	Distal Intergenic	high	0.90	-0.41	4.12E-04	APOB	cited in AML	72
cg25962699	Other Intron	high	0.90	-0.39	2.17E-05	SLC7A14	non-leukemia cancer types	72
cg08166767	Promoter (<=1kb)	high	0.90	-0.33	2.66E-05	LCE2A	never cited	72

cg13441112	1st Intron	high	0.90	-0.33	3.25E-05	CFHR4	non-leukemia cancer types	72
cg01253818	Other Intron	high	0.73	-0.31	1.23E-05	PPP2R2C	non-leukemia cancer types	
cg24296920	Promoter (<=1kb)	high	1.43	-0.20	1.03E-04	ARMS2	non-leukemia cancer types	
cg22234930	Promoter (1-2kb)	high	0.90	-0.42	3.04E-06	PKM	cited in AML	181
cg00736104	Distal Intergenic	high	0.90	-0.36	8.89E-05	SUDS3	non-leukemia cancer types	181
cg07202214	Promoter (<=1kb)	high	0.90	-0.21	2.17E-05	LRRC32	cited in AML	181
cg13026772	1st Intron	high	0.90	-0.23	2.17E-05	PKNOX2	non-AML leukemia types	
cg07302934	Promoter (1-2kb)	high	1.38	-0.30	2.54E-07	GLIS2	cited in AML	
cg21756194	Promoter (1-2kb)	high	1.11	-0.44	2.17E-05	CALCR	non-AML leukemia types	
cg27590787	Distal Intergenic	high	0.73	-0.47	1.59E-06	PNCK	cited in AML	
cg02999224	Promoter (<=1kb)	high	0.90	-0.47	3.73E-07	SLC7A7	cited in AML	62
cg10558233	Distal Intergenic	high	0.90	-0.62	2.17E-05	MIR378D2	non-leukemia cancer types	62
cg13541713	Promoter (2-3kb)	high	0.90	-0.51	1.89E-07	SYNPO2	non-leukemia cancer types	62
cg02147126	Promoter (<=1kb)	high	0.90	-0.42	2.77E-05	AZU1	cited in AML	62
cg05641048	1st Intron	high	1.38	-0.37	3.73E-05	GCNT3	non-leukemia cancer types	
cg06427176	Distal Intergenic	high	0.80	-0.21	1.81E-05	ADAMTS2	cited in AML	
cg15843496	Promoter (<=1kb)	high	1.38	-0.21	1.18E-05	OR11H12	never cited	
cg21122370	Promoter (<=1kb)	high	0.73	-0.39	2.65E-05	SLIT3	cited in AML	
cg03495053	Other Exon	high	1.25	-0.29	4.57E-05	THBS2	non-AML leukemia types	
cg12910797	Promoter (<=1kb)	high	1.11	-0.75	2.17E-05	HOXB3	cited in AML	199
cg22053945	Promoter (<=1kb)	high	1.11	-0.71	2.17E-05	HOXB3	cited in AML	199
cg26342141	Distal Intergenic	high	0.89	-0.25	1.61E-05	MIR2113	non-leukemia cancer types	
cg19052164	Distal Intergenic	high	0.73	-0.34	1.09E-04	PLEKHG4B	cited in PubMed	
cg26256521	Distal Intergenic	high	1.25	-0.24	6.21E-05	MIR4710	never cited	
cg05905844	Distal Intergenic	high	1.11	-0.36	5.59E-06	CHRM2	non-leukemia cancer types	
cg00306893	Distal Intergenic	high	1.57	-0.33	6.28E-05	MECOM	cited in AML	
cg08548882	1st Intron	high	1.11	-0.42	2.17E-05	PLEKHG1	non-leukemia cancer types	84

cg23908019	Other Exon	high	1.11	-0.32	2.17E-05	OCA2	non-leukemia cancer types	84
cg13139361	Distal Intergenic	high	1.38	-0.31	5.23E-05	C1D	non-leukemia cancer types	
cg26492744	Promoter (2-3kb)	high	0.73	-0.35	1.01E-05	EFNB1	cited in AML	
cg14408356	Other Intron	high	1.57	-0.22	6.28E-05	DTX1	non-AML leukemia types	
cg22152605	Promoter (1-2kb)	high	1.11	-0.49	2.17E-05	FPR1	cited in AML	
cg26681975	Promoter (<=1kb)	high	1.38	-0.30	1.24E-04	PNPLA1	non-AML leukemia types	
cg00683788	Promoter (<=1kb)	high	1.11	-0.29	2.17E-05	PDYN	non-leukemia cancer types	
cg21943117	Distal Intergenic	high	0.73	-0.24	2.30E-05	ACTRT2	cited in PubMed	
cg07147383	Promoter (2-3kb)	high	1.38	-0.39	5.88E-07	FSCN2	non-leukemia cancer types	277
cg17819250	Distal Intergenic	high	1.38	-0.38	1.85E-05	RN7SK	non-leukemia cancer types	277
cg12512337	Distal Intergenic	high	1.38	-0.24	2.65E-05	GSX1	non-leukemia cancer types	277
cg08577913	Promoter (<=1kb)	high	1.38	-0.31	2.65E-05	TRIM21	cited in AML	
cg12630277	Promoter (<=1kb)	high	1.38	-0.28	6.90E-06	GJD4	cited in PubMed	
cg26090020	Promoter (2-3kb)	high	0.64	-0.29	5.75E-04	C17orf102	never cited	132
cg20043105	3' UTR	high	0.64	-0.25	3.89E-05	LINC01551	cited in PubMed	132
cg14663914	Promoter (<=1kb)	high	1.11	-0.37	1.79E-04	AZU1	cited in AML	51
cg12249234	1st Intron	high	1.11	-0.47	2.17E-05	KSR1	cited in AML	51
cg15697257	Promoter (<=1kb)	high	1.11	-0.36	2.17E-05	SYNPO	non-AML leukemia types	51
cg05876069	Promoter (<=1kb)	high	1.11	-0.48	2.17E-05	SYNPO	non-AML leukemia types	51
cg16643542	Promoter (<=1kb)	high	1.11	-0.38	1.45E-05	AZU1	cited in AML	51
cg15610437	Promoter (<=1kb)	high	1.11	-0.36	3.97E-05	AZU1	cited in AML	51
cg11119767	Other Intron	high	1.11	-0.42	2.17E-05	MAP3K20	non-leukemia cancer types	51
cg00426709	Distal Intergenic	high	0.73	-0.27	3.26E-04	PRDM13	non-leukemia cancer types	
cg24693341	3' UTR	high	1.38	-0.38	2.97E-05	PHOX2B	non-AML leukemia types	
cg16708938	Downstream (<=300)	high	1.38	-0.30	2.33E-05	SIK1	cited in AML	
cg01446692	Promoter (<=1kb)	high	1.38	-0.50	1.02E-04	CER1	non-leukemia cancer types	33
cg17504164	Distal Intergenic	high	1.38	-0.48	2.65E-05	ADGRL4	non-leukemia cancer types	33

cg11560431	Other Intron	high	1.38	-0.44	2.65E-05	SLC22A23	non-leukemia cancer types	33
cg20776947	Promoter (2-3kb)	high	1.38	-0.37	4.77E-06	P2RX2	non-leukemia cancer types	33
cg24004178	Distal Intergenic	high	0.73	-0.25	5.82E-06	TR	cited in AML	
cg23122650	1st Intron	high	1.38	-0.44	5.56E-07	COBL	non-AML leukemia types	
cg26765567	Promoter (2-3kb)	high	0.90	-0.43	6.37E-05	FGF4	cited in AML	
cg07637239	Promoter (<=1kb)	high	1.38	-0.33	2.65E-05	KCNK18	non-AML leukemia types	
cg09406107	Distal Intergenic	high	1.38	-0.37	2.15E-05	AGAP1	non-AML leukemia types	1
cg14539466	Promoter (<=1kb)	high	1.38	-0.47	2.65E-05	MPDZ	non-AML leukemia types	1
cg07336872	Distal Intergenic	high	1.38	-0.40	2.65E-05	ULBP3	cited in AML	1
cg03145200	Promoter (<=1kb)	high	1.38	-0.56	2.65E-05	IL21R	cited in AML	1
cg14750475	Other Intron	high	1.38	-0.32	2.90E-06	RRAS	cited in AML	1
cg04940329	Promoter (<=1kb)	high	1.38	-0.51	1.19E-08	KRT23	non-leukemia cancer types	1
cg24720967	Distal Intergenic	high	1.38	-0.36	2.65E-05	RHOT1	non-leukemia cancer types	1
cg27260684	Promoter (2-3kb)	high	1.38	-0.52	2.65E-05	KIAA0513	non-leukemia cancer types	1
cg04118102	Distal Intergenic	high	1.38	-0.40	2.65E-05	ADORA2B	non-leukemia cancer types	1
cg04571189	Distal Intergenic	high	1.38	-0.47	1.46E-06	ODC1	cited in AML	1
cg18915156	Distal Intergenic	high	1.38	-0.46	4.42E-06	LRRC75A	cited in AML	1
cg15690511	Promoter (<=1kb)	high	1.38	-0.37	9.67E-06	OR4C12	non-leukemia cancer types	1
cg18236066	Other Intron	high	1.38	-0.43	7.15E-06	RPH3A	non-leukemia cancer types	1
cg12380764	Promoter (1-2kb)	high	1.38	-0.37	3.51E-06	IL19	non-AML leukemia types	1
cg23866916	1st Intron	high	1.38	-0.43	2.65E-05	SBNO2	non-AML leukemia types	1
cg27541604	Promoter (<=1kb)	high	1.38	-0.55	2.65E-05	AIM2	cited in AML	1
cg06244240	Distal Intergenic	high	1.38	-0.36	1.16E-06	METRNL	non-leukemia cancer types	1
cg21083556	Promoter (2-3kb)	high	1.38	-0.26	1.27E-07	ADSSL1	non-AML leukemia types	1
cg03625911	Promoter (<=1kb)	high	1.38	-0.44	4.04E-08	CHI3L1	cited in AML	1
cg12458039	Other Intron	high	1.38	-0.48	3.26E-04	FAM20C	cited in AML	1
cg17085688	Other Exon	high	1.38	-0.62	2.65E-05	GNGT1	non-leukemia cancer types	1

cg18022554	1st Intron	high	1.38	-0.30	2.65E-05	HCN4	non-leukemia cancer types	1
cg11145776	Promoter (<=1kb)	high	1.38	-0.51	1.05E-06	SLC6A12	non-leukemia cancer types	1
cg11806633	1st Intron	high	1.38	-0.49	2.65E-05	ARHGEF10L	non-leukemia cancer types	1
cg27119904	Other Intron	high	1.38	-0.34	5.82E-05	RASA3	cited in AML	1
cg03774957	Distal Intergenic	high	1.38	-0.58	2.65E-05	PCDH1	cited in AML	1
cg21856784	Promoter (<=1kb)	high	1.38	-0.50	2.65E-05	TRIM15	non-AML leukemia types	1
cg15978561	Other Intron	high	1.38	-0.61	2.65E-05	HDAC4	cited in AML	1
cg23313963	Other Exon	high	1.38	-0.30	2.65E-05	TNXB	non-AML leukemia types	1
cg15102179	Downstream (<=300)	high	1.38	-0.30	9.48E-05	P1L4	non-AML leukemia types	1
cg00411072	Promoter (1-2kb)	high	1.38	-0.66	2.65E-05	HOXB3	cited in AML	1
cg21551253	Distal Intergenic	high	1.38	-0.53	2.65E-05	ADGRD1	cited in AML	1
cg03833794	5' UTR	high	1.38	-0.68	2.65E-05	SGSH	non-leukemia cancer types	1
cg16522250	Other Intron	high	1.38	-0.39	2.65E-05	CNTN6	non-leukemia cancer types	1
cg12806681	Other Intron	high	1.38	-0.46	2.65E-05	AHRR	non-AML leukemia types	1
cg07127883	Distal Intergenic	high	1.38	-0.32	2.65E-05	SHQ1	non-AML leukemia types	1
cg02226672	Other Intron	high	1.38	-0.35	1.94E-06	SMPD3	cited in AML	1
cg01058360	Other Intron	high	1.38	-0.68	2.65E-05	PRKAG2	non-leukemia cancer types	1
cg24490227	Distal Intergenic	high	1.38	-0.54	2.65E-05	JAM3	cited in AML	1
cg00114012	Promoter (1-2kb)	high	1.38	-0.34	6.55E-08	SLC2A8	non-leukemia cancer types	1
cg00864684	1st Intron	high	1.38	-0.40	2.65E-05	CHST15	non-leukemia cancer types	1
cg25011257	Promoter (<=1kb)	high	1.38	-0.34	5.80E-05	TH	cited in AML	1
cg00697095	Promoter (<=1kb)	high	1.38	-0.42	2.65E-05	GRB7	non-AML leukemia types	1
cg17400947	Promoter (2-3kb)	high	1.38	-0.46	2.65E-05	GALNT18	cited in PubMed	1
cg23312375	Other Intron	high	1.38	-0.49	2.65E-05	RASA3	cited in AML	1
cg03991871	Other Intron	high	1.38	-0.55	2.65E-05	AHRR	non-AML leukemia types	1
cg08136806	Promoter (<=1kb)	high	1.38	-0.58	2.65E-05	KRT6C	non-leukemia cancer types	1
cg08105471	Other Intron	high	1.38	-0.29	4.33E-06	CNTN3	non-AML leukemia types	1

cg04637264	Distal Intergenic	high	1.38	-0.53	2.65E-05	WISP3	non-leukemia cancer types	1
cg15646543	3' UTR	high	1.38	-0.63	2.65E-05	PCDH1	cited in AML	1
cg05178291	Promoter (<=1kb)	high	1.38	-0.24	2.19E-06	SAA1	cited in AML	1
cg00667298	Other Intron	high	1.38	-0.45	3.02E-07	GABBR1	non-leukemia cancer types	1
cg15072976	Promoter (<=1kb)	high	1.38	-0.43	2.39E-07	GAL3ST2	non-leukemia cancer types	1
cg00540067	Promoter (1-2kb)	high	1.38	-0.36	1.37E-06	KLF15	non-AML leukemia types	1
cg04843555	Distal Intergenic	high	1.38	-0.45	2.65E-05	RN7SK	non-leukemia cancer types	1
cg07409200	Promoter (1-2kb)	high	1.38	-0.36	5.28E-07	FAM216B	never cited	1
cg22425467	Promoter (<=1kb)	high	1.38	-0.45	7.88E-08	TRIM15	non-AML leukemia types	1
cg08735550	3' UTR	high	1.38	-0.47	2.65E-05	RGS11	non-leukemia cancer types	1
cg26857521	Distal Intergenic	high	1.38	-0.33	7.70E-04	PEX10	cited in PubMed	1
cg16704797	Other Intron	high	1.38	-0.41	2.65E-05	KLHL29	non-leukemia cancer types	1
cg08980014	Promoter (<=1kb)	high	1.38	-0.64	2.65E-05	ARHGEF10	non-leukemia cancer types	1
cg00720829	Promoter (<=1kb)	high	1.38	-0.51	2.65E-05	TRIM15	non-AML leukemia types	1
cg22779896	Distal Intergenic	high	1.38	-0.42	2.65E-05	KIAA0232	cited in PubMed	1
cg05701418	Promoter (<=1kb)	high	1.38	-0.56	2.65E-05	TRIM15	non-AML leukemia types	1
cg14039246	Other Intron	high	1.38	-0.45	9.90E-06	ECHDC2	non-leukemia cancer types	1
cg01604946	Other Intron	high	1.38	-0.55	2.65E-05	SH3TC2	non-AML leukemia types	1
cg05870586	Other Intron	high	1.38	-0.58	2.65E-05	HDAC4	cited in AML	1
cg08190125	Other Intron	high	1.38	-0.44	2.65E-05	IGHG1	non-AML leukemia types	1
cg02570920	Distal Intergenic	high	1.38	-0.37	2.65E-05	RN7SK	non-leukemia cancer types	1
cg17023856	Promoter (<=1kb)	high	1.38	-0.37	3.45E-06	PRKCZ	non-AML leukemia types	1
cg11691844	1st Intron	high	1.38	-0.40	2.65E-05	SYTL2	non-leukemia cancer types	1
cg03608093	Other Intron	high	1.38	-0.46	2.65E-05	DEAF1	non-AML leukemia types	1
cg16603012	Promoter (1-2kb)	high	1.38	-0.61	2.65E-05	APRT	cited in AML	1
cg27152299	Promoter (<=1kb)	high	1.38	-0.47	5.16E-07	KRTAP5-7	non-leukemia cancer types	1
cg08422803	Promoter (<=1kb)	high	1.38	-0.34	1.09E-04	ITGB2	cited in AML	1

cg25627098	Promoter (<=1kb)	high	1.38	-0.28	2.65E-05	SPEM2	never cited	1
cg23726831	Other Intron	high	1.38	-0.35	2.65E-05	SLC4A4	non-AML leukemia types	1
cg10135708	Promoter (<=1kb)	high	1.38	-0.42	1.39E-07	UCN2	non-AML leukemia types	1
cg16928335	Promoter (<=1kb)	high	1.38	-0.37	2.16E-06	SH2D1A	cited in AML	1
cg08936645	Other Intron	high	1.38	-0.54	2.65E-05	TBC1D1	non-leukemia cancer types	1
cg26120971	Distal Intergenic	high	1.38	-0.27	5.61E-09	MED30	non-leukemia cancer types	1
cg11800608	Promoter (<=1kb)	high	1.38	-0.54	3.47E-07	C20orf85	non-leukemia cancer types	1
cg16596317	Other Intron	high	1.38	-0.53	1.04E-07	BCL10	cited in AML	1
cg13557773	Other Intron	high	1.38	-0.50	2.65E-05	RASA3	cited in AML	1
cg22733910	Promoter (<=1kb)	high	1.38	-0.32	2.65E-05	PDE4B	non-AML leukemia types	34
cg13525397	Other Intron	high	1.38	-0.34	1.12E-06	HCG22	non-leukemia cancer types	34
cg19972648	Promoter (<=1kb)	high	1.38	-0.43	2.65E-05	KCNMA1	cited in AML	34
cg03604424	1st Intron	high	1.38	-0.36	2.90E-05	TRIO	cited in AML	34
cg08549011	Other Intron	high	1.38	-0.54	2.65E-05	FSTL4	non-leukemia cancer types	34
cg12690978	Other Intron	high	0.64	-0.31	2.13E-05	MFAP5	non-leukemia cancer types	
cg00017842	Distal Intergenic	high	0.90	-0.33	4.09E-05	EN1	cited in AML	43
cg14660328	Distal Intergenic	high	0.90	-0.34	1.58E-05	TENM4	non-leukemia cancer types	43
cg03564793	3' UTR	high	1.38	-0.51	2.65E-05	COL12A1	cited in AML	129
cg22778788	Promoter (1-2kb)	high	1.38	-0.36	2.65E-05	NKX2-3	cited in AML	129
cg07798610	Promoter (<=1kb)	high	0.73	-0.59	2.65E-05	PRSS21	non-AML leukemia types	
cg05303280	Promoter (1-2kb)	high	1.11	-0.27	7.45E-05	GLDN	non-leukemia cancer types	
cg08814947	Promoter (<=1kb)	high	1.38	-0.34	4.40E-07	KLK11	non-leukemia cancer types	
cg03233426	Promoter (<=1kb)	high	1.38	-0.42	2.73E-06	TMEM100	non-leukemia cancer types	
cg22129183	1st Intron	high	0.90	-0.32	1.76E-06	EVA1A	non-leukemia cancer types	70
cg10909152	Promoter (<=1kb)	high	0.90	-0.50	2.17E-05	SIVA1	cited in AML	70
cg23026228	Distal Intergenic	high	0.73	-0.29	1.20E-05	FNDC1	non-leukemia cancer types	125
cg04285362	Other Intron	high	0.73	-0.35	4.36E-05	SNORA63	never cited	125

cg02558625	1st Intron	high	0.73	-0.51	2.65E-05	COL4A1	non-AML leukemia types	125
cg21006686	Promoter (<=1kb)	high	1.11	-0.40	5.57E-05	NOS1	cited in AML	
cg02855850	Promoter (1-2kb)	high	1.38	-0.42	2.40E-06	IVL	cited in AML	37
cg00870837	Distal Intergenic	high	1.38	-0.32	2.65E-05	C1QTNF8	non-leukemia cancer types	37
cg09418852	Distal Intergenic	high	1.38	-0.39	2.65E-05	SQOR	non-leukemia cancer types	37
cg13805537	1st Intron	high	1.38	-0.31	2.65E-05	FAM102A	non-leukemia cancer types	37
cg23121615	Distal Intergenic	high	1.11	-0.27	1.28E-05	C8orf31	non-leukemia cancer types	
cg19743254	1st Intron	high	1.38	-0.48	2.65E-05	OPCML	non-leukemia cancer types	
cg23304023	Promoter (2-3kb)	high	1.38	-0.44	1.23E-05	TACC2	cited in AML	
cg24768113	Distal Intergenic	high	1.11	-0.35	5.22E-04	FIBIN	non-leukemia cancer types	
cg23345292	Promoter (<=1kb)	high	0.73	-0.31	3.37E-06	LOXHD1	non-leukemia cancer types	242
cg06728135	Distal Intergenic	high	0.73	-0.36	1.28E-06	IRX2	cited in AML	242
cg25242423	Promoter (<=1kb)	high	0.73	-0.28	4.20E-06	RTBDN	non-leukemia cancer types	
cg16451324	Promoter (<=1kb)	high	1.38	-0.37	7.14E-05	PDE1A	non-AML leukemia types	44
cg08661007	Promoter (<=1kb)	high	1.38	-0.31	6.20E-06	ROBO1	cited in AML	44
cg15534052	Distal Intergenic	high	1.43	-0.22	1.03E-04	MC2R	non-AML leukemia types	
cg17524162	Other Intron	high	0.73	-0.52	2.65E-05	HLA-DQA2	non-leukemia cancer types	
cg20016673	Other Exon	high	0.64	-0.31	6.28E-05	NTNG1	non-leukemia cancer types	
cg11747462	1st Intron	high	1.38	-0.31	2.65E-05	OPCML	non-leukemia cancer types	
cg25784280	Promoter (<=1kb)	high	0.73	-0.58	2.65E-05	DT	non-leukemia cancer types	97
cg23670353	Other Intron	high	0.73	-0.52	2.65E-05	FGGY	non-leukemia cancer types	97
cg13196652	1st Intron	high	1.11	-0.22	2.17E-05	ADCY8	non-leukemia cancer types	192
cg18746826	Other Intron	high	1.11	-0.32	1.47E-06	SCARA5	non-leukemia cancer types	192
cg10085326	Promoter (<=1kb)	high	0.73	-0.40	2.65E-05	MMP13	non-AML leukemia types	
cg08036172	Other Intron	high	0.90	-0.42	2.17E-05	MGLL	non-leukemia cancer types	14
cg07345515	Other Intron	high	0.90	-0.52	2.17E-05	TNXB	non-AML leukemia types	14
cg21335375	Promoter (<=1kb)	high	0.90	-0.29	2.17E-05	CCL3	cited in AML	14

cg12707346	Distal Intergenic	high	0.90	-0.29	1.72E-04	RASSF3	non-AML leukemia types	14
cg07470708	Promoter (2-3kb)	high	0.90	-0.41	2.17E-05	NTF4	non-AML leukemia types	14
cg04348689	1st Intron	high	0.90	-0.57	2.17E-05	BTBD7	non-leukemia cancer types	14
cg00275828	Promoter (<=1kb)	high	0.90	-0.37	2.84E-06	KRTAP2-4	non-leukemia cancer types	14
cg04751839	Promoter (1-2kb)	high	0.90	-0.30	2.15E-04	GRTP1	non-AML leukemia types	
cg16287284	Other Intron	high	1.43	-0.31	7.02E-04	SLC5A8	cited in AML	
cg08616516	Promoter (<=1kb)	high	1.00	-0.24	2.12E-04	GRM5	non-leukemia cancer types	
cg17878899	Promoter (<=1kb)	high	0.90	-0.36	2.17E-05	KIAA1210	non-leukemia cancer types	232
cg02709924	Promoter (<=1kb)	high	0.90	-0.38	5.63E-06	NRG1	cited in AML	232
cg00573887	Distal Intergenic	high	0.73	-0.31	3.34E-08	RN7SK	non-leukemia cancer types	176
cg05807489	Distal Intergenic	high	0.73	-0.37	3.18E-05	SOX8	non-leukemia cancer types	176
cg18052106	Distal Intergenic	high	0.73	-0.46	1.82E-06	EPHA7	cited in AML	58
cg27535687	Other Intron	high	0.73	-0.40	1.84E-06	CPLX4	non-leukemia cancer types	58
cg01982835	Promoter (<=1kb)	high	0.73	-0.49	6.01E-06	DLGAP4	non-leukemia cancer types	58
cg25673598	Promoter (2-3kb)	high	1.11	-0.39	2.17E-05	EPN2	non-leukemia cancer types	
cg14387312	Distal Intergenic	high	1.11	-0.48	2.17E-05	RASL11B	non-AML leukemia types	138
cg07015886	Promoter (<=1kb)	high	1.11	-0.41	2.17E-05	TLR5	cited in AML	138
cg08027265	3' UTR	high	1.11	-0.34	1.26E-06	NUDT1	cited in AML	138
cg12935818	Promoter (<=1kb)	high	1.11	-0.38	6.45E-07	RAB17	non-leukemia cancer types	138
cg09578829	Other Intron	high	1.11	-0.35	2.17E-05	TBC1D1	non-leukemia cancer types	138
cg07236190	Promoter (<=1kb)	high	1.11	-0.34	2.51E-06	AMDHD1	non-leukemia cancer types	138
cg10769201	Other Intron	high	1.11	-0.38	9.36E-06	VWA3B	cited in PubMed	138
cg24997585	3' UTR	high	1.11	-0.32	2.17E-05	GABRB3	non-AML leukemia types	138
cg23030159	Distal Intergenic	high	1.11	-0.27	2.17E-05	UNCX	cited in AML	138
cg10142837	Distal Intergenic	high	0.90	-0.36	1.51E-05	PITX2	cited in AML	
cg18432441	1st Intron	high	0.90	-0.56	2.17E-05	TUB	non-AML leukemia types	71
cg10320783	Other Intron	high	0.90	-0.39	2.17E-05	CADM1	cited in AML	71

cg21318380	3' UTR	high	0.90	-0.24	2.92E-04	KCNG1	cited in PubMed	71
cg26346796	Other Intron	high	0.90	-0.41	4.79E-06	TNXB	non-AML leukemia types	71
cg09490523	Distal Intergenic	high	1.11	-0.40	4.49E-05	BCAR1	cited in AML	
cg08525713	Distal Intergenic	high	1.11	-0.50	2.17E-05	DH5	non-leukemia cancer types	38
cg24102792	Distal Intergenic	high	1.11	-0.23	2.17E-05	TEX29	cited in PubMed	38
cg01181681	Promoter (<=1kb)	high	1.11	-0.39	2.17E-05	TLR5	cited in AML	38
cg23244948	Distal Intergenic	high	1.11	-0.24	2.17E-05	RPL10L	non-leukemia cancer types	38
cg27183007	Promoter (<=1kb)	high	1.11	-0.29	5.27E-06	ZPBP	non-leukemia cancer types	38
cg17413460	3' UTR	high	1.11	-0.40	1.18E-04	HAL	cited in AML	38
cg13720705	Distal Intergenic	high	0.90	-0.46	2.17E-05	MTRNR2L7	never cited	
cg10888138	Distal Intergenic	high	1.11	-0.21	1.35E-05	SHISA2	non-leukemia cancer types	
cg18194850	1st Intron	high	0.90	-0.37	2.17E-05	SUCLG2	non-leukemia cancer types	98
cg17242362	Other Intron	high	0.90	-0.43	2.27E-07	ATXN7L1	non-leukemia cancer types	98
cg23878404	Promoter (<=1kb)	high	0.90	-0.48	1.09E-05	KRTAP1-5	non-leukemia cancer types	98
cg09268963	3' UTR	high	0.90	-0.25	8.77E-05	SYNE2	cited in AML	98
cg01252455	Other Intron	high	0.90	-0.32	2.33E-07	CPLX2	non-leukemia cancer types	98
cg25060339	Promoter (2-3kb)	high	1.38	-0.34	2.03E-04	MIR203B	cited in PubMed	108
cg23696618	Promoter (<=1kb)	high	1.38	-0.21	2.65E-05	SERPINB10	cited in AML	108
cg26914334	Other Intron	high	1.38	-0.28	2.06E-06	GRIK4	cited in AML	108
cg03229996	Promoter (2-3kb)	high	0.80	-0.22	1.23E-05	ZNF469	non-leukemia cancer types	
cg16179969	Distal Intergenic	high	1.00	-0.23	2.06E-04	ACAN	cited in AML	
cg07175433	Promoter (2-3kb)	high	0.73	-0.40	7.55E-05	KCNIP4	non-AML leukemia types	
cg07940804	Promoter (<=1kb)	high	0.73	-0.37	1.81E-05	ACTRT1	non-leukemia cancer types	55
cg15731296	Promoter (<=1kb)	high	0.73	-0.43	5.40E-06	PRRG3	non-leukemia cancer types	55
cg09718371	Other Intron	high	1.38	-0.34	2.65E-05	JAKMIP3	cited in PubMed	
cg22027471	Promoter (<=1kb)	high	1.25	-0.25	4.57E-05	SLC5A4	non-leukemia cancer types	
cg10451200	Promoter (<=1kb)	high	1.25	-0.26	4.57E-05	GRM5	non-leukemia cancer types	162

cg19526076	Distal Intergenic	high	1.25	-0.25	2.07E-04	KLF12	non-AML leukemia types	162
cg15050865	Promoter (<=1kb)	high	1.11	-0.39	2.17E-05	CDH18	non-leukemia cancer types	
cg15379170	1st Intron	high	1.38	-0.30	7.36E-06	EFHD1	non-leukemia cancer types	
cg03099780	1st Intron	high	0.73	-0.38	8.77E-05	MBNL2	non-leukemia cancer types	
cg08674227	Distal Intergenic	high	1.38	-0.43	1.78E-05	XKRX	cited in PubMed	74
cg01126560	Promoter (<=1kb)	high	1.38	-0.35	2.65E-05	PAXX	non-leukemia cancer types	74
cg00497905	Other Exon	high	1.38	-0.37	2.65E-05	MYO7A	non-leukemia cancer types	74
cg20959965	Distal Intergenic	high	1.38	-0.42	7.80E-06	CYBB	cited in AML	74
cg14410557	Distal Intergenic	high	1.38	-0.31	9.79E-06	C9orf62	never cited	74
cg26651775	Promoter (<=1kb)	high	1.38	-0.59	3.26E-04	METRN	non-leukemia cancer types	74
cg24860560	Distal Intergenic	high	1.38	-0.35	2.65E-05	MIR4472-1	never cited	74
cg24852442	Other Exon	high	1.38	-0.37	8.87E-07	MYO7A	non-leukemia cancer types	74
cg20860188	1st Intron	high	1.38	-0.58	2.65E-05	KLHL29	non-leukemia cancer types	74
cg10040821	Other Intron	high	1.11	-0.54	2.78E-04	ANKS1B	non-AML leukemia types	9
cg03544781	Distal Intergenic	high	1.11	-0.69	2.17E-05	PDP1	non-AML leukemia types	9
cg25880242	Distal Intergenic	high	1.11	-0.22	2.17E-05	ACTRT2	cited in PubMed	9
cg00840694	Promoter (1-2kb)	high	1.11	-0.33	2.17E-05	MYOM2	non-leukemia cancer types	9
cg20152871	Distal Intergenic	high	1.11	-0.38	4.69E-05	MIR1208	cited in PubMed	9
cg02585931	Promoter (<=1kb)	high	1.11	-0.24	9.71E-07	GALR3	non-leukemia cancer types	9
cg21549497	3' UTR	high	1.11	-0.27	1.37E-07	CRYAA	non-leukemia cancer types	9
cg11068289	Distal Intergenic	high	1.11	-0.60	2.17E-05	CHMP6	non-AML leukemia types	9
cg19091930	Promoter (<=1kb)	high	1.11	-0.51	2.17E-05	LRRC14B	never cited	9
cg13010014	Other Exon	high	1.11	-0.52	2.17E-05	ROBO3	cited in AML	9
cg06291334	Promoter (<=1kb)	high	1.11	-0.34	2.17E-05	SPOP	non-AML leukemia types	9
cg22101045	Distal Intergenic	high	1.11	-0.40	2.17E-05	NUP160	non-AML leukemia types	9
cg18559799	Promoter (1-2kb)	high	1.11	-0.24	4.03E-06	PPY	cited in AML	9
cg21564495	1st Intron	high	1.11	-0.43	1.40E-07	FAM19A5	non-leukemia cancer types	9

cg18778097	Other Exon	high	1.11	-0.37	1.71E-04	NLRP7	non-AML leukemia types	9
cg23057567	Other Intron	high	1.11	-0.45	6.18E-06	PNMA8B	never cited	9
cg10287786	Promoter (1-2kb)	high	1.11	-0.37	8.22E-06	DSCAML1	cited in AML	9
cg26677288	Other Intron	high	1.11	-0.71	2.17E-05	KIF26B	non-leukemia cancer types	9
cg12838168	1st Intron	high	1.11	-0.48	2.17E-05	LRRC15	non-leukemia cancer types	9
cg02886188	Distal Intergenic	high	1.11	-0.52	2.17E-05	DCTD	cited in AML	9
cg14432251	Distal Intergenic	high	1.11	-0.41	2.17E-05	DJB6	non-AML leukemia types	9
cg03333699	Promoter (<=1kb)	high	1.11	-0.40	6.77E-07	ADAP1	non-leukemia cancer types	9
cg19794207	5' UTR	high	1.11	-0.30	1.09E-04	GRIN1	non-leukemia cancer types	9
cg26865084	Distal Intergenic	high	1.11	-0.39	8.59E-07	SMOC2	non-leukemia cancer types	9
cg16726532	Distal Intergenic	high	1.11	-0.27	1.44E-05	AEBP2	cited in AML	9
cg11211263	1st Intron	high	1.11	-0.41	4.27E-07	STUM	non-leukemia cancer types	9
cg09696747	Distal Intergenic	high	1.11	-0.51	2.17E-05	TEX29	cited in PubMed	9
cg16257533	Other Intron	high	1.11	-0.60	2.17E-05	NTM	cited in AML	9
cg00234046	1st Intron	high	1.11	-0.30	1.86E-05	CDH23	non-leukemia cancer types	9
cg00588517	Promoter (<=1kb)	high	1.11	-0.38	3.96E-06	C2	cited in AML	9
cg13491662	Distal Intergenic	high	1.11	-0.27	2.91E-05	C2orf27B	never cited	9
cg00396699	Other Intron	high	1.11	-0.30	2.17E-05	CAC1H	non-AML leukemia types	9
cg15715746	Promoter (<=1kb)	high	1.38	-0.31	2.65E-05	MAGEB2	cited in AML	53
cg08706312	Promoter (<=1kb)	high	1.38	-0.23	2.65E-05	MAGEB1	non-leukemia cancer types	53
cg13183298	Distal Intergenic	high	1.11	-0.32	5.83E-06	PLCH2	non-leukemia cancer types	131
cg02143487	Distal Intergenic	high	1.11	-0.29	2.78E-04	TMEM105	cited in PubMed	131
cg14095048	Distal Intergenic	high	1.11	-0.27	2.17E-05	TMEM211	never cited	200
cg19250417	Promoter (2-3kb)	high	1.11	-0.24	4.11E-07	CRMP1	non-AML leukemia types	200
cg00139681	Distal Intergenic	high	1.11	-0.62	2.17E-05	CCDC71L	cited in PubMed	8
cg05046377	Promoter (<=1kb)	high	1.11	-0.37	2.17E-05	OR51A7	cited in PubMed	8
cg17742099	Other Intron	high	1.11	-0.39	2.17E-05	GABBR1	non-leukemia cancer types	8

cg10819238	1st Intron	high	1.11	-0.50	1.05E-05	SBNO2	non-AML leukemia types	8
cg09284275	Other Intron	high	1.11	-0.37	6.63E-05	MYH11	cited in AML	8
cg10818566	Other Intron	high	1.11	-0.43	1.08E-07	TTC7A	non-leukemia cancer types	8
cg20063450	Promoter (2-3kb)	high	1.11	-0.53	6.27E-08	KRT32	non-leukemia cancer types	8
cg15230985	Other Intron	high	1.11	-0.49	2.17E-05	RPTOR	cited in AML	8
cg27310092	Distal Intergenic	high	1.11	-0.41	2.17E-05	S100A10	cited in AML	8
cg26928972	Promoter (<=1kb)	high	1.11	-0.56	2.17E-05	CSTA	non-leukemia cancer types	8
cg11939346	Promoter (<=1kb)	high	1.11	-0.28	2.17E-05	KALRN	non-leukemia cancer types	8
cg06586713	Promoter (<=1kb)	high	1.11	-0.24	2.17E-05	PCLO	non-AML leukemia types	8
cg26925644	Promoter (<=1kb)	high	1.11	-0.64	2.17E-05	PHLDB1	non-leukemia cancer types	8
cg23083774	Promoter (<=1kb)	high	1.11	-0.33	7.35E-06	PLPPR3	cited in PubMed	8
cg01883046	Distal Intergenic	high	1.11	-0.54	2.17E-05	SP3	cited in AML	8
cg14161165	1st Intron	high	1.11	-0.30	2.17E-05	ASTN2	non-leukemia cancer types	8
cg14187687	Other Intron	high	1.11	-0.58	2.17E-05	SAMD4A	non-leukemia cancer types	8
cg04949225	1st Intron	high	1.11	-0.62	2.17E-05	DLEU1	cited in AML	8
cg16452651	Promoter (2-3kb)	high	1.11	-0.47	6.66E-07	ITSN1	non-leukemia cancer types	8
cg02258846	3' UTR	high	1.11	-0.53	6.90E-08	SCML4	non-AML leukemia types	8
cg12866960	Other Intron	high	1.11	-0.51	3.74E-07	IRAK3	cited in AML	8
cg24341657	Promoter (2-3kb)	high	1.11	-0.35	2.17E-05	DOK7	cited in AML	8
cg22009908	Other Intron	high	1.11	-0.40	2.17E-05	EF5	non-AML leukemia types	8
cg00078513	Promoter (<=1kb)	high	1.11	-0.24	2.90E-05	SNORD115-40	never cited	8
cg14457875	Promoter (1-2kb)	high	1.11	-0.26	8.15E-06	MUC21	non-leukemia cancer types	8
cg14462670	Distal Intergenic	high	1.11	-0.43	2.17E-05	CRK	cited in AML	8
cg21243944	Distal Intergenic	high	1.11	-0.57	2.93E-07	RNU6ATAC	cited in PubMed	8
cg02098075	Other Exon	high	1.11	-0.69	2.17E-05	EFCAB1	non-leukemia cancer types	8
cg19984911	Promoter (<=1kb)	high	1.11	-0.70	2.17E-05	SYNPO	non-AML leukemia types	8
cg07549474	Promoter (<=1kb)	high	1.11	-0.33	3.66E-05	MAGEC2	non-AML leukemia types	8

cg06172871	Promoter (<=1kb)	high	1.11	-0.54	8.51E-08	HP	cited in AML	8
cg00987534	Distal Intergenic	high	1.11	-0.60	2.17E-05	CLDN3	non-leukemia cancer types	8
cg14022913	Promoter (1-2kb)	high	1.11	-0.60	2.17E-05	NEIL3	non-leukemia cancer types	8
cg15167202	Promoter (<=1kb)	high	1.11	-0.48	2.17E-05	SYNPO	non-AML leukemia types	8
cg09824603	Distal Intergenic	high	1.11	-0.41	1.35E-05	IGFBP3	cited in AML	8
cg27268708	Distal Intergenic	high	1.11	-0.60	2.17E-05	HS3ST1	non-AML leukemia types	8
cg01579636	Promoter (<=1kb)	high	1.11	-0.26	9.10E-06	IL17B	cited in AML	8
cg12738008	Other Exon	high	1.11	-0.52	2.17E-05	MYOM2	non-leukemia cancer types	8
cg24955682	Other Intron	high	1.11	-0.27	2.17E-05	HLA-G	cited in AML	8
cg06578434	1st Intron	high	1.11	-0.49	1.50E-09	SBNO2	non-AML leukemia types	8
cg25941151	Promoter (<=1kb)	high	1.11	-0.39	8.65E-06	TYR	cited in AML	8
cg09648454	Other Intron	high	1.11	-0.56	2.17E-05	ABCC12	non-leukemia cancer types	8
cg13575139	Distal Intergenic	high	1.11	-0.46	2.17E-05	KCTD6	non-leukemia cancer types	8
cg17631184	Promoter (<=1kb)	high	1.11	-0.64	2.17E-05	CTTN	non-AML leukemia types	8
cg17943672	Other Intron	high	1.11	-0.53	8.91E-08	TCAIM	cited in PubMed	8
cg26657086	Promoter (1-2kb)	high	1.11	-0.48	1.23E-05	BTNL2	non-leukemia cancer types	8
cg03579045	Other Intron	high	1.11	-0.37	6.65E-05	GATA4	cited in AML	8
cg21448927	Distal Intergenic	high	1.11	-0.25	5.76E-06	FNDC1	non-leukemia cancer types	8
cg23482746	Other Intron	high	1.11	-0.34	4.30E-06	TMEM266	cited in PubMed	8
cg02961101	Distal Intergenic	high	1.11	-0.50	2.17E-05	SIAH1	cited in AML	8
cg13694680	Promoter (1-2kb)	high	1.11	-0.35	1.48E-05	FIBIN	non-leukemia cancer types	8
cg26415633	Promoter (<=1kb)	high	1.11	-0.30	1.96E-05	KLK1	non-AML leukemia types	8
cg02809611	Promoter (<=1kb)	high	1.11	-0.44	3.09E-06	OR1F1	non-leukemia cancer types	8
cg19027636	Promoter (1-2kb)	high	1.11	-0.29	2.17E-05	NSD1	cited in AML	8
cg25113360	Promoter (<=1kb)	high	0.73	-0.32	2.65E-05	GRIK4	cited in AML	99
cg05556461	Distal Intergenic	high	0.73	-0.36	2.65E-05	CARTPT	non-leukemia cancer types	99
cg19139729	Promoter (<=1kb)	high	1.38	-0.32	2.65E-05	SULT2A1	non-leukemia cancer types	

cg24822127	Promoter (<=1kb)	high	1.11	-0.47	1.88E-07	FATE1	non-leukemia cancer types	
cg07776049	Distal Intergenic	high	1.38	-0.33	5.78E-05	SNTG2	cited in PubMed	124
cg24640101	Promoter (<=1kb)	high	1.38	-0.21	3.03E-05	SNORD115-37	never cited	124
cg26958838	Distal Intergenic	high	1.57	-0.30	6.28E-05	IRX2	cited in AML	
cg12669395	Promoter (1-2kb)	high	1.38	-0.40	4.77E-06	DDR1	cited in AML	130
cg00583426	Other Intron	high	1.38	-0.37	2.65E-05	CAC1H	non-AML leukemia types	130
cg19175742	Promoter (<=1kb)	high	1.38	-0.32	6.64E-06	AP3B2	non-leukemia cancer types	130
cg08747676	Promoter (1-2kb)	high	1.11	-0.32	3.46E-05	C1QTNF8	non-leukemia cancer types	
cg16966496	Distal Intergenic	high	1.38	-0.42	1.97E-06	TBX3	non-AML leukemia types	92
cg01998808	Distal Intergenic	high	1.38	-0.22	1.77E-05	LMF1	non-leukemia cancer types	92
cg16034268	Distal Intergenic	high	1.38	-0.34	3.16E-06	SFRP1	cited in AML	92
cg10052840	Promoter (1-2kb)	high	1.38	-0.34	8.35E-06	SEMA6B	cited in AML	83
cg15597096	Distal Intergenic	high	1.38	-0.40	3.90E-05	CSF3R	cited in AML	83
cg24323597	Promoter (<=1kb)	high	1.38	-0.21	2.65E-05	KALRN	non-leukemia cancer types	83
cg00074348	Promoter (1-2kb)	high	1.38	-0.30	1.49E-05	APLNR	cited in AML	29
cg21591938	Distal Intergenic	high	1.38	-0.45	2.65E-05	FAR2	cited in PubMed	29
cg17823175	Promoter (<=1kb)	high	1.38	-0.40	1.77E-05	AZU1	cited in AML	29
cg22620071	Distal Intergenic	high	1.38	-0.49	2.65E-05	YTHDC2	non-leukemia cancer types	29
cg24517501	Promoter (<=1kb)	high	1.38	-0.46	1.62E-05	GFI1	cited in AML	29
cg08625482	Distal Intergenic	high	1.38	-0.40	1.32E-05	NEFL	non-leukemia cancer types	29
cg05294112	Distal Intergenic	high	1.38	-0.41	7.20E-05	SOX1	cited in AML	29
cg09674502	Promoter (<=1kb)	high	1.38	-0.46	2.65E-05	GFI1	cited in AML	29
cg16631083	1st Intron	high	1.38	-0.41	4.76E-08	HUNK	non-leukemia cancer types	29
cg02987482	1st Intron	high	1.38	-0.49	2.65E-05	MLLT1	cited in AML	29
cg01766941	Promoter (1-2kb)	high	1.38	-0.55	2.65E-05	GFI1	cited in AML	29
cg20689476	Promoter (1-2kb)	high	1.38	-0.29	1.71E-05	PPP2R2C	non-leukemia cancer types	29
cg18004847	1st Intron	high	1.38	-0.49	2.65E-05	SBNO2	non-AML leukemia types	29

cg04777348	Promoter (<=1kb)	high	1.38	-0.56	2.65E-05	GFI1	cited in AML	29
cg07717083	Other Intron	high	1.38	-0.36	2.01E-05	TNXB	non-AML leukemia types	29
cg18618429	Promoter (<=1kb)	high	1.38	-0.36	2.65E-05	CSTA	non-leukemia cancer types	29
cg09488090	Distal Intergenic	high	1.38	-0.38	2.65E-05	PMFBP1	cited in PubMed	18
cg26394380	Promoter (<=1kb)	high	1.38	-0.32	9.01E-08	SFTPB	non-leukemia cancer types	18
cg16544010	Promoter (<=1kb)	high	1.38	-0.29	3.12E-07	DLK1	cited in AML	18
cg13250566	Distal Intergenic	high	1.38	-0.36	3.44E-05	TUBG2	non-leukemia cancer types	18
cg15060366	Promoter (<=1kb)	high	0.90	-0.47	2.17E-05	PCSK2	non-leukemia cancer types	
cg14561934	Promoter (1-2kb)	high	1.11	-0.40	7.06E-06	FAM171A1	non-leukemia cancer types	
cg00947324	Other Intron	high	1.25	-0.21	4.57E-05	AK7	non-AML leukemia types	
cg26123605	Distal Intergenic	high	1.43	-0.21	1.03E-04	ZIC1	cited in AML	
cg14431020	Other Intron	high	0.89	-0.21	8.23E-05	ELMO1	cited in AML	
cg23749637	Promoter (<=1kb)	high	0.80	-0.31	4.57E-05	NXN	non-leukemia cancer types	
cg07812957	3' UTR	high	0.73	-0.53	2.65E-05	KLF2	cited in AML	25
cg14544831	Promoter (1-2kb)	high	0.73	-0.27	2.65E-05	BCL2	cited in AML	25
cg23009780	Distal Intergenic	high	0.73	-0.38	2.65E-05	ADRA2B	non-leukemia cancer types	25
cg26201596	Distal Intergenic	high	0.73	-0.44	4.67E-06	DIP2C	non-leukemia cancer types	
cg03706086	Distal Intergenic	high	0.73	-0.52	2.65E-05	NCOA2	cited in AML	10
cg01293740	Promoter (2-3kb)	high	0.73	-0.38	2.65E-05	CACNG8	non-leukemia cancer types	10
cg09842053	Promoter (<=1kb)	high	0.73	-0.51	2.65E-05	XDH	non-AML leukemia types	10
cg24764810	Other Intron	high	0.73	-0.36	2.06E-06	HCG22	non-leukemia cancer types	10
cg11228126	Distal Intergenic	high	1.00	-0.23	1.55E-05	NEUROG3	non-AML leukemia types	
cg17919471	Promoter (<=1kb)	high	0.73	-0.26	7.35E-05	XAGE3	non-leukemia cancer types	
cg06729381	Other Intron	high	0.90	-0.48	2.17E-05	SYT7	non-leukemia cancer types	164
cg21878759	Promoter (<=1kb)	high	0.90	-0.39	1.52E-05	LOXHD1	non-leukemia cancer types	164
cg14765834	Other Exon	high	0.90	-0.52	2.17E-05	YBX2	non-leukemia cancer types	101
cg20951266	1st Intron	high	0.90	-0.33	6.88E-06	SMCP	non-leukemia cancer types	101

cg16591659	Distal Intergenic	high	0.90	-0.26	1.13E-07	NPTX1	non-leukemia cancer types	101
cg14962049	Other Intron	high	0.90	-0.30	2.78E-04	PRELID2	non-leukemia cancer types	101
cg26331243	Other Intron	high	0.90	-0.26	1.36E-06	CCDC33	non-leukemia cancer types	
cg14520512	Promoter (<=1kb)	high	0.90	-0.32	3.15E-06	MBNL3	non-AML leukemia types	59
cg24508310	1st Intron	high	0.90	-0.36	2.17E-05	BCOR	cited in AML	59
cg25927227	Other Intron	high	0.90	-0.51	2.28E-06	SFRP1	cited in AML	59
cg11229415	Promoter (<=1kb)	high	0.90	-0.33	1.33E-06	PLCH2	non-leukemia cancer types	23
cg11612905	Other Exon	high	0.90	-0.34	2.17E-05	DGKD	non-AML leukemia types	23
cg01759110	Promoter (<=1kb)	high	0.90	-0.54	2.17E-05	ADAMDEC1	non-leukemia cancer types	23
cg00328597	Other Intron	high	0.90	-0.45	5.66E-06	ACTN2	cited in AML	23
cg19145082	Distal Intergenic	high	0.90	-0.56	2.17E-05	CHST2	non-AML leukemia types	23
cg20048109	Other Intron	high	0.90	-0.45	6.14E-06	MAGI2	non-AML leukemia types	23
cg05573626	Other Exon	high	0.90	-0.34	1.25E-04	ZNF423	cited in AML	23
cg17086773	Distal Intergenic	high	0.90	-0.70	2.17E-05	CD200R1L	cited in PubMed	23
cg16375358	Promoter (<=1kb)	high	0.90	-0.42	7.92E-06	CACNG5	non-leukemia cancer types	23
cg04755857	Other Intron	high	0.73	-0.33	2.35E-04	EVC	non-AML leukemia types	81
cg08313382	Distal Intergenic	high	0.73	-0.40	1.10E-05	MIR4278	never cited	81
cg01206723	Distal Intergenic	high	0.73	-0.41	3.68E-06	RNU4-1	cited in PubMed	81
cg16491739	Distal Intergenic	high	1.11	-0.45	3.02E-06	C14orf180	cited in PubMed	
cg14737125	3' UTR	high	1.11	-0.30	2.17E-05	GBX2	cited in AML	
cg06079509	Other Exon	high	0.90	-0.26	5.34E-05	WFS1	non-leukemia cancer types	
cg10331779	Promoter (<=1kb)	high	0.64	-0.26	3.97E-05	CTNND2	non-leukemia cancer types	
cg17588373	Promoter (<=1kb)	high	1.11	-0.32	6.99E-05	GPM6B	cited in AML	
cg27426921	Distal Intergenic	high	1.11	-0.24	1.48E-06	PFKP	cited in AML	
cg12580770	Promoter (<=1kb)	high	1.25	-0.36	3.99E-04	HTR5A	non-leukemia cancer types	
cg08318283	Downstream (<=300)	high	0.90	-0.52	2.17E-05	HCN4	non-leukemia cancer types	30
cg05035315	1st Intron	high	0.90	-0.30	2.94E-06	OPCML	non-leukemia cancer types	30

cg04697056	Other Intron	high	0.90	-0.47	2.37E-06	FAT1	cited in AML	30
cg04086012	Promoter (<=1kb)	high	0.90	-0.21	3.35E-06	TRIML1	cited in PubMed	30
cg05576949	Promoter (1-2kb)	high	0.90	-0.62	2.17E-05	IGF2BP2	cited in AML	30
cg11873482	Promoter (<=1kb)	high	1.38	-0.39	1.78E-05	TAC1	non-AML leukemia types	47
cg04139223	Distal Intergenic	high	1.38	-0.37	2.65E-05	SLC9A3	non-leukemia cancer types	47
cg14206523	Distal Intergenic	high	1.11	-0.31	1.12E-06	GJD2	non-leukemia cancer types	
cg11889730	Distal Intergenic	high	0.90	-0.25	6.01E-05	MTRNR2L7	never cited	
cg14737484	Other Intron	high	1.38	-0.20	2.65E-05	TNXB	non-AML leukemia types	
cg04318657	Promoter (1-2kb)	low	0.90	-0.32	3.29E-05	PRKX	non-AML leukemia types	301
cg11638347	Promoter (<=1kb)	low	0.90	-0.26	5.80E-05	HLCS	non-leukemia cancer types	301
cg18142353	Promoter (<=1kb)	low	0.90	-0.38	2.17E-05	LRP6	cited in AML	301
cg11678461	1st Intron	low	0.90	-0.57	1.67E-06	OSBPL5	non-leukemia cancer types	301
cg22202121	Promoter (<=1kb)	low	0.73	-0.31	7.99E-06	ZNF292	non-AML leukemia types	
cg05255275	Promoter (<=1kb)	high	1.00	-0.26	4.11E-05	C14orf39	non-leukemia cancer types	
cg01377936	Promoter (<=1kb)	high	0.90	-0.49	2.17E-05	DMD	non-AML leukemia types	69
cg16101493	Promoter (1-2kb)	high	0.90	-0.22	2.17E-05	POU4F3	cited in AML	69
cg10815229	Promoter (<=1kb)	high	0.90	-0.34	2.17E-05	HELT	non-AML leukemia types	
cg06532574	Promoter (2-3kb)	low	0.73	-0.38	2.65E-05	ELL2	cited in AML	290
cg18568145	Promoter (<=1kb)	low	0.73	-0.28	4.57E-05	FAM189B	non-leukemia cancer types	290

Annex X Genes with more than one CpG as potential biomarkers in AML-M2 patients.

gene	probes	location	Cluster
BAIAP2	cg06578276	Other Intron	hypermethylation
	cg09083945	Promoter (2-3kb)	hypermethylation
C1QTNF8	cg00870837	Distal Intergenic	hypermethylation
	cg08747676	Promoter (1-2kb)	hypermethylation
CACNA1H	cg00583426	Other Intron	hypermethylation
	cg00396699	Other Intron	hypermethylation
CSTA	cg26928972	Promoter (<=1kb)	hypermethylation
	cg18618429	Promoter (<=1kb)	hypermethylation
DLX4	cg10592171	Promoter (2-3kb)	hypomethylation
	cg12224030	Promoter (1-2kb)	hypomethylation
ENTPD3	cg17264618	Promoter (<=1kb)	hypomethylation
	cg13409248	Promoter (<=1kb)	hypomethylation
FIBIN	cg24768113	Distal Intergenic	hypermethylation
	cg13694680	Promoter (1-2kb)	hypermethylation
FLI1	cg17239923	Promoter (<=1kb)	hypomethylation
	cg10542562	Promoter (<=1kb)	hypomethylation
	cg08586366	Promoter (1-2kb)	hypomethylation
FNDC1	cg23026228	Distal Intergenic	hypermethylation
	cg21448927	Distal Intergenic	hypermethylation
GABBR1	cg17742099	Other Intron	hypermethylation
	cg27297993	Other Exon	hypermethylation
	cg00667298	Other Intron	hypermethylation
GFI1	cg24517501	Promoter (<=1kb)	hypermethylation
	cg09674502	Promoter (<=1kb)	hypermethylation
	cg01766941	Promoter (1-2kb)	hypermethylation
	cg04777348	Promoter (<=1kb)	hypermethylation
GNMT	cg17345569	Promoter (<=1kb)	hypomethylation
	cg09436375	Promoter (<=1kb)	hypomethylation
GRIK4	cg25113360	Promoter (<=1kb)	hypermethylation
	cg26914334	Other Intron	hypermethylation
GRM5	cg23575349	Promoter (1-2kb)	hypermethylation
	cg10451200	Promoter (<=1kb)	hypermethylation
	cg08616516	Promoter (<=1kb)	hypermethylation
HCG22	cg13525397	Other Intron	hypermethylation
	cg24764810	Other Intron	hypermethylation
HCN4	cg08318283	Downstream (<=300)	hypermethylation
	cg18022554	1st Intron	hypermethylation
HDAC4	cg15978561	Other Intron	hypermethylation
	cg05870586	Other Intron	hypermethylation
HLA-DMB	cg20392842	Promoter (<=1kb)	hypomethylation
	cg16236263	Promoter (<=1kb)	hypomethylation
	cg16300030	Promoter (<=1kb)	hypomethylation

gene	probes	location	Cluster
HOXB3	cg00411072	Promoter (1-2kb)	hypermethylation
	cg12910797	Promoter (<=1kb)	hypermethylation
	cg22053945	Promoter (<=1kb)	hypermethylation
IRX2	cg26958838	Distal Intergenic	hypermethylation
	cg06728135	Distal Intergenic	hypermethylation
IRX3	cg08076437	Downstream (<=300)	hypomethylation
	cg01951879	Downstream (<=300)	hypomethylation
	cg08347500	Downstream (<=300)	hypomethylation
	cg05071046	Distal Intergenic	hypomethylation
KALRN	cg11939346	Promoter (<=1kb)	hypermethylation
	cg24323597	Promoter (<=1kb)	hypermethylation
KIAA1217	cg25042430	Promoter (1-2kb)	hypomethylation
	cg23196346	Other Intron	hypomethylation
KLHL29	cg16704797	Other Intron	hypermethylation
	cg20860188	1st Intron	hypermethylation
LOXHD1	cg21878759	Promoter (<=1kb)	hypermethylation
	cg23345292	Promoter (<=1kb)	hypermethylation
MTRNR2L7	cg11889730	Distal Intergenic	hypermethylation
	cg13720705	Distal Intergenic	hypermethylation
MYO7A	cg00497905	Other Exon	hypermethylation
	cg24852442	Other Exon	hypermethylation
	cg00840694	Promoter (1-2kb)	hypermethylation
	cg12738008	Other Exon	hypermethylation
NEUROG3	cg11228126	Distal Intergenic	hypermethylation
	cg24640390	Distal Intergenic	hypomethylation
NSD1	cg08369368	Promoter (<=1kb)	hypomethylation
	cg19027636	Promoter (1-2kb)	hypermethylation
NTM	cg16257533	Other Intron	hypermethylation
	cg05184519	Other Intron	hypermethylation
NXN	cg23749637	Promoter (<=1kb)	hypermethylation
	cg25050975	Other Intron	hypermethylation
OPCML	cg05035315	1st Intron	hypermethylation
	cg19743254	1st Intron	hypermethylation
	cg11747462	1st Intron	hypermethylation
OSBPL5	cg22074576	1st Intron	hypomethylation
	cg23357130	1st Intron	hypomethylation
	cg11678461	1st Intron	hypomethylation
PCDH1	cg03774957	Distal Intergenic	hypermethylation
	cg15646543	3' UTR	hypermethylation
PDE4B	cg22733910	Promoter (<=1kb)	hypermethylation
	cg23045908	Promoter (1-2kb)	hypomethylation
PLCH2	cg11229415	Promoter (<=1kb)	hypermethylation
	cg13183298	Distal Intergenic	hypermethylation

gene	probes	location	Cluster
PLEKHG4B	cg19052164	Distal Intergenic	hypermethylation
	cg13691209	Distal Intergenic	hypermethylation
PPP2R2C	cg01253818	Other Intron	hypermethylation
	cg20689476	Promoter (1-2kb)	hypermethylation
PRDM8	cg18073471	Promoter (<=1kb)	hypomethylation
	cg22902505	Promoter (<=1kb)	hypomethylation
PRKAG2	cg01058360	Other Intron	hypermethylation
	cg06333800	Other Intron	hypermethylation
RASA3	cg27119904	Other Intron	hypermethylation
	cg23312375	Other Intron	hypermethylation
	cg13557773	Other Intron	hypermethylation
RN7SK	cg01116873	Distal Intergenic	hypermethylation
	cg00573887	Distal Intergenic	hypermethylation
	cg04843555	Distal Intergenic	hypermethylation
	cg02570920	Distal Intergenic	hypermethylation
	cg17819250	Distal Intergenic	hypermethylation
ROBO1	cg08147563	1st Intron	hypermethylation
	cg08661007	Promoter (<=1kb)	hypermethylation
SBNO2	cg10819238	1st Intron	hypermethylation
	cg23866916	1st Intron	hypermethylation
	cg18004847	1st Intron	hypermethylation
	cg06578434	1st Intron	hypermethylation
SFRP1	cg25927227	Other Intron	hypermethylation
	cg16034268	Distal Intergenic	hypermethylation
SH3BP2	cg07991621	Promoter (<=1kb)	hypomethylation
	cg10745272	Promoter (<=1kb)	hypomethylation
SLC4A4	cg17691657	Promoter (<=1kb)	hypomethylation
	cg23726831	Other Intron	hypermethylation
SORBS3	cg03572859	Promoter (<=1kb)	hypomethylation
	cg17142470	Promoter (<=1kb)	hypomethylation
SP3	cg01883046	Distal Intergenic	hypermethylation
	cg13223682	Distal Intergenic	hypermethylation
SYNPO	cg15697257	Promoter (<=1kb)	hypermethylation
	cg19984911	Promoter (<=1kb)	hypermethylation
	cg15167202	Promoter (<=1kb)	hypermethylation
	cg05876069	Promoter (<=1kb)	hypermethylation
TBC1D1	cg09578829	Other Intron	hypermethylation
	cg08936645	Other Intron	hypermethylation
TBX3	cg22830507	Distal Intergenic	hypermethylation
	cg16966496	Distal Intergenic	hypermethylation
	cg19175386	Distal Intergenic	hypomethylation
TEX29	cg24102792	Distal Intergenic	hypermethylation
	cg09696747	Distal Intergenic	hypermethylation

gene	probes	location	Cluster
TLR5	cg07015886	Promoter (<=1kb)	hypermethylation
	cg01181681	Promoter (<=1kb)	hypermethylation
TMEM105	cg00036408	Distal Intergenic	hypermethylation
	cg02143487	Distal Intergenic	hypermethylation
TNS3	cg06588645	Promoter (2-3kb)	hypomethylation
	cg17858880	Promoter (2-3kb)	hypomethylation
TNXB	cg07345515	Other Intron	hypermethylation
	cg23313963	Other Exon	hypermethylation
	cg07717083	Other Intron	hypermethylation
	cg26346796	Other Intron	hypermethylation
	cg14737484	Other Intron	hypermethylation
TRIM15	cg21856784	Promoter (<=1kb)	hypermethylation
	cg22425467	Promoter (<=1kb)	hypermethylation
	cg00720829	Promoter (<=1kb)	hypermethylation
	cg05701418	Promoter (<=1kb)	hypermethylation
TRNA	cg16207110	Promoter (1-2kb)	hypomethylation
	cg24004178	Distal Intergenic	hypermethylation
UNC13D	cg07010633	Other Intron	hypomethylation
	cg02627403	3' UTR	hypomethylation
	cg12407791	Other Intron	hypomethylation
XYLT1	cg06321596	Promoter (1-2kb)	hypomethylation
	cg04313565	Promoter (2-3kb)	hypomethylation
	cg04359840	Promoter (1-2kb)	hypomethylation
	cg16794579	Promoter (2-3kb)	hypomethylation
ZNF423	cg05573626	Other Exon	hypermethylation
	cg26578156	1st Intron	hypermethylation

Annex XI Additional information about the 4 candidate biomarkers of prognostic of gene expression in patients with AML-M4 categorized in the intermediate prognostic risk group.

gene	status	Ratio	foldchange	*p-value*	bibliographic
CCNK	low	1.20	0.33	0.015769	cited in AML
RPUSD4	high	0.64	0.35	0.004117	non-leukemia cancer types
ATAD3C	high	1.18	0.21	0.000004	non-leukemia cancer types
TRIM2	high	1.30	0.37	0.044184	non-leukemia cancer types

Annex XII List of the gene sets shared by the majority of the intermediate-poor AML-M4 that were differentially enriched in comparison with the intermediate-favorable subgroups. For each gene set is represented the number and the percentage of intermediate-poor subgroups that have the gene sets enriched (n and percentage), a representative *p-value* and the status (upregulated (up) or downregulated (down)).

Set	n	Percentage	*p-value*	status
GO:0008380 RNA splicing	4	100	0.002	up
GO:0010948 negative regulation of cell cycle process	4	100	0.002	up
GO:0006397 mRNA processing	4	100	0.003	up
GO:0010498 proteasomal protein catabolic process	4	100	0.003	up
GO:0006401 RNA catabolic process	4	100	0.003	up
GO:1901991 negative regulation of mitotic cell cycle phase transition	4	100	0.004	up
GO:1901988 negative regulation of cell cycle phase transition	4	100	0.005	up
GO:0043161 proteasome-mediated ubiquitin-dependent protein catabolic process	4	100	0.006	up
GO:0009145 purine nucleoside triphosphate biosynthetic process	4	100	0.006	up
GO:0009206 purine ribonucleoside triphosphate biosynthetic process	4	100	0.008	up
GO:0006402 mRNA catabolic process	4	100	0.008	up
GO:0000375 RNA splicing, via transesterification reactions	4	100	0.009	up
GO:0009144 purine nucleoside triphosphate metabolic process	4	100	0.009	up
GO:0009199 ribonucleoside triphosphate metabolic process	4	100	0.009	up
GO:0090501 RNA phosphodiester bond hydrolysis	4	100	0.011	up
GO:0000377 RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	4	100	0.011	up
GO:0000398 mRNA splicing, via spliceosome	4	100	0.011	up
GO:0006754 ATP biosynthetic process	4	100	0.012	up
GO:0009201 ribonucleoside triphosphate biosynthetic process	4	100	0.012	up
GO:0031145 anaphase-promoting complex-dependent catabolic process	4	100	0.013	up
GO:0009205 purine ribonucleoside triphosphate metabolic process	4	100	0.013	up
GO:0009141 nucleoside triphosphate metabolic process	4	100	0.017	up
GO:1901990 regulation of mitotic cell cycle phase transition	4	100	0.018	up
GO:0006120 mitochondrial electron transport, NADH to ubiquinone	4	100	0.019	up
GO:0009142 nucleoside triphosphate biosynthetic process	4	100	0.024	up
GO:0042775 mitochondrial ATP synthesis coupled electron transport	4	100	0.024	up
GO:1901987 regulation of cell cycle phase transition	4	100	0.024	up

Set	n	Percentage	*p-value*	status
GO:1902750 negative regulation of cell cycle G2/M phase transition	4	100	0.025	up
GO:0010972 negative regulation of G2/M transition of mitotic cell cycle	4	100	0.027	up
GO:0042769 DNA damage response, detection of DNA damage	4	100	0.028	up
GO:0045930 negative regulation of mitotic cell cycle	4	100	0.028	up
GO:0035195 gene silencing by miRNA	4	100	0.028	up
GO:0042773 ATP synthesis coupled electron transport	4	100	0.029	up
GO:1904030 negative regulation of cyclin-dependent protein kinase activity	4	100	0.033	up
GO:0015985 energy coupled proton transport, down electrochemical gradient	4	100	0.035	up
GO:0015986 ATP synthesis coupled proton transport	4	100	0.035	up
GO:0045736 negative regulation of cyclin-dependent protein serine/threonine kinase activity	4	100	0.035	up
GO:0090305 nucleic acid phosphodiester bond hydrolysis	4	100	0.035	up
GO:0005746 mitochondrial respirasome	4	100	0.036	up
GO:0006119 oxidative phosphorylation	4	100	0.036	up
GO:0040029 regulation of gene expression, epigenetic	4	100	0.036	up
GO:0006417 regulation of translation	4	100	0.038	up
GO:0034248 regulation of cellular amide metabolic process	4	100	0.040	up
GO:0070469 respirasome	4	100	0.041	up
GO:0006457 protein folding	4	100	0.041	up
GO:0046034 ATP metabolic process	4	100	0.041	up
GO:1903311 regulation of mRNA metabolic process	4	100	0.044	up
GO:0016441 posttranscriptional gene silencing	4	100	0.044	up
GO:0035194 posttranscriptional gene silencing by RNA	4	100	0.044	up
GO:0061013 regulation of mRNA catabolic process	4	100	0.046	up
GO:0006283 transcription-coupled nucleotide-excision repair	4	100	0.046	up
GO:0043488 regulation of mRNA stability	4	100	0.048	up
GO:0007606 sensory perception of chemical stimulus	4	100	0.008	down
GO:0050907 detection of chemical stimulus involved in sensory perception	4	100	0.011	down
GO:0050906 detection of stimulus involved in sensory perception	4	100	0.012	down
GO:0009593 detection of chemical stimulus	4	100	0.016	down
GO:0048754 branching morphogenesis of an epithelial tube	4	100	0.016	down
GO:0050909 sensory perception of taste	4	100	0.023	down
GO:0048665 neuron fate specification	4	100	0.032	down
GO:0061564 axon development	4	100	0.032	down
GO:0070509 calcium ion import	4	100	0.034	down
GO:0061138 morphogenesis of a branching epithelium	4	100	0.035	down
GO:0051606 detection of stimulus	4	100	0.038	down

Set	n	Percentage	*p-value*	status
GO:0001763 morphogenesis of a branching structure	4	100	0.039	down
GO:0050912 detection of chemical stimulus involved in sensory perception of taste	4	100	0.045	down
GO:0050806 positive regulation of synaptic transmission	4	100	0.047	down

Annex XIII The remaining 225 identified CpG sites whose DNA methylation were able to predict survival in patients with AML-M4 categorized in the intermediate prognostic risk group.

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg02440744	0.00015	0.5104	10	13	0.08779	*SLC26A5*	9.02840
cg17664577	0.00008	0.0758	8	13	0.91341	*MMP9*	8.92099
cg12432236	0.00032	0.1619	13	10	0.27731	*PCDH17*	8.90266
cg18060330	0.00019	0.7864	12	11	0.26746	*BTNL2*	8.57623
cg08168379	0.00024	0.5964	13	10	0.59773	*SALL1*	8.44727
cg21909948	0.00027	0.8074	10	13	0.51451	*IQSEC2*	8.30867
cg14100184	0.00033	0.3863	12	11	0.40558	*GNG13*	8.25389
cg05744332	0.00010	0.5701	9	14	0.13839	*MNX1*	7.72140
cg06871764	0.00015	0.6887	11	12	0.53785	*BTNL2*	7.57844
cg03161453	0.00061	0.8877	10	13	0.41965	*BCOR*	7.56155
cg13060157	0.00079	0.129	14	9	0.37735	*FAM19A3*	7.50433
cg16683746	0.00060	0.2662	12	11	0.10921	*RUNX1T1*	7.49478
cg12462026	0.00077	0.8209	14	9	0.84996	*HS6ST2*	7.45942
cg11703139	0.00064	0.9079	11	12	0.82928	*GUCY2F*	7.41295
cg27307168	0.00083	0.8152	13	10	0.53474	*RBMX*	7.39429
cg16049600	0.00031	0.7902	9	14	0.92464	*PCDHB11*	7.19769
cg07003115	0.00078	0.5532	14	9	0.23089	*MANEAL*	7.12757
cg14605748	0.00107	0.8787	10	12	0.89499	*AMOT*	7.01445
cg03780733	0.00104	0.6103	12	11	0.44125	*PCDHB7*	6.87882
cg12454245	0.00131	0.9227	12	11	0.71165	*NDUFB11*	6.80032

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg13795116	0.00150	0.9066	11	12	0.44125	*CLCN4*	6.72658
cg10249705	0.00053	0.5404	10	13	0.20315	*GUCY1A2*	6.60473
cg10703826	0.00061	0.328	9	14	0.08291	*TBX15*	6.46416
cg06801028	0.00017	0.3065	10	13	0.82799	*NCOA4*	6.35859
cg23850281	0.00066	0.8371	10	13	0.82799	*ADGRG2*	6.30660
cg24753473	0.00099	0.1543	12	11	0.14769	*MAP2*	6.16553
cg18996274	0.00085	0.8338	10	13	0.80389	*CYP26B1*	6.15876
cg09766820	0.00100	0.1842	10	12	0.97367	*LHX8*	6.09998
cg02060618	0.00099	0.6802	11	12	0.37170	*BMP15*	5.98057
cg02586212	0.00100	0.1812	12	10	0.86892	*RGS1*	5.87767
cg25879561	0.00092	0.3639	12	11	0.51772	*SNRPN*	5.83237
cg14988083	0.00411	0.2634	13	10	0.73278	*FGFR3*	5.64096
cg02593884	0.00411	0.6706	13	10	0.73278	*FLYWCH1*	5.64096
cg22190023	0.00086	0.6523	10	13	0.68657	*PCDHB7*	5.59047
cg06047020	0.00101	0.5837	13	10	0.10652	*GPC6*	5.58894
cg20757404	0.00086	0.5219	9	14	0.39462	*THEG*	5.57012
cg18496212	0.00147	0.1983	12	11	1.00000	*MITF*	5.46430
cg23756474	0.00113	0.1183	11	12	0.95088	*PCSK2*	5.43285
cg24533097	0.00190	0.6004	12	11	0.45974	*PCDHB11*	5.37955
cg17342925	0.00178	0.4294	9	14	0.43058	*EN1*	5.35627
cg08571680	0.00277	0.4805	12	11	0.40558	*TBX10*	5.28736
cg22851944	0.00143	0.1097	11	12	0.49798	*GRIK2*	5.23365
cg16062292	0.00074	0.5308	14	9	0.15597	*TKTL1*	5.17998
cg24508310	0.00178	0.7836	10	13	0.90119	*BCOR*	5.15726
cg26439139	0.00075	0.844	9	13	0.61619	*SGCD*	5.09647
cg19223521	0.00215	0.243	12	11	0.55837	*EN1*	5.09617

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg23992130	0.00224	0.8459	10	13	0.53474	*LONRF3*	5.00583
cg00412554	0.00413	0.8935	10	13	0.55536	*KLHL13*	4.97668
cg05946623	0.00127	0.5593	10	13	0.55536	*CDH8*	4.89196
cg02275924	0.00234	0.8851	9	14	0.89964	*MID1*	4.84769
cg12437013	0.00978	0.4753	14	9	0.94972	*TMCO3*	4.82762
cg20881335	0.00377	0.4993	11	12	0.20661	*GLRA2*	4.61475
cg16792071	0.00202	0.7562	11	12	0.35543	*ADGRA1*	4.32252
cg24489686	0.00526	0.8347	10	12	0.81728	*FGF13*	4.31138
cg27281882	0.00282	0.8836	9	14	0.80087	*PAK5*	4.22973
cg14215711	0.00270	0.3135	10	12	0.62053	*PIP4K2A*	4.15450
cg24740868	0.00337	0.6604	10	13	0.55536	*C1orf87*	4.13511
cg01325409	0.00419	0.7325	9	14	0.75255	*SLC24A5*	4.02275
cg12104246	0.01278	0.5247	13	10	0.57636	*C6orf62*	3.94986
cg09857513	0.00426	0.5109	11	12	0.13926	*WNT16*	3.93015
cg17544177	0.01350	0.3628	14	9	0.57037	*KCNIP2*	3.91834
cg19433175	0.00374	0.2462	13	10	0.51451	*TPTE*	3.85599
cg10566660	0.01482	0.2034	13	10	0.70954	*GTF3A*	3.85021
cg04514392	0.01482	0.7459	13	10	0.70954	*CCDC54*	3.85021
cg13971849	0.01482	0.527	13	10	0.70954	*PLEKHA2*	3.85021
cg11067407	0.01482	0.2285	13	10	0.70954	*TMPRSS5*	3.85021
cg02719508	0.01459	0.2974	12	9	0.45511	*AHNAK2*	3.84457
cg18417245	0.00318	0.7546	10	13	0.61945	*PCDHB11*	3.83701
cg06720722	0.01031	0.5955	11	12	0.51772	*TP63*	3.82081
cg15084269	0.01564	0.1206	14	9	0.70518	*STX6*	3.81891
cg04160030	0.00801	0.7215	12	11	0.73473	*FUCA1*	3.78775
cg15965134	0.01019	0.299	9	13	0.26999	*SOX14*	3.69967

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg21889703	0.01288	0.672	10	12	0.69205	*BCLAF1*	3.69920
cg22979531	0.00875	0.4952	10	13	0.92581	*TRNA*	3.68436
cg11340260	0.01247	0.5388	12	11	0.25440	*GP1BA*	3.68335
cg19196221	0.01148	0.8373	13	10	0.35176	*EPN1*	3.67546
cg13883633	0.01151	0.6845	12	11	0.37170	*MGA*	3.66123
cg06718139	0.01187	0.7797	12	11	0.95088	*KIDINS220*	3.65986
cg14265709	0.01111	0.2997	14	9	0.31302	*SLCO5A1*	3.62372
cg17501774	0.02142	0.8107	13	10	0.82799	*ZNF697*	3.61802
cg17435266	0.02142	0.0511	13	10	0.82799	*GGACT*	3.61802
cg00066854	0.01476	0.4063	11	12	0.33963	*GPAM*	3.61696
cg14211055	0.00946	0.8883	11	12	0.64405	*MCM3AP*	3.61460
cg08806184	0.00585	0.609	9	14	0.08866	*DPYSL5*	3.54556
cg21822834	0.01205	0.8245	10	13	0.90119	*AKT1*	3.53793
cg23866916	0.01205	0.586	10	13	0.90119	*SBNO2*	3.53793
cg25845326	0.01476	0.8361	12	11	1.00000	*MRGPRE*	3.51238
cg13444289	0.00683	0.8804	11	12	0.24179	*HMGB3*	3.49570
cg05986288	0.01430	0.7621	10	13	0.59773	*HMGCR*	3.47425
cg00406338	0.01430	0.8267	10	13	0.59773	*NPEPL1*	3.47425
cg05094081	0.01135	0.0994	14	9	0.87474	*DLX1*	3.46848
cg18437033	0.01083	0.5905	13	10	0.21439	*TMEM132D*	3.43290
cg10068740	0.01844	0.876	11	12	0.75806	*NSD3*	3.42159
cg17761815	0.01841	0.6218	11	12	0.49798	*IL20RA*	3.41729
cg11940177	0.01319	0.4068	9	14	0.92464	*PGAM1*	3.41141
cg02276944	0.01756	0.3116	12	11	0.29496	*GPD2*	3.40884
cg00007076	0.01883	0.3583	12	11	1.00000	*RRS1*	3.39041
cg22620071	0.01903	0.7668	9	13	0.89363	*YTHDC2*	3.37194

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg22040039	0.01505	0.6649	10	13	0.49469	*ALDH2*	3.35970
cg11683364	0.02500	0.4195	9	12	0.94327	*LGR6*	3.35855
cg04722901	0.01742	0.6657	14	9	0.72873	*MYO10*	3.35060
cg00773060	0.01888	0.6413	14	9	0.52833	*TBCE*	3.34219
cg13552999	0.02173	0.1488	13	10	0.16248	*PTPN21*	3.32146
cg20779373	0.01081	0.2799	12	11	0.85337	*GRIK3*	3.31505
cg23422268	0.01718	0.6138	10	13	0.87667	*PAX2*	3.30257
cg07623567	0.02111	0.1842	14	9	0.59197	*HLA-DMB*	3.27841
cg26703507	0.02006	0.4007	14	9	0.13839	*SLC20A1*	3.27525
cg10026995	0.01296	0.2885	9	14	0.59197	*BRSK2*	3.27391
cg07015886	0.02208	0.3461	14	9	0.48792	*TLR5*	3.26918
cg13066481	0.02416	0.3842	11	12	0.73473	*MYLK*	3.26666
cg21446172	0.01996	0.79	10	13	0.85226	*CAPN8*	3.24451
cg26530319	0.02512	0.5686	12	11	0.18532	*HLX*	3.21152
cg27217742	0.02267	0.3969	10	13	0.55536	*RGS12*	3.15549
cg17758673	0.02267	0.5948	10	13	0.55536	*RGS12*	3.15549
cg24516497	0.02267	0.7128	10	13	0.55536	*CYB5D2*	3.15549
cg03523740	0.02502	0.3399	14	9	0.39462	*TXLNA*	3.15346
cg25276892	0.01775	0.4523	13	10	0.80389	*TNRC6B*	3.13568
cg14223135	0.02120	0.3545	13	10	0.80389	*TPSD1*	3.13474
cg01056004	0.02566	0.1753	14	9	0.06286	*SLIT1*	3.13267
cg01062020	0.01151	0.5836	10	13	0.90119	*SH2D1B*	3.12207
cg16629523	0.02367	0.1737	11	12	0.44125	*CTTN*	3.07790
cg18103730	0.02068	0.3807	11	12	0.25440	*GALC*	3.06347
cg03679544	0.02914	0.4545	14	9	0.20726	*TIAM2*	3.05919
cg12492938	0.01382	0.5174	12	11	0.42320	*LHX5*	3.05683

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg05798339	0.02395	0.4564	12	11	0.37170	*SRGAP3*	3.04357
cg07616394	0.02330	0.1488	13	9	0.16034	*HHEX*	3.02880
cg27315497	0.03229	0.2975	14	9	0.12237	*SLC43A1*	3.01541
cg26729380	0.03467	0.0962	14	9	0.48792	*TNF*	2.97725
cg07107171	0.02017	0.1063	9	13	0.78915	*TNR*	2.97149
cg13922669	0.02386	0.3608	13	10	0.16248	*LUZP2*	2.97077
cg11405695	0.02512	0.5607	13	10	0.26382	*ATAD3C*	2.96629
cg00469897	0.03610	0.2705	14	9	0.17519	*TNS3*	2.95649
cg08083041	0.02565	0.6398	13	10	0.45631	*CEMIP*	2.93873
cg02237906	0.02759	0.4905	12	11	0.97543	*RAB37*	2.93268
cg06398251	0.03805	0.5302	14	9	0.20726	*EIF4G1*	2.92760
cg27228413	0.02016	0.7936	11	12	0.73473	*MRPL46*	2.89307
cg15541611	0.04126	0.3178	14	9	0.43058	*C10orf95*	2.88499
cg02507296	0.04126	0.3182	14	9	0.43058	*C10orf95*	2.88499
cg13977486	0.04126	0.141	14	9	0.43058	*C10orf95*	2.88499
cg19268453	0.04126	0.4329	14	9	0.43058	*HLA-DMB*	2.88499
cg27331471	0.03052	0.5257	10	13	0.77997	*CKM*	2.88079
cg14086922	0.04126	0.3495	14	9	0.31302	*MICAL3*	2.86927
cg25335557	0.02912	0.1914	10	12	0.09888	*GBX2*	2.86905
cg21033675	0.03227	0.5638	13	10	0.66389	*MRGPRX4*	2.84637
cg20108357	0.03449	0.5377	13	10	0.12067	*BDNF*	2.84360
cg16708938	0.04518	0.2561	14	9	0.17519	*SIK1*	2.83579
cg14534144	0.04518	0.6984	14	9	0.17519	*TMCO3*	2.83579
cg23167246	0.04518	0.6787	14	9	0.17519	*TMCO3*	2.83579
cg23328404	0.04596	0.1072	14	9	0.54915	*CSGALNACT1*	2.82684
cg03996020	0.04596	0.3490	14	9	0.54915	*DNAJB6*	2.82684

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg01374870	0.04823	0.2427	13	9	0.31596	*HLA-DMB*	2.81714
cg24134261	0.04781	0.2347	13	9	0.25574	*RASGRP3*	2.80565
cg24175188	0.03503	0.3556	14	9	0.17519	*PXK*	2.79534
cg04411041	0.03767	0.3249	13	10	0.77997	*FAM180B*	2.75815
cg00343906	0.04682	0.3716	13	10	0.51451	*NADK*	2.64890
cg05464008	0.04894	0.4773	14	9	0.50791	*MCF2L*	2.62874
cg01289541	0.04925	0.2420	13	10	0.87667	*SLC7A14*	2.62160
cg04688330	0.04925	0.2584	13	10	0.87667	*SH3PXD2A*	2.62160
cg11657817	0.02532	0.4635	14	9	0.82533	*CST11*	2.45262
cg27166581	0.04481	0.3245	14	9	0.82533	*EFNA3*	2.45262
cg25417405	0.02532	0.4629	14	9	0.80087	*SLC27A2*	1.98682
cg27166673	0.04308	0.3748	13	10	0.87667	*ARHGAP6*	0.38711
cg11362604	0.04691	0.4002	9	14	0.13839	*MEIS2*	0.37707
cg04025964	0.02774	0.3221	12	11	0.10256	*NR5A2*	0.36180
cg08230177	0.03205	0.1255	11	12	0.85337	*TMEM174*	0.35967
cg03926025	0.02967	0.4809	12	11	0.53785	*HLA-E*	0.35694
cg02952295	0.02819	0.5784	13	10	0.14461	*TRPM8*	0.35508
cg06684850	0.02534	0.1452	14	9	0.46836	*BDNF*	0.35374
cg11005845	0.02742	0.3879	10	13	0.61945	*LDOC1*	0.35190
cg00603890	0.02667	0.504	9	14	0.29814	*CXorf56*	0.33619
cg06363801	0.02667	0.2491	9	14	0.29814	*MOSPD1*	0.33619
cg17236781	0.02468	0.3977	9	14	0.84996	*ZDHHC9*	0.33236
cg00264378	0.02468	0.4142	9	14	0.84996	*CLCN5*	0.33236
cg23939077	0.02468	0.5881	9	14	0.84996	*TSR2*	0.33236
cg04297329	0.01523	0.424	11	12	1.00000	*NAP1L2*	0.31651
cg20046330	0.01668	0.4645	10	13	0.70954	*STMN2*	0.31348

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg24361761	0.03664	0.6662	8	12	0.16460	*GPR158*	0.30644
cg20421446	0.02038	0.8421	9	14	0.36055	*NRN1*	0.30474
cg26730416	0.01834	0.3979	9	14	0.72873	*RRM1*	0.29821
cg19937979	0.01261	0.6907	9	14	0.84996	*CCDC177*	0.29813
cg16927040	0.00892	0.2913	14	9	0.21885	*SST*	0.29523
cg05120331	0.00898	0.2973	12	11	0.78160	*CCNA1*	0.29409
cg02301364	0.01617	0.041	14	9	0.89964	*PRPS1*	0.28678
cg06628473	0.01200	0.6694	14	9	0.28374	*MCC*	0.28136
cg20372230	0.00573	0.4849	13	10	0.73278	*LEP*	0.28095
cg13921220	0.00915	0.4655	11	12	0.35543	*IGSF21*	0.28077
cg01891172	0.00741	0.5599	10	13	0.49469	*KLHL34*	0.27835
cg02218496	0.00389	0.4667	12	11	0.68883	*DLX1*	0.27214
cg25556752	0.00482	0.1330	12	11	1.00000	*CLCN4*	0.27143
cg13986294	0.00770	0.5197	14	9	0.48792	*NFIB*	0.26894
cg01375382	0.01069	0.1185	14	9	0.65893	*RPS4Y1*	0.26440
cg05786601	0.01069	0.0243	14	9	0.65893	*AR*	0.26440
cg09525227	0.00984	0.1032	14	9	0.41237	*ESX1*	0.26295
cg11871628	0.00455	0.4405	10	13	0.66389	*CITED1*	0.26231
cg03933846	0.01160	0.5352	12	11	0.57926	*TMSB15A*	0.26218
cg06289882	0.00543	0.4807	9	14	0.80087	*RBMX2*	0.26074
cg13048466	0.00498	0.5167	11	12	0.11619	*WNT4*	0.26023
cg10246296	0.01100	0.0660	9	12	0.80332	*CLCN4*	0.25950
cg11325578	0.00640	0.4504	9	14	0.61394	*GPR143*	0.25519
cg07428004	0.00257	0.5065	13	10	1.00000	*LEP*	0.25321
cg03136493	0.00814	0.7767	13	9	0.81505	*TBXT*	0.24787
cg14541448	0.00707	0.0511	14	9	0.57037	*PTCHD1*	0.24678

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg02838825	0.00822	0.6269	13	10	0.43776	*TARBP1*	0.24522
cg15682807	0.00570	0.0182	14	9	0.94972	*ITM2A*	0.24478
cg00981643	0.00730	0.3515	12	11	0.80535	*MECP2*	0.24040
cg21167269	0.00333	0.6508	11	10	0.83253	*HSD17B3*	0.23792
cg05019001	0.00514	0.0260	14	9	0.57037	*AR*	0.23746
cg01479413	0.00514	0.0446	14	9	0.57037	*ARHGEF6*	0.23746
cg10418630	0.00364	0.2614	10	13	0.75626	*GPC4*	0.23686
cg01039990	0.00364	0.4254	10	13	0.75626	*ZIC3*	0.23686
cg16414561	0.00364	0.4091	10	13	0.75626	*ARX*	0.23686
cg23921534	0.00320	0.4788	11	12	0.60052	*POU3F4*	0.23396
cg19407410	0.00533	0.4716	14	9	0.57037	*PCDH19*	0.23269
cg25073957	0.00533	0.2492	14	9	0.32838	*RNF128*	0.23269
cg17875227	0.00534	0.0344	14	9	0.57037	*MORF4L2*	0.23198
cg25555657	0.00677	0.0421	13	10	0.95050	*FTSJ1*	0.23028
cg19153710	0.00677	0.0927	13	10	0.95050	*PHF8*	0.23028
cg02728721	0.00211	0.4534	11	12	0.85337	*LAMP5*	0.22945
cg24829975	0.00494	0.0408	13	10	0.90119	*ARMCX3*	0.22907
cg05782751	0.00549	0.1278	13	10	0.95050	*MCTS1*	0.22411
cg12527112	0.00549	0.0567	13	10	0.95050	*UPF3B*	0.22411
cg03317455	0.00549	0.0825	13	10	0.95050	*MAOA*	0.22411
cg02213813	0.00549	0.0299	13	10	0.95050	*MAMLD1*	0.22411
cg08395108	0.00549	0.0562	13	10	0.95050	*MAGED2*	0.22411
cg19912739	0.00320	0.0394	14	9	0.65893	*MAMLD1*	0.22195
cg01212677	0.00501	0.0600	14	9	0.94972	*PDK3*	0.22163
cg12324831	0.00501	0.0624	14	9	0.94972	*VBP1*	0.22163
cg22766145	0.00202	0.2685	13	10	0.32058	*BHLHE22*	0.21725

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg25614094	0.00302	0.2463	14	9	0.10112	*OPRK1*	0.21595
cg16491617	0.00302	0.1228	14	9	0.10112	*OPRK1*	0.21595
cg07764473	0.00199	0.5997	13	10	0.68657	*BCOR*	0.21581
cg17861230	0.00164	0.5071	14	9	0.57037	*PDE4C*	0.21399
cg26142661	0.00310	0.1296	13	10	0.66389	*ZMAT1*	0.21325
cg21744850	0.00257	0.4019	12	11	0.47865	*DGKK*	0.21294
cg21491240	0.00231	0.0303	14	9	0.48792	*HTATSF1*	0.20919
cg02156782	0.00231	0.0644	14	9	0.48792	*PPP1R3F*	0.20919
cg06211724	0.00251	0.2994	13	10	0.29127	*LAMC2*	0.20910
cg05883195	0.00576	0.7439	10	13	0.59773	*SOX8*	0.20887
cg08908089	0.00290	0.5298	13	10	0.90119	*APBA2*	0.20458
cg09208571	0.00271	0.2534	13	10	0.85226	*MAGED2*	0.20443
cg14270434	0.00166	0.6251	13	10	0.49469	*FOXE1*	0.20399
cg14091713	0.00224	0.0571	13	10	0.53474	*RP2*	0.19977
cg12713960	0.00202	0.0328	14	9	0.52833	*GLOD5*	0.19772
cg15075851	0.00344	0.1840	12	11	0.66629	*HPRT1*	0.19760
cg18973863	0.00152	0.7192	9	14	0.21885	*MBNL2*	0.19516
cg09001953	0.00104	0.0899	12	11	0.68883	*UFSP2*	0.19473
cg16235803	0.00222	0.4290	9	14	0.61394	*WNK3*	0.19402
cg00583618	0.00178	0.0174	13	10	0.90119	*MAGIX*	0.19390
cg13699152	0.00178	0.0196	13	10	0.90119	*GK*	0.19390
cg01098871	0.00294	0.0428	12	11	1.00000	*WDR45*	0.19371
cg03536032	0.00276	0.2463	11	12	0.45974	*ARHGAP6*	0.19252
cg22473846	0.00070	0.2874	13	10	0.55536	*OSMR*	0.19179
cg16290737	0.00264	0.1661	11	11	0.34062	*CHGA*	0.18947
cg16328412	0.00129	0.5234	10	13	0.43776	*IGSF1*	0.18941

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg23496314	0.00135	0.0376	13	10	0.70954	*BCOR*	0.18601
cg15281331	0.00084	0.5640	9	14	0.63627	*JAKMIP3*	0.18548
cg05921207	0.00085	0.4371	14	9	0.39462	*CHRDL1*	0.18508
cg13077484	0.00097	0.0641	14	9	0.94972	*DLG3*	0.18426
cg07210835	0.00097	0.0414	14	9	0.94972	*PLP2*	0.18426
cg27404676	0.00121	0.1562	14	9	0.70518	*TENT5D*	0.18418
cg07351143	0.00138	0.4899	14	9	0.39462	*SPAG6*	0.18126
cg10578938	0.00198	0.7131	13	8	0.23150	*CYFIP2*	0.18121
cg15211677	0.00240	0.0671	14	9	0.75255	*TCEAL9*	0.17985
cg00180631	0.00194	0.1710	13	10	0.40200	*MTM1*	0.17781
cg18452799	0.00161	0.0841	14	9	0.37735	*TRMT2B*	0.17556
cg16930349	0.00139	0.0347	13	10	0.43776	*GRIPAP1*	0.17499
cg18742441	0.00096	0.0215	13	10	0.45631	*ATP6AP1*	0.17408
cg21887683	0.00096	0.0216	13	10	0.45631	*HTATSF1*	0.17408
cg16391404	0.00096	0.1638	13	10	0.45631	*ZNF711*	0.17408
cg01191902	0.00136	0.0326	13	10	0.95050	*PRAF2*	0.17317
cg15322420	0.00146	0.0446	13	10	0.66389	*MORF4L2*	0.17316
cg10848980	0.00085	0.0237	14	9	0.44924	*PRAF2*	0.17239
cg03165176	0.00159	0.7308	14	9	0.80087	*APC2*	0.17068
cg18556676	0.00101	0.5281	13	10	0.82799	*ABCC9*	0.16910
cg05855948	0.00112	0.4432	13	10	0.64151	*KCTD1*	0.16793
cg01488378	0.00102	0.0458	14	9	0.34423	*SLC35A2*	0.16587
cg07903918	0.00077	0.3521	12	11	0.87760	*GABBR2*	0.16499
cg13879937	0.00221	0.8185	9	14	0.61394	*EHD4*	0.16400
cg00698744	0.00078	0.0680	12	11	0.16570	*TSPYL2*	0.16211
cg06068202	0.00106	0.3228	12	11	0.80535	*GPR50*	0.16202

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg00227584	0.00106	0.1171	12	11	0.80535	*TSPYL2*	0.16202
cg13822691	0.00106	0.1188	12	11	0.80535	*MSN*	0.16202
cg20880647	0.00106	0.1004	12	11	0.80535	*RNF128*	0.16202
cg15788661	0.00106	0.1289	12	11	0.80535	*FAM155B*	0.16202
cg15706156	0.00106	0.0231	12	11	0.80535	*GABRQ*	0.16202
cg07320017	0.00106	0.1574	12	11	0.80535	*MCF2*	0.16202
cg17973147	0.00106	0.1051	12	11	0.80535	*JADE3*	0.16202
cg09443457	0.00106	0.4139	12	11	0.80535	*FAM47C*	0.16202
cg02116333	0.00106	0.0298	12	11	0.80535	*HSD17B10*	0.16202
cg06650776	0.00106	0.0399	12	11	0.80535	*BEX3*	0.16202
cg02938958	0.00106	0.0363	12	11	0.80535	*ARX*	0.16202
cg01353788	0.00106	0.0198	12	11	0.80535	*AFF2*	0.16202
cg15050093	0.00106	0.0413	12	11	0.80535	*RPL39*	0.16202
cg14022645	0.00106	0.0283	12	11	0.80535	*TFE3*	0.16202
cg19679687	0.00106	0.2907	12	11	0.80535	*LANCL3*	0.16202
cg23050981	0.00106	0.0417	12	11	0.80535	*L1CAM*	0.16202
cg26583344	0.00096	0.0326	13	10	0.80389	*TMEM255A*	0.16055
cg23694557	0.00096	0.0596	13	10	0.80389	*IGSF1*	0.16055
cg09970175	0.00019	0.2903	10	13	0.73278	*SEMA6D*	0.15868
cg19736647	0.00075	0.0345	14	9	0.13019	*AIFM1*	0.15843
cg10994149	0.00040	0.7046	11	12	0.37170	*ANXA2R*	0.15667
cg00398130	0.00044	0.4211	12	11	0.95088	*STMN2*	0.14922
cg13183496	0.00131	0.0374	11	12	0.71165	*FAM120C*	0.14705
cg08100265	0.00131	0.1238	11	12	0.71165	*THOC2*	0.14705
cg00687135	0.00081	0.3885	14	9	0.13839	*ZNF385D*	0.14678
cg02279124	0.00017	0.4991	9	14	0.39462	*SRPK3*	0.14417

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg07390463	0.00016	0.6155	14	9	0.92464	*ALG10*	0.13970
cg04474375	0.00086	0.2962	10	13	0.85226	*FGF13*	0.13916
cg00177239	0.00031	0.1733	14	9	0.61394	*FAM160B1*	0.13893
cg14232291	0.00034	0.5861	12	11	0.28098	*KLHL34*	0.13618
cg18747090	0.00021	0.5765	12	11	0.95088	*PNPLA4*	0.13406
cg13072112	0.00023	0.3746	12	11	0.30939	*SOX3*	0.13096
cg01908395	0.00023	0.2919	12	11	0.30939	*MSX2*	0.13096
cg24648715	0.00054	0.0403	11	11	0.97379	*TCEAL3*	0.12853
cg17407511	0.00017	0.3197	13	10	0.59773	*SRPX*	0.12670
cg05926586	0.00075	0.8654	11	10	0.77806	*CCDC33*	0.12550
cg01003197	0.00036	0.0794	13	10	0.90119	*OPHN1*	0.12208
cg06943593	0.00036	0.0202	13	10	0.90119	*ARX*	0.12208
cg15024277	0.00036	0.0405	13	10	0.90119	*BEX3*	0.12208
cg24139895	0.00036	0.0554	13	10	0.90119	*NXT2*	0.12208
cg18134562	0.00046	0.3419	11	12	0.87760	*PLS3*	0.12004
cg25052176	0.00026	0.3806	11	12	0.60052	*WNK3*	0.11406
cg07758529	0.00023	0.4763	12	11	0.60052	*IL1RAPL2*	0.11321
cg14156792	0.00011	0.4565	14	9	0.57037	*SAMD11*	0.10189
cg14499563	0.00012	0.2678	14	9	0.82533	*CCNA1*	0.09959
cg06228453	0.00020	0.5394	9	14	0.63627	*MORC4*	0.08697
cg25127732	0.00020	0.4341	9	14	0.63627	*KLHL34*	0.08697
cg20950264	0.00016	0.3900	10	13	1.00000	*EFNB1*	0.08606
cg16639692	0.00003	0.6381	14	9	0.10112	*ANXA2R*	0.08256
cg15395971	0.00010	0.4911	13	10	0.75626	*F3*	0.07661
cg21477075	0.00007	0.8157	14	9	0.70518	*KIF25*	0.07399
cg22696549	0.00004	0.2194	10	13	0.75626	*NR0B1*	0.06885

CpG sites	*p-value*	Optimal cutpoint	Group 1 (n)	Group 2 (n)	Age test (*p-value*)	Gene	HR
cg20710266	0.00001	0.2462	13	10	0.97524	*NR2F2*	0.05806
cg20371650	0.00007	0.3641	9	14	0.50791	*PRAF2*	0.04326
cg15718594	0.02532	0.1791	12	10	0.71655	*BATF3*	
cg10349687	0.02532	0.7131	13	9	0.66389	*DNAJB6*	
cg04267772	0.02532	0.4301	12	11	0.85337	*CARHSP1*	
cg11311332	0.02532	0.7568	11	12	0.97543	*PODXL*	
cg21606490	0.04481	0.0878	11	12	0.51772	*NTNG1*	
cg03112433	0.00022	0.4704	12	11	0.71165	*CDK14*	
cg07924081	0.01405	0.1527	14	9	0.84996	*PPP1R13L*	
cg24630778	0.04481	0.7687	11	11	0.74246	*GALNT9*	
cg26307359	0.02532	0.0577	13	10	0.59773	*SEZ6*	
cg02311725	0.02532	0.274	14	9	0.18544	*HCK*	
cg08118344	0.04481	0.4382	11	12	0.28098	*RAP1GAP*	
cg01353586	0.02532	0.1719	11	11	0.79258	*HS3ST4*	
cg12024530	0.04481	0.3202	14	9	0.29814	*C12orf10*	
cg03975922	0.04481	0.3871	12	11	0.32428	*ZMAT2*	
cg27557428	0.02532	0.0540	12	10	1.00000	*TMEM9*	
cg16322565	0.02532	0.4527	14	9	0.32838	*NR1I2*	
cg26135172	0.04481	0.0938	13	10	0.75626	*LIMD1*	
cg21454485	0.02265	0.5287	13	10	0.61945	*CD84*	
cg02568531	0.02532	0.3937	14	9	0.18544	*PNPLA2*	
cg05448271	0.03128	0.7846	10	12	0.09897	*KLF6*	
cg12857702	0.00316	0.1287	14	9	0.61394	*ATRX*	
cg01032398	0.02532	0.6783	14	9	0.57037	*APOE*	
cg15378486	0.02532	0.3017	14	9	1.00000	*FSCN2*	
cg15320998	0.02532	0.1523	14	9	0.77660	*ZNF212*	

CpG sites	***p-value***	**Optimal cutpoint**	**Group 1 (n)**	**Group 2 (n)**	**Age test (*p-value*)**	**Gene**	**HR**
cg11792874	0.04481	0.4584	14	9	0.77660	*ZFHX2*	
cg00926657	0.04481	0.4101	14	9	0.77660	*MAFG*	

Annex XIV Additional information about the 375 candidate biomarkers of prognostic of DNA methylation in patients with AML-M4 categorized in the intermediate prognostic risk group.

CpG sites	location	status	Ratio	delta beta	*p-value*	Gene	cluster
cg25914522	Promoter (2-3kb)	low	1.43	-0.33	1.03E-04	*RBMY1F*	
cg04929022	1st Intron	low	0.92	-0.30	1.48E-06	*VGLL1*	
cg06294373	Other Exon	low	0.91	-0.24	3.25E-05	*UMOD*	
cg06394109	Distal Intergenic	low	1.56	-0.50	2.45E-06	*C1QTNF8*	
cg14312439	Promoter (<=1kb)	low	1.56	-0.36	2.45E-06	*CCR3*	
cg17560693	Promoter (<=1kb)	low	1.00	-0.20	2.84E-06	*TBX22*	
cg16803185	Promoter (1-2kb)	low	1.30	-0.34	1.75E-06	*PLS3*	
cg15467834	Distal Intergenic	low	1.30	-0.36	1.75E-06	*CRYAA*	
cg19720260	Promoter (<=1kb)	low	1.30	-0.36	3.68E-06	*NXPE2*	
cg21230162	Distal Intergenic	low	0.64	-0.31	4.65E-06	*CRIPAK*	
cg21329507	Promoter (<=1kb)	low	0.64	-0.38	2.45E-06	*TMEM255A*	
cg25946304	Promoter (<=1kb)	low	0.77	-0.27	4.42E-05	*S1PR5*	1
cg13185308	Promoter (<=1kb)	low	0.77	-0.32	1.75E-06	*ABCC8*	1
cg13149245	Downstream (<=300)	low	1.56	-0.30	1.00E-06	*PIF1*	
cg22405653	Promoter (1-2kb)	low	0.64	-0.39	6.45E-07	*KRTAP21-1*	
cg02440744	Promoter (<=1kb)	low	0.77	-0.40	1.75E-06	*SLC26A5*	
cg17664577	Other Exon	low	0.62	-0.23	9.83E-06	*MMP9*	
cg12432236	1st Exon	low	1.30	-0.46	6.30E-05	*PCDH17*	
cg18060330	Promoter (1-2kb)	low	1.09	-0.42	1.48E-06	*BTNL2*	
cg08168379	Distal Intergenic	low	1.30	-0.43	1.75E-06	*SALL1*	
cg21909948	Other Intron	low	0.77	-0.22	1.97E-06	*IQSEC2*	
cg14100184	Promoter (<=1kb)	low	1.09	-0.29	7.59E-07	*GNG13*	
cg05744332	Promoter (2-3kb)	low	0.64	-0.39	6.85E-06	*MNX1*	
cg06871764	Promoter (1-2kb)	low	0.92	-0.37	1.48E-06	*BTNL2*	
cg03161453	1st Intron	low	0.77	-0.27	1.75E-06	*BCOR*	
cg13060157	Distal Intergenic	low	1.56	-0.47	2.45E-06	*FAM19A3*	

cg16683746	Promoter (1-2kb)	low	1.09	-0.39	1.48E-06	*RUNX1T1*	
cg12462026	Promoter (<=1kb)	low	1.56	-0.30	2.45E-06	*HS6ST2*	
cg11703139	Promoter (<=1kb)	low	0.92	-0.20	1.48E-06	*GUCY2F*	
cg27307168	Distal Intergenic	low	1.30	-0.23	1.75E-06	*RBMX*	
cg16049600	Promoter (<=1kb)	low	0.64	-0.51	2.45E-06	*PCDHB11*	
cg07003115	Promoter (<=1kb)	low	1.56	-0.31	1.19E-06	*MANEAL*	
cg14605748	Promoter (<=1kb)	low	0.83	-0.22	3.09E-06	*AMOT*	
cg03780733	Promoter (<=1kb)	low	1.09	-0.42	1.48E-06	*PCDHB7*	
cg12454245	Promoter (2-3kb)	low	1.09	-0.27	1.48E-06	*NDUFB11*	
cg13795116	3' UTR	low	0.92	-0.24	1.48E-06	*CLCN4*	
cg10249705	Promoter (<=1kb)	low	0.77	-0.53	3.13E-08	*GUCY1A2*	
cg10703826	Promoter (<=1kb)	low	0.64	-0.51	8.21E-05	*TBX15*	
cg06801028	Promoter (<=1kb)	low	0.77	-0.32	4.62E-08	*NCOA4*	
cg23850281	Promoter (2-3kb)	low	0.77	-0.29	1.75E-06	*ADGRG2*	
cg24753473	Promoter (<=1kb)	low	1.09	-0.47	1.48E-06	*MAP2*	
cg18996274	Distal Intergenic	low	0.77	-0.23	1.75E-06	*CYP26B1*	
cg09766820	Promoter (1-2kb)	low	0.83	-0.21	3.09E-06	*LHX8*	
cg02060618	Promoter (<=1kb)	low	0.92	-0.22	3.09E-05	*BMP15*	
cg02586212	Promoter (<=1kb)	low	1.20	-0.36	3.09E-06	*RGS1*	
cg25879561	Promoter (<=1kb)	low	1.09	-0.30	9.99E-06	*SNRPN*	
cg14988083	Promoter (1-2kb)	low	1.30	-0.31	1.92E-06	*FGFR3*	298
cg02593884	Promoter (1-2kb)	low	1.30	-0.26	8.30E-08	*FLYWCH1*	298
cg22190023	Promoter (<=1kb)	low	0.77	-0.44	6.30E-05	*PCDHB7*	
cg06047020	Promoter (1-2kb)	low	1.30	-0.41	6.30E-05	*GPC6*	
cg20757404	Promoter (2-3kb)	low	0.64	-0.35	2.45E-06	*THEG*	
cg18496212	1st Intron	low	1.09	-0.30	1.48E-06	*MITF*	
cg23756474	Other Intron	low	0.92	-0.48	1.48E-06	*PCSK2*	
cg24533097	Promoter (<=1kb)	low	1.09	-0.38	5.52E-05	*PCDHB11*	

cg17342925	Distal Intergenic	low	0.64	-0.28	6.59E-06	*EN1*	
cg08571680	Promoter (<=1kb)	low	1.09	-0.30	1.08E-07	*TBX10*	
cg22851944	Promoter (<=1kb)	low	0.92	-0.37	1.48E-06	*GRIK2*	
cg16062292	3' UTR	low	1.56	-0.30	6.60E-08	*TKTL1*	
cg24508310	1st Intron	low	0.77	-0.30	8.37E-06	*BCOR*	
cg26439139	Other Intron	low	0.69	-0.22	4.02E-06	*SGCD*	
cg19223521	Distal Intergenic	low	1.09	-0.44	1.48E-06	*EN1*	
cg23992130	Other Intron	low	0.77	-0.37	1.75E-06	*LONRF3*	
cg00412554	Promoter (<=1kb)	low	0.77	-0.28	1.75E-06	*KLHL13*	
cg05946623	Promoter (<=1kb)	low	0.77	-0.34	1.23E-05	*CDH8*	
cg02275924	Promoter (<=1kb)	low	0.64	-0.47	2.45E-06	*MID1*	
cg12437013	Other Intron	low	1.56	-0.31	2.60E-07	*TMCO3*	
cg20881335	Promoter (<=1kb)	low	0.92	-0.49	3.12E-07	*GLRA2*	
cg16792071	Distal Intergenic	low	0.92	-0.20	1.48E-06	*ADGRA1*	
cg24489686	Other Intron	low	0.83	-0.21	3.09E-06	*FGF13*	
cg27281882	Promoter (1-2kb)	low	0.64	-0.22	2.45E-06	*PAK5*	
cg14215711	Other Intron	low	0.83	-0.24	1.09E-07	*PIP4K2A*	
cg24740868	Promoter (<=1kb)	low	0.77	-0.32	2.87E-05	*C1orf87*	
cg01325409	Promoter (<=1kb)	low	0.64	-0.20	3.63E-06	*SLC24A5*	
cg12104246	Promoter (<=1kb)	low	1.30	-0.43	2.20E-07	*C6orf62*	
cg09857513	Promoter (<=1kb)	low	0.92	-0.31	2.60E-06	*WNT16*	
cg17544177	Promoter (<=1kb)	low	1.56	-0.52	2.45E-06	*KCNIP2*	
cg19433175	Distal Intergenic	low	1.30	-0.25	2.60E-06	*TPTE*	
cg10566660	Distal Intergenic	low	1.30	-0.24	8.17E-07	*GTF3A*	3
cg04514392	Distal Intergenic	low	1.30	-0.59	1.75E-06	*CCDC54*	3
cg13971849	Other Intron	low	1.30	-0.24	5.81E-08	*PLEKHA2*	3
cg11067407	Distal Intergenic	low	1.30	-0.21	1.75E-06	*TMPRSS5*	3
cg02719508	Promoter (<=1kb)	low	1.33	-0.23	1.01E-04	*AHNAK2*	
cg18417245	Promoter (<=1kb)	low	0.77	-0.37	1.75E-06	*PCDHB11*	
cg06720722	Promoter (<=1kb)	low	0.92	-0.53	5.52E-05	*TP63*	

cg15084269	Promoter (1-2kb)	low	1.56	-0.25	2.45E-06	*STX6*	
cg04160030	Promoter (<=1kb)	low	1.09	-0.40	1.48E-06	*FUCA1*	
cg15965134	Promoter (2-3kb)	low	0.69	-0.23	4.81E-08	*SOX14*	
cg21889703	1st Intron	low	0.83	-0.28	5.90E-07	*BCLAF1*	
cg22979531	Distal Intergenic	low	0.77	-0.31	4.82E-06	*TRNA*	
cg11340260	Promoter (<=1kb)	low	1.09	-0.34	8.04E-06	*GP1BA*	
cg19196221	Distal Intergenic	low	1.30	-0.22	1.75E-06	*EPN1*	
cg13883633	Promoter (<=1kb)	low	1.09	-0.28	1.72E-05	*MGA*	
cg06718139	3' UTR	low	1.09	-0.27	1.48E-06	*KIDINS220*	
cg14265709	1st Intron	low	1.56	-0.52	2.45E-06	*SLCO5A1*	
cg17501774	1st Intron	low	1.30	-0.25	1.75E-06	*ZNF697*	4
cg17435266	Promoter (<=1kb)	low	1.30	-0.27	1.75E-06	*GGACT*	4
cg00066854	Distal Intergenic	low	0.92	-0.40	4.59E-07	*GPAM*	
cg14211055	Promoter (<=1kb)	low	0.92	-0.42	1.48E-06	*MCM3AP*	
cg08806184	Promoter (2-3kb)	low	0.64	-0.32	2.56E-06	*DPYSL5*	
cg21822834	Promoter (1-2kb)	low	0.77	-0.28	1.75E-06	*AKT1*	5
cg23866916	1st Intron	low	0.77	-0.38	1.30E-08	*SBNO2*	5
cg25845326	Other Exon	low	1.09	-0.33	1.48E-06	*MRGPRE*	
cg13444289	3' UTR	low	0.92	-0.23	1.48E-06	*HMGB3*	
cg05986288	Distal Intergenic	low	0.77	-0.32	7.23E-06	*HMGCR*	6
cg00406338	Promoter (<=1kb)	low	0.77	-0.26	1.75E-06	*NPEPL1*	6
cg05094081	Promoter (<=1kb)	low	1.56	-0.34	8.21E-05	*DLX1*	
cg18437033	1st Intron	low	1.30	-0.46	1.75E-06	*TMEM132D*	
cg10068740	Other Intron	low	0.92	-0.23	1.48E-06	*NSD3*	
cg17761815	Other Exon	low	0.92	-0.37	5.52E-05	*IL20RA*	
cg11940177	Promoter (1-2kb)	low	0.64	-0.47	2.45E-06	*PGAM1*	
cg02276944	Promoter (<=1kb)	low	1.09	-0.27	1.48E-06	*GPD2*	
cg00007076	Promoter (1-2kb)	low	1.09	-0.36	2.39E-06	*RRS1*	
cg22620071	Distal Intergenic	low	0.69	-0.29	4.02E-06	*YTHDC2*	
cg22040039	Distal Intergenic	low	0.77	-0.27	1.27E-06	*ALDH2*	
cg11683364	Promoter (2-3kb)	low	0.75	-0.20	1.19E-04	*LGR6*	

cg04722901	Other Intron	low	1.56	-0.23	2.41E-06	*MYO10*	
cg00773060	Other Intron	low	1.56	-0.30	3.24E-08	*TBCE*	
cg13552999	Promoter (<=1kb)	low	1.30	-0.34	1.75E-06	*PTPN21*	
cg20779373	1st Intron	low	1.09	-0.28	8.53E-08	*GRIK3*	
cg23422268	Distal Intergenic	low	0.77	-0.51	1.18E-08	*PAX2*	
cg07623567	Promoter (<=1kb)	low	1.56	-0.27	2.45E-06	*HLA-DMB*	
cg26703507	Promoter (1-2kb)	low	1.56	-0.35	1.76E-05	*SLC20A1*	
cg10026995	Other Exon	low	0.64	-0.24	6.12E-09	*BRSK2*	
cg07015886	Promoter (<=1kb)	low	1.56	-0.29	9.69E-07	*TLR5*	
cg13066481	Other Intron	low	0.92	-0.30	2.55E-05	*MYLK*	
cg21446172	Other Intron	low	0.77	-0.28	1.75E-06	*CAPN8*	
cg26530319	Distal Intergenic	low	1.09	-0.41	1.02E-06	*HLX*	
cg27217742	Other Intron	low	0.77	-0.34	5.26E-08	*RGS12*	7
cg17758673	Other Intron	low	0.77	-0.56	1.75E-06	*RGS12*	7
cg24516497	Downstream (<=300)	low	0.77	-0.38	8.09E-08	*CYB5D2*	7
cg03523740	Promoter (<=1kb)	low	1.56	-0.21	7.70E-06	*TXLNA*	
cg25276892	Promoter (<=1kb)	low	1.30	-0.52	1.11E-07	*TNRC6B*	
cg14223135	Distal Intergenic	low	1.30	-0.39	4.79E-08	*TPSD1*	
cg01056004	Promoter (2-3kb)	low	1.56	-0.43	2.45E-06	*SLIT1*	
cg01062020	Promoter (<=1kb)	low	0.77	-0.39	1.75E-06	*SH2D1B*	
cg16629523	Other Intron	low	0.92	-0.29	1.48E-06	*CTTN*	
cg18103730	Promoter (<=1kb)	low	0.92	-0.56	1.48E-06	*GALC*	
cg03679544	Promoter (<=1kb)	low	1.56	-0.54	2.45E-08	*TIAM2*	
cg12492938	Distal Intergenic	low	1.09	-0.36	5.05E-08	*LHX5*	
cg05798339	Distal Intergenic	low	1.09	-0.42	1.17E-08	*SRGAP3*	
cg07616394	Promoter (2-3kb)	low	1.44	-0.24	4.02E-06	*HHEX*	
cg27315497	Promoter (<=1kb)	low	1.56	-0.41	2.45E-06	*SLC43A1*	
cg26729380	Promoter (<=1kb)	low	1.56	-0.29	8.21E-05	*TNF*	
cg07107171	Promoter (<=1kb)	low	0.69	-0.27	4.02E-06	*TNR*	
cg13922669	Promoter (<=1kb)	low	1.30	-0.27	7.13E-07	*LUZP2*	

cg11405695	Promoter (<=1kb)	low	1.30	-0.33	1.76E-05	*ATAD3C*	
cg00469897	1st Intron	low	1.56	-0.39	9.90E-07	*TNS3*	
cg08083041	Promoter (1-2kb)	low	1.30	-0.32	4.61E-07	*CEMIP*	
cg02237906	Promoter (<=1kb)	low	1.09	-0.44	6.86E-06	*RAB37*	
cg06398251	Promoter (<=1kb)	low	1.56	-0.34	5.52E-07	*EIF4G1*	
cg27228413	Distal Intergenic	low	0.92	-0.22	1.48E-06	*MRPL46*	
cg15541611	Promoter (<=1kb)	low	1.56	-0.34	1.72E-08	*C10orf95*	8
cg02507296	Promoter (<=1kb)	low	1.56	-0.29	5.45E-08	*C10orf95*	8
cg13977486	Promoter (<=1kb)	low	1.56	-0.24	2.45E-06	*C10orf95*	8
cg19268453	Promoter (<=1kb)	low	1.56	-0.27	3.78E-06	*HLA-DMB*	8
cg27331471	3' UTR	low	0.77	-0.50	1.75E-06	*CKM*	
cg14086922	Downstream (<=300)	low	1.56	-0.34	1.84E-05	*MICAL3*	
cg25335557	Distal Intergenic	low	0.83	-0.26	3.09E-06	*GBX2*	
cg21033675	Promoter (<=1kb)	low	1.30	-0.27	2.17E-06	*MRGPRX4*	
cg20108357	Promoter (2-3kb)	low	1.30	-0.39	1.42E-05	*BDNF*	
cg16708938	Downstream (<=300)	low	1.56	-0.26	3.28E-06	*SIK1*	9
cg14534144	Other Exon	low	1.56	-0.63	8.21E-05	*TMCO3*	9
cg23167246	Other Exon	low	1.56	-0.64	8.15E-05	*TMCO3*	9
cg23328404	Promoter (<=1kb)	low	1.56	-0.31	2.45E-06	*CSGALNACT1*	9
cg03996020	Other Intron	low	1.56	-0.49	2.07E-07	*DNAJB6*	9
cg01374870	Promoter (<=1kb)	low	1.44	-0.25	1.00E-05	*HLA-DMB*	
cg24134261	Promoter (<=1kb)	low	1.44	-0.23	3.38E-05	*RASGRP3*	
cg24175188	Other Intron	low	1.56	-0.38	2.45E-06	*PXK*	
cg04411041	Promoter (1-2kb)	low	1.30	-0.20	1.11E-07	*FAM180B*	
cg00343906	Promoter (<=1kb)	low	1.30	-0.38	2.80E-06	*NADK*	
cg05464008	Other Intron	low	1.56	-0.39	2.45E-06	*MCF2L*	
cg01289541	Other Intron	low	1.30	-0.25	1.07E-06	*SLC7A14*	10
cg04688330	Promoter (1-2kb)	low	1.30	-0.23	2.29E-05	*SH3PXD2A*	10
cg11657817	Promoter (<=1kb)	low	1.56	-0.25	1.55E-06	*CST11*	11
cg27166581	1st Intron	low	1.56	-0.51	2.45E-06	*EFNA3*	11

cg25417405	Promoter (<=1kb)	high	1.56	-0.35	1.76E-06	*SLC27A2*	
cg27166673	Promoter (<=1kb)	high	1.30	-0.55	9.07E-08	*ARHGAP6*	
cg11362604	Promoter (<=1kb)	high	0.64	-0.34	2.45E-06	*MEIS2*	
cg04025964	Promoter (1-2kb)	high	1.09	-0.56	1.48E-06	*NR5A2*	
cg08230177	Distal Intergenic	high	0.92	-0.41	1.48E-06	*TMEM174*	
cg03926025	Distal Intergenic	high	1.09	-0.32	1.48E-06	*HLA-E*	
cg02952295	Other Intron	high	1.30	-0.58	1.75E-06	*TRPM8*	
cg06684850	Promoter (<=1kb)	high	1.56	-0.49	2.45E-06	*BDNF*	
cg11005845	Promoter (<=1kb)	high	0.77	-0.38	6.51E-06	*LDOC1*	
cg00603890	Promoter (<=1kb)	high	0.64	-0.47	2.45E-06	*CXorf56*	12
cg06363801	Promoter (<=1kb)	high	0.64	-0.44	2.45E-06	*MOSPD1*	12
cg17236781	Promoter (<=1kb)	high	0.64	-0.29	2.45E-06	*ZDHHC9*	13
cg00264378	Promoter (<=1kb)	high	0.64	-0.48	2.45E-06	*CLCN5*	13
cg23939077	Promoter (<=1kb)	high	0.64	-0.48	2.45E-06	*TSR2*	13
cg04297329	Promoter (<=1kb)	high	0.92	-0.44	6.38E-06	*NAP1L2*	
cg20046330	Promoter (<=1kb)	high	0.77	-0.38	5.10E-06	*STMN2*	
cg24361761	Other Intron	high	0.67	-0.27	3.76E-06	*GPR158*	
cg20421446	Distal Intergenic	high	0.64	-0.24	2.45E-06	*NRN1*	
cg26730416	Distal Intergenic	high	0.64	-0.57	2.45E-06	*RRM1*	
cg19937979	Promoter (1-2kb)	high	0.64	-0.37	2.90E-07	*CCDC177*	
cg16927040	Promoter (<=1kb)	high	1.56	-0.41	9.89E-08	*SST*	
cg05120331	Promoter (<=1kb)	high	1.09	-0.46	1.48E-06	*CCNA1*	
cg02301364	Promoter (<=1kb)	high	1.56	-0.28	2.45E-06	*PRPS1*	
cg06628473	Other Intron	high	1.56	-0.25	4.05E-07	*MCC*	
cg20372230	Distal Intergenic	high	1.30	-0.47	1.75E-06	*LEP*	
cg13921220	Other Intron	high	0.92	-0.34	1.26E-07	*IGSF21*	
cg01891172	Promoter (<=1kb)	high	0.77	-0.45	1.75E-06	*KLHL34*	
cg02218496	Promoter (2-3kb)	high	1.09	-0.33	8.06E-07	*DLX1*	

cg25556752	Promoter (<=1kb)	high	1.09	-0.38	1.48E-06	*CLCN4*	
cg13986294	Promoter (2-3kb)	high	1.56	-0.41	2.45E-06	*NFIB*	
cg01375382	Promoter (<=1kb)	high	1.56	-0.40	2.45E-06	*RPS4Y1*	14
cg05786601	Promoter (<=1kb)	high	1.56	-0.30	8.21E-05	*AR*	14
cg09525227	Promoter (<=1kb)	high	1.56	-0.35	2.45E-06	*ESX1*	
cg11871628	Promoter (1-2kb)	high	0.77	-0.55	1.75E-06	*CITED1*	
cg03933846	Promoter (<=1kb)	high	1.09	-0.54	1.48E-06	*TMSB15A*	
cg06289882	Promoter (<=1kb)	high	0.64	-0.64	2.45E-06	*RBMX2*	
cg13048466	Distal Intergenic	high	0.92	-0.36	4.91E-08	*WNT4*	
cg10246296	Promoter (<=1kb)	high	0.75	-0.22	1.42E-04	*CLCN4*	
cg11325578	Promoter (<=1kb)	high	0.64	-0.52	2.45E-06	*GPR143*	
cg07428004	Distal Intergenic	high	1.30	-0.43	1.25E-07	*LEP*	
cg03136493	Distal Intergenic	high	1.44	-0.27	4.02E-06	*TBXT*	
cg14541448	Promoter (1-2kb)	high	1.56	-0.51	2.45E-06	*PTCHD1*	
cg02838825	Promoter (1-2kb)	high	1.30	-0.43	1.75E-06	*TARBP1*	
cg15682807	Promoter (<=1kb)	high	1.56	-0.30	2.45E-06	*ITM2A*	
cg00981643	Promoter (<=1kb)	high	1.09	-0.33	1.09E-07	*MECP2*	
cg21167269	Distal Intergenic	high	1.10	-0.32	3.95E-05	*HSD17B3*	
cg05019001	Promoter (2-3kb)	high	1.56	-0.32	2.45E-06	*AR*	15
cg01479413	Promoter (<=1kb)	high	1.56	-0.37	2.45E-06	*ARHGEF6*	15
cg10418630	Promoter (<=1kb)	high	0.77	-0.34	1.75E-06	*GPC4*	16
cg01039990	Distal Intergenic	high	0.77	-0.32	6.69E-06	*ZIC3*	16
cg16414561	Promoter (<=1kb)	high	0.77	-0.52	6.30E-05	*ARX*	16
cg23921534	Promoter (<=1kb)	high	0.92	-0.43	5.84E-06	*POU3F4*	
cg19407410	Promoter (<=1kb)	high	1.56	-0.57	2.45E-06	*PCDH19*	
cg25073957	Promoter (<=1kb)	high	1.56	-0.43	2.45E-06	*RNF128*	
cg17875227	Promoter (<=1kb)	high	1.56	-0.21	8.21E-05	*MORF4L2*	

cg25555657	Promoter (<=1kb)	high	1.30	-0.20	6.30E-05	*FTSJ1*	17
cg19153710	Promoter (<=1kb)	high	1.30	-0.28	1.75E-06	*PHF8*	17
cg02728721	Distal Intergenic	high	0.92	-0.33	1.76E-07	*LAMP5*	
cg24829975	Promoter (<=1kb)	high	1.30	-0.29	1.75E-06	*ARMCX3*	
cg05782751	Promoter (<=1kb)	high	1.30	-0.24	1.75E-06	*MCTS1*	18
cg12527112	Promoter (<=1kb)	high	1.30	-0.37	1.75E-06	*UPF3B*	18
cg03317455	Promoter (<=1kb)	high	1.30	-0.38	1.75E-06	*MAOA*	18
cg02213813	Promoter (2-3kb)	high	1.30	-0.33	6.30E-05	*MAMLD1*	18
cg08395108	Promoter (<=1kb)	high	1.30	-0.36	1.75E-06	*MAGED2*	18
cg19912739	Promoter (<=1kb)	high	1.56	-0.31	8.21E-05	*MAMLD1*	
cg01212677	Promoter (<=1kb)	high	1.56	-0.35	2.45E-06	*PDK3*	19
cg12324831	Promoter (<=1kb)	high	1.56	-0.29	8.21E-05	*VBP1*	19
cg22766145	Promoter (<=1kb)	high	1.30	-0.40	1.66E-07	*BHLHE22*	
cg25614094	Promoter (<=1kb)	high	1.56	-0.50	5.55E-07	*OPRK1*	20
cg16491617	Promoter (<=1kb)	high	1.56	-0.49	2.45E-06	*OPRK1*	20
cg07764473	Promoter (<=1kb)	high	1.30	-0.41	1.42E-05	*BCOR*	
cg17861230	Promoter (<=1kb)	high	1.56	-0.37	5.17E-07	*PDE4C*	
cg26142661	Promoter (<=1kb)	high	1.30	-0.44	1.75E-06	*ZMAT1*	
cg21744850	Promoter (1-2kb)	high	1.09	-0.42	4.92E-06	*DGKK*	
cg21491240	Promoter (<=1kb)	high	1.56	-0.25	2.45E-06	*HTATSF1*	21
cg02156782	Promoter (<=1kb)	high	1.56	-0.34	2.45E-06	*PPP1R3F*	21
cg06211724	Promoter (<=1kb)	high	1.30	-0.38	5.20E-06	*LAMC2*	
cg05883195	Distal Intergenic	high	0.77	-0.26	2.62E-06	*SOX8*	
cg08908089	Promoter (<=1kb)	high	1.30	-0.36	2.98E-06	*APBA2*	
cg09208571	Promoter (<=1kb)	high	1.30	-0.38	6.30E-05	*MAGED2*	
cg14270434	Promoter (1-2kb)	high	1.30	-0.48	1.75E-06	*FOXE1*	
cg14091713	Promoter (<=1kb)	high	1.30	-0.32	1.75E-06	*RP2*	

cg12713960	Distal Intergenic	high	1.56	-0.32	2.45E-06	*GLOD5*	
cg15075851	Promoter (<=1kb)	high	1.09	-0.41	1.48E-06	*HPRT1*	
cg18973863	Promoter (<=1kb)	high	0.64	-0.30	2.45E-06	*MBNL2*	
cg09001953	Promoter (<=1kb)	high	1.09	-0.41	1.48E-06	*UFSP2*	
cg16235803	Promoter (<=1kb)	high	0.64	-0.39	5.11E-06	*WNK3*	
cg00583618	Promoter (<=1kb)	high	1.30	-0.41	6.23E-05	*MAGIX*	22
cg13699152	Promoter (<=1kb)	high	1.30	-0.32	1.75E-06	*GK*	22
cg01098871	Promoter (<=1kb)	high	1.09	-0.35	1.48E-06	*WDR45*	
cg03536032	Promoter (<=1kb)	high	0.92	-0.34	1.48E-06	*ARHGAP6*	
cg22473846	Promoter (<=1kb)	high	1.30	-0.30	3.73E-06	*OSMR*	
cg16290737	Promoter (<=1kb)	high	1.00	-0.29	2.84E-06	*CHGA*	
cg16328412	Promoter (<=1kb)	high	0.77	-0.38	3.52E-06	*IGSF1*	
cg23496314	Promoter (<=1kb)	high	1.30	-0.22	1.75E-06	*BCOR*	
cg15281331	Distal Intergenic	high	0.64	-0.45	2.45E-06	*JAKMIP3*	
cg05921207	Promoter (<=1kb)	high	1.56	-0.38	2.45E-06	*CHRDL1*	
cg13077484	Promoter (<=1kb)	high	1.56	-0.44	2.45E-06	*DLG3*	23
cg07210835	Promoter (<=1kb)	high	1.56	-0.26	8.18E-05	*PLP2*	23
cg27404676	Promoter (<=1kb)	high	1.56	-0.52	2.45E-06	*TENT5D*	
cg07351143	Distal Intergenic	high	1.56	-0.34	2.45E-06	*SPAG6*	
cg10578938	Promoter (<=1kb)	high	1.63	-0.26	9.83E-06	*CYFIP2*	
cg15211677	Promoter (<=1kb)	high	1.56	-0.31	2.45E-06	*TCEAL9*	
cg00180631	Promoter (<=1kb)	high	1.30	-0.42	1.75E-06	*MTM1*	
cg18452799	Promoter (<=1kb)	high	1.56	-0.29	2.45E-06	*TRMT2B*	
cg16930349	Promoter (<=1kb)	high	1.30	-0.22	1.75E-06	*GRIPAP1*	
cg18742441	Promoter (<=1kb)	high	1.30	-0.34	6.30E-05	*ATP6AP1*	24
cg21887683	Promoter (<=1kb)	high	1.30	-0.35	6.30E-05	*HTATSF1*	24
cg16391404	Promoter (<=1kb)	high	1.30	-0.29	1.75E-06	*ZNF711*	24

cg01191902	Promoter (<=1kb)	high	1.30	-0.36	1.75E-06	*PRAF2*	
cg15322420	Promoter (<=1kb)	high	1.30	-0.36	6.30E-05	*MORF4L2*	
cg10848980	Promoter (<=1kb)	high	1.56	-0.31	2.45E-06	*PRAF2*	
cg03165176	5' UTR	high	1.56	-0.24	2.45E-06	*APC2*	
cg18556676	Promoter (<=1kb)	high	1.30	-0.31	1.04E-05	*ABCC9*	
cg05855948	Promoter (2-3kb)	high	1.30	-0.48	1.75E-06	*KCTD1*	
cg01488378	Promoter (<=1kb)	high	1.56	-0.28	8.21E-05	*SLC35A2*	
cg07903918	Promoter (<=1kb)	high	1.09	-0.30	1.48E-06	*GABBR2*	
cg13879937	Promoter (<=1kb)	high	0.64	-0.27	2.45E-06	*EHD4*	
cg00698744	Distal Intergenic	high	1.09	-0.25	1.48E-06	*TSPYL2*	
cg06068202	Promoter (1-2kb)	high	1.09	-0.48	1.48E-06	*GPR50*	25
cg00227584	Distal Intergenic	high	1.09	-0.52	1.48E-06	*TSPYL2*	25
cg13822691	Promoter (<=1kb)	high	1.09	-0.45	1.48E-06	*MSN*	25
cg20880647	Promoter (<=1kb)	high	1.09	-0.43	1.48E-06	*RNF128*	25
cg15788661	Promoter (<=1kb)	high	1.09	-0.45	1.48E-06	*FAM155B*	25
cg15706156	Promoter (<=1kb)	high	1.09	-0.36	5.52E-05	*GABRQ*	25
cg07320017	Promoter (<=1kb)	high	1.09	-0.30	1.48E-06	*MCF2*	25
cg17973147	Promoter (<=1kb)	high	1.09	-0.29	1.48E-06	*JADE3*	25
cg09443457	Distal Intergenic	high	1.09	-0.40	1.71E-08	*FAM47C*	25
cg02116333	Promoter (<=1kb)	high	1.09	-0.34	1.48E-06	*HSD17B10*	25
cg06650776	Promoter (<=1kb)	high	1.09	-0.51	1.48E-06	*BEX3*	25
cg02938958	Other Exon	high	1.09	-0.48	1.48E-06	*ARX*	25
cg01353788	Promoter (<=1kb)	high	1.09	-0.43	1.48E-06	*AFF2*	25
cg15050093	Promoter (<=1kb)	high	1.09	-0.42	1.48E-06	*RPL39*	25
cg14022645	Promoter (<=1kb)	high	1.09	-0.29	5.52E-05	*TFE3*	25
cg19679687	Promoter (<=1kb)	high	1.09	-0.37	6.60E-08	*LANCL3*	25
cg23050981	Promoter (<=1kb)	high	1.09	-0.22	1.48E-06	*L1CAM*	25

cg26583344	Promoter (1-2kb)	high	1.30	-0.30	1.75E-06	*TMEM255A*	26
cg23694557	Promoter (<=1kb)	high	1.30	-0.46	1.75E-06	*IGSF1*	26
cg09970175	Promoter (<=1kb)	high	0.77	-0.45	1.75E-06	*SEMA6D*	
cg19736647	Promoter (<=1kb)	high	1.56	-0.34	2.45E-06	*AIFM1*	
cg10994149	Downstrea m (<=300)	high	0.92	-0.48	1.48E-06	*ANXA2R*	
cg00398130	Promoter (2-3kb)	high	1.09	-0.37	4.15E-06	*STMN2*	
cg13183496	Promoter (<=1kb)	high	0.92	-0.42	1.48E-06	*FAM120C*	27
cg08100265	Promoter (<=1kb)	high	0.92	-0.36	1.48E-06	*THOC2*	27
cg00687135	Promoter (<=1kb)	high	1.56	-0.38	3.93E-07	*ZNF385D*	
cg02279124	Promoter (<=1kb)	high	0.64	-0.25	2.91E-06	*SRPK3*	
cg07390463	Distal Intergenic	high	1.56	-0.37	2.45E-06	*ALG10*	
cg04474375	Promoter (<=1kb)	high	0.77	-0.41	1.75E-06	*FGF13*	
cg00177239	Promoter (<=1kb)	high	1.56	-0.33	2.45E-06	*FAM160B1*	
cg14232291	Promoter (<=1kb)	high	1.09	-0.41	4.63E-05	*KLHL34*	
cg18747090	Promoter (<=1kb)	high	1.09	-0.52	1.48E-06	*PNPLA4*	
cg13072112	Promoter (1-2kb)	high	1.09	-0.40	1.48E-06	*SOX3*	28
cg01908395	Distal Intergenic	high	1.09	-0.34	8.37E-06	*MSX2*	28
cg24648715	Promoter (<=1kb)	high	1.00	-0.25	2.84E-06	*TCEAL3*	
cg17407511	Promoter (<=1kb)	high	1.30	-0.38	2.26E-07	*SRPX*	
cg05926586	Other Intron	high	1.10	-0.20	5.67E-06	*CCDC33*	
cg01003197	Promoter (<=1kb)	high	1.30	-0.50	1.75E-06	*OPHN1*	29
cg06943593	Other Intron	high	1.30	-0.34	6.30E-05	*ARX*	29
cg15024277	Promoter (<=1kb)	high	1.30	-0.39	1.75E-06	*BEX3*	29
cg24139895	Promoter (<=1kb)	high	1.30	-0.28	1.75E-06	*NXT2*	29
cg18134562	Promoter (<=1kb)	high	0.92	-0.47	1.48E-06	*PLS3*	
cg25052176	Promoter (1-2kb)	high	0.92	-0.50	1.48E-06	*WNK3*	
cg07758529	Promoter (2-3kb)	high	1.09	-0.54	1.48E-06	*IL1RAPL2*	
cg14156792	Other Intron	high	1.56	-0.37	7.63E-06	*SAMD11*	

cg14499563	Promoter (<=1kb)	high	1.56	-0.45	1.98E-06	*CCNA1*	
cg06228453	Promoter (<=1kb)	high	0.64	-0.48	2.45E-06	*MORC4*	30
cg25127732	Promoter (<=1kb)	high	0.64	-0.33	1.30E-05	*KLHL34*	30
cg20950264	Other Intron	high	0.77	-0.26	1.55E-07	*EFNB1*	
cg16639692	Promoter (2-3kb)	high	1.56	-0.45	2.45E-06	*ANXA2R*	
cg15395971	Promoter (2-3kb)	high	1.30	-0.37	1.69E-06	*F3*	
cg21477075	Other Intron	high	1.56	-0.22	8.21E-05	*KIF25*	
cg22696549	Promoter (<=1kb)	high	0.77	-0.32	1.75E-06	*NR0B1*	
cg20710266	Promoter (1-2kb)	high	1.30	-0.38	2.99E-07	*NR2F2*	
cg20371650	Promoter (<=1kb)	high	0.64	-0.32	2.45E-06	*PRAF2*	
cg15718594	Promoter (1-2kb)	low	1.20	-0.23	3.09E-06	*BATF3*	
cg10349687	Distal Intergenic	low	1.44	-0.24	7.09E-07	*DNAJB6*	
cg04267772	Promoter (<=1kb)	low	1.09	-0.43	2.77E-07	*CARHSP1*	
cg11311332	Distal Intergenic	low	0.92	-0.38	1.48E-06	*PODXL*	
cg21606490	3' UTR	low	0.92	-0.45	1.48E-06	*NTNG1*	
cg03112433	Promoter (<=1kb)	high	1.09	-0.45	9.57E-07	*CDK14*	
cg07924081	Promoter (2-3kb)	low	1.56	-0.20	2.45E-06	*PPP1R13L*	
cg24630778	Promoter (2-3kb)	low	1.00	-0.32	2.84E-06	*GALNT9*	
cg26307359	Promoter (<=1kb)	low	1.30	-0.48	1.75E-06	*SEZ6*	
cg02311725	Promoter (<=1kb)	high	1.56	-0.28	8.31E-06	*HCK*	
cg08118344	Other Intron	low	0.92	-0.26	2.76E-07	*RAP1GAP*	
cg01353586	Promoter (<=1kb)	low	1.00	-0.23	2.84E-06	*HS3ST4*	
cg12024530	Promoter (<=1kb)	low	1.56	-0.36	2.50E-08	*C12orf10*	
cg03975922	Promoter (<=1kb)	low	1.09	-0.27	5.64E-07	*ZMAT2*	
cg27557428	Promoter (<=1kb)	low	1.20	-0.22	3.09E-06	*TMEM9*	
cg16322565	Other Exon	low	1.56	-0.33	5.14E-07	*NR1I2*	
cg26135172	Distal Intergenic	low	1.30	-0.27	1.75E-06	*LIMD1*	
cg21454485	1st Intron	low	1.30	-0.28	9.18E-06	*CD84*	
cg02568531	Promoter (1-2kb)	low	1.56	-0.37	1.58E-06	*PNPLA2*	

cg05448271	1st Intron	high	0.83	-0.24	3.09E-06	*KLF6*	
cg12857702	Promoter (<=1kb)	high	1.56	-0.32	2.45E-06	*ATRX*	
cg01032398	Promoter (<=1kb)	low	1.56	-0.23	4.28E-07	*APOE*	
cg15378486	Distal Intergenic	low	1.56	-0.32	8.71E-08	*FSCN2*	
cg15320998	Promoter (<=1kb)	high	1.56	-0.41	2.45E-06	*ZNF212*	
cg11792874	Other Intron	low	1.56	-0.27	3.47E-06	*ZFHX2*	31
cg00926657	Promoter (<=1kb)	low	1.56	-0.47	8.21E-05	*MAFG*	31

Annex XV The remaining 17 identified genes whose gene expression were able to predict survival in patients with AML-M5 categorized in the intermediate prognostic risk group.

Gene	p-value	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (p-value)	HR
AQP11	0.0243	4.4296	6	9	0.5157	4.0034
WDR36	0.0246	10.2089	8	8	0.4939	3.9321
CTAGE6	0.0246	0.9845	8	8	0.3710	3.9321
CSMD1	0.0433	3.9458	7	9	0.9155	3.3080
ATP6V0E1	0.0427	11.5052	8	7	0.4171	0.2784
USHBP1	0.0427	0.8465	8	7	0.6428	0.2784
RNASET2	0.0233	11.1725	9	7	0.3397	0.2583
SARAF	0.0246	12.0394	8	8	0.2926	0.2543
ZBP1	0.0246	5.2369	8	8	0.4939	0.2543
ABAT	0.0295	8.7918	7	9	1.0000	0.2449
GDE1	0.0113	10.7249	8	8	0.7126	0.1955
MEI1	0.0079	7.6111	7	9	0.5958	0.1803
SKAP2	0.0189	11.8406	6	9	0.5949	0.1752
B2M	0.0086	15.5936	7	9	0.7908	0.1476
TXNDC12	0.0023	10.6061	8	8	1.0000	0.1471
ATP6V1G1	0.0004	10.2707	8	8	0.9162	0.0550
PPP1R2	0.0002	9.9615	8	6	1.0000	0.0467

Annex XVI Additional information about the 32 candidate biomarkers of prognostic of gene expression in patients with AML-M5 categorized in the intermediate prognostic risk group.

gene	status	Ratio	foldchange	*p-value*	bibliographic
TTC30B	low	1.00	0.37	0.0002	non-AML leukemia types
FNTB	low	1.00	0.33	0.0002	non-leukemia cancer types
CDKN2AIP	low	0.78	0.33	0.0002	non-AML leukemia types
VANGL1	low	0.88	0.33	0.0003	non-AML leukemia types
ATN1	low	1.29	0.31	0.0002	non-AML leukemia types
AMACR	low	1.29	0.36	0.0002	non-AML leukemia types
PLA2G4A	low	1.00	0.33	0.0006	cited in AML
TBX4	low	0.67	-Inf	0.0004	non-leukemia cancer types
ABRAXAS2	low	0.67	0.35	0.0004	non-leukemia cancer types
C9orf3	low	1.00	0.38	0.0002	non-leukemia cancer types
RTTN	low	1.29	0.34	0.0002	non-leukemia cancer types
ZNF625	low	1.14	0.34	0.0002	non-leukemia cancer types
FANK1	low	1.14	0.33	0.0001	non-leukemia cancer types
CDH24	low	1.29	0.36	0.0006	non-leukemia cancer types
ZSCAN20	low	1.29	0.39	0.0002	cited in PubMed
AQP11	low	0.67	0.40	0.0004	non-leukemia cancer types
WDR36	low	1.00	0.31	0.0002	non-AML leukemia types
CTAGE6	low	1.00	-0.69	0.0003	never cited
CSMD1	low	0.78	0.14	0.0001	cited in AML
ATP6V0E1	high	1.14	0.30	0.0003	non-leukemia cancer types
USHBP1	high	1.14	-0.51	0.0013	cited in PubMed
RNASET2	high	1.29	0.30	0.0002	non-AML leukemia types
SARAF	high	1.00	0.29	0.0002	cited in AML
ZBP1	high	1.00	0.36	0.0002	non-leukemia cancer types
ABAT	high	0.78	0.32	0.0000	cited in AML
GDE1	high	1.00	0.31	0.0002	non-leukemia cancer types
MEI1	high	0.78	0.35	0.0002	non-leukemia cancer types
SKAP2	high	0.67	0.29	0.0004	cited in AML
B2M	high	0.78	0.24	0.0002	cited in AML
TXNDC12	high	1.00	0.31	0.0002	non-leukemia cancer types
ATP6V1G1	high	1.00	0.31	0.0002	non-leukemia cancer types
PPP1R2	high	1.33	0.32	0.0007	non-leukemia cancer types

Annex XVII List of the gene sets shared by the majority of the intermediate-poor AML-M5 that were differentially enriched in comparison with the intermediate-favorable subgroups. For each gene set is represented the number and the percentage of intermediate-poor subgroups that have the gene sets enriched (n and percentage), a representative *p-value* and the status (upregulated (up) or downregulated (down)).

Set	n	Percentage	*p-value*	Status
GO:0044782 cilium organization	31	100	0.0001	Up
GO:0042073 intraciliary transport	31	100	0.0002	Up
GO:0098840 protein transport along microtubule	31	100	0.0004	Up
GO:0099118 microtubule-based protein transport	31	100	0.0004	Up
GO:0061512 protein localization to cilium	31	100	0.0004	Up
GO:0035082 axoneme assembly	31	100	0.0006	Up
GO:0001578 microtubule bundle formation	31	100	0.0010	Up
GO:0035735 intraciliary transport involved in cilium assembly	31	100	0.0011	Up
GO:0010970 transport along microtubule	31	100	0.0012	Up
GO:0099111 microtubule-based transport	31	100	0.0012	Up
GO:0060271 cilium assembly	31	100	0.0018	Up
GO:0030705 cytoskeleton-dependent intracellular transport	31	100	0.0018	Up
GO:1905349 ciliary transition zone assembly	31	100	0.0063	Up
GO:0048199 vesicle targeting, to, from or within Golgi	31	100	0.0064	Up
GO:0097712 vesicle targeting, trans-Golgi to periciliary membrane compartment	31	100	0.0073	Up
GO:0006903 vesicle targeting	31	100	0.0095	Up
GO:0007224 smoothened signaling pathway	31	100	0.0280	Up
GO:0008589 regulation of smoothened signaling pathway	31	100	0.0336	Up
GO:0051650 establishment of vesicle localization	31	100	0.0447	Up
GO:0009953 dorsal/ventral pattern formation	31	100	0.0476	Up
GO:0007281 germ cell development	30	97	0.0434	Up
GO:0007286 spermatid development	30	97	0.0471	Up
GO:0098681 synaptic ribbon	29	94	0.0180	Up
GO:0045880 positive regulation of smoothened signaling pathway	29	94	0.0314	Up
GO:0007368 determination of left/right symmetry	29	94	0.0355	Up
GO:0003351 epithelial cilium movement involved in extracellular fluid movement	29	94	0.0406	Up
GO:0009799 specification of symmetry	29	94	0.0457	Up
GO:0009855 determination of bilateral symmetry	29	94	0.0465	Up
GO:0048515 spermatid differentiation	29	94	0.0470	Up
GO:0009063 cellular amino acid catabolic process	29	94	0.0482	Up
GO:0003341 cilium movement	28	90	0.0441	Up
GO:0019882 antigen processing and presentation	31	100	0.0002	Down
GO:0048002 antigen processing and presentation of peptide antigen	31	100	0.0007	Down

Set	n	Percentage	*p-value*	Status
GO:0019884 antigen processing and presentation of exogenous antigen	31	100	0.0012	Down
GO:0002478 antigen processing and presentation of exogenous peptide antigen	31	100	0.0029	Down
GO:0097478 leaflet of membrane bilayer	31	100	0.0033	Down
GO:0060333 interferon-gamma-mediated signaling pathway	31	100	0.0036	Down
GO:0070098 chemokine-mediated signaling pathway	31	100	0.0055	Down
GO:1990868 response to chemokine	31	100	0.0057	Down
GO:1990869 cellular response to chemokine	31	100	0.0057	Down
GO:0002504 antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	31	100	0.0058	Down
GO:0019886 antigen processing and presentation of exogenous peptide antigen via MHC class II	31	100	0.0064	Down
GO:0002495 antigen processing and presentation of peptide antigen via MHC class II	31	100	0.0065	Down
GO:0034341 response to interferon-gamma	31	100	0.0069	Down
GO:2000106 regulation of leukocyte apoptotic process	31	100	0.0110	Down
GO:0071346 cellular response to interferon-gamma	31	100	0.0111	Down
GO:0030593 neutrophil chemotaxis	31	100	0.0124	Down
GO:0007159 leukocyte cell-cell adhesion	31	100	0.0125	Down
GO:1901215 negative regulation of neuron death	31	100	0.0151	Down
GO:1902894 negative regulation of pri-miRNA transcription by RNA polymerase II	31	100	0.0191	Down
GO:1990266 neutrophil migration	31	100	0.0192	Down
GO:0050852 T cell receptor signaling pathway	31	100	0.0208	Down
GO:0010959 regulation of metal ion transport	31	100	0.0208	Down
GO:0050851 antigen receptor-mediated signaling pathway	31	100	0.0215	Down
GO:0022407 regulation of cell-cell adhesion	31	100	0.0264	Down
GO:2000107 negative regulation of leukocyte apoptotic process	31	100	0.0274	Down
GO:1903037 regulation of leukocyte cell-cell adhesion	31	100	0.0327	Down
GO:0050792 regulation of viral process	31	100	0.0338	Down
GO:0050870 positive regulation of T cell activation	31	100	0.0348	Down
GO:0006816 calcium ion transport	31	100	0.0351	Down
GO:0046633 alpha-beta T cell proliferation	31	100	0.0371	Down
GO:1903039 positive regulation of leukocyte cell-cell adhesion	31	100	0.0388	Down
GO:0046640 regulation of alpha-beta T cell proliferation	31	100	0.0403	Down
GO:0043903 regulation of symbiosis, encompassing mutualism through parasitism	31	100	0.0406	Down
GO:0046641 positive regulation of alpha-beta T cell proliferation	31	100	0.0417	Down
GO:2001026 regulation of endothelial cell chemotaxis	31	100	0.0431	Down
GO:0042102 positive regulation of T cell proliferation	31	100	0.0432	Down
GO:0002250 adaptive immune response	31	100	0.0448	Down

Set	n	Percentage	*p-value*	Status
GO:0090022 regulation of neutrophil chemotaxis	31	100	0.0452	Down
GO:0022409 positive regulation of cell-cell adhesion	31	100	0.0456	Down
GO:2001028 positive regulation of endothelial cell chemotaxis	31	100	0.0469	Down
GO:0002253 activation of immune response	30	97	0.0000	Down
GO:0002429 immune response-activating cell surface receptor signaling pathway	30	97	0.0000	Down
GO:0002757 immune response-activating signal transduction	30	97	0.0000	Down
GO:0002768 immune response-regulating cell surface receptor signaling pathway	30	97	0.0000	Down
GO:0002764 immune response-regulating signaling pathway	30	97	0.0000	Down
GO:0002697 regulation of immune effector process	30	97	0.0000	Down
GO:0042110 T cell activation	30	97	0.0000	Down
GO:0051249 regulation of lymphocyte activation	30	97	0.0000	Down
GO:0060326 cell chemotaxis	30	97	0.0000	Down
GO:0050863 regulation of T cell activation	30	97	0.0000	Down
GO:0032103 positive regulation of response to external stimulus	30	97	0.0000	Down
GO:0002694 regulation of leukocyte activation	30	97	0.0000	Down
GO:0002460 adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	30	97	0.0001	Down
GO:0032943 mononuclear cell proliferation	30	97	0.0001	Down
GO:0002831 regulation of response to biotic stimulus	30	97	0.0001	Down
GO:0002683 negative regulation of immune system process	30	97	0.0001	Down
GO:0071216 cellular response to biotic stimulus	30	97	0.0001	Down
GO:0002696 positive regulation of leukocyte activation	30	97	0.0001	Down
GO:0009617 response to bacterium	30	97	0.0001	Down
GO:0046651 lymphocyte proliferation	30	97	0.0001	Down
GO:0050670 regulation of lymphocyte proliferation	30	97	0.0001	Down
GO:0050867 positive regulation of cell activation	30	97	0.0001	Down
GO:0032944 regulation of mononuclear cell proliferation	30	97	0.0001	Down
GO:0002521 leukocyte differentiation	30	97	0.0001	Down
GO:0030595 leukocyte chemotaxis	30	97	0.0001	Down
GO:0070663 regulation of leukocyte proliferation	30	97	0.0002	Down
GO:0045785 positive regulation of cell adhesion	30	97	0.0002	Down
GO:0032496 response to lipopolysaccharide	30	97	0.0002	Down
GO:0051251 positive regulation of lymphocyte activation	30	97	0.0002	Down
GO:0002237 response to molecule of bacterial origin	30	97	0.0002	Down
GO:0071219 cellular response to molecule of bacterial origin	30	97	0.0002	Down
GO:0002449 lymphocyte mediated immunity	30	97	0.0002	Down

Set	n	Percentage	*p-value*	Status
GO:0070661 leukocyte proliferation	30	97	0.0002	Down
GO:0071621 granulocyte chemotaxis	30	97	0.0002	Down
GO:0042129 regulation of T cell proliferation	30	97	0.0002	Down
GO:0042098 T cell proliferation	30	97	0.0003	Down
GO:0071222 cellular response to lipopolysaccharide	30	97	0.0003	Down
GO:0030449 regulation of complement activation	30	97	0.0004	Down
GO:0002920 regulation of humoral immune response	30	97	0.0005	Down
GO:0022408 negative regulation of cell-cell adhesion	30	97	0.0006	Down
GO:0140375 immune receptor activity	30	97	0.0008	Down
GO:0050777 negative regulation of immune response	30	97	0.0008	Down
GO:0031349 positive regulation of defense response	30	97	0.0009	Down
GO:0001819 positive regulation of cytokine production	30	97	0.0010	Down
GO:0006909 phagocytosis	30	97	0.0010	Down
GO:0019724 B cell mediated immunity	30	97	0.0011	Down
GO:1903038 negative regulation of leukocyte cell-cell adhesion	30	97	0.0011	Down
GO:0097530 granulocyte migration	30	97	0.0013	Down
GO:0097529 myeloid leukocyte migration	30	97	0.0013	Down
GO:1902107 positive regulation of leukocyte differentiation	30	97	0.0014	Down
GO:0050900 leukocyte migration	30	97	0.0014	Down
GO:0002698 negative regulation of immune effector process	30	97	0.0014	Down
GO:0002224 toll-like receptor signaling pathway	30	97	0.0017	Down
GO:1902105 regulation of leukocyte differentiation	30	97	0.0017	Down
GO:0002221 pattern recognition receptor signaling pathway	30	97	0.0017	Down
GO:0016064 immunoglobulin mediated immune response	30	97	0.0022	Down
GO:0006959 humoral immune response	30	97	0.0022	Down
GO:0030098 lymphocyte differentiation	30	97	0.0026	Down
GO:0046634 regulation of alpha-beta T cell activation	30	97	0.0028	Down
GO:0046631 alpha-beta T cell activation	30	97	0.0030	Down
GO:0050727 regulation of inflammatory response	30	97	0.0030	Down
GO:0050868 negative regulation of T cell activation	30	97	0.0033	Down
GO:0070374 positive regulation of ERK1 and ERK2 cascade	30	97	0.0033	Down
GO:0045088 regulation of innate immune response	30	97	0.0034	Down
GO:0002819 regulation of adaptive immune response	30	97	0.0035	Down
GO:0050921 positive regulation of chemotaxis	30	97	0.0036	Down
GO:0007162 negative regulation of cell adhesion	30	97	0.0036	Down
GO:0031341 regulation of cell killing	30	97	0.0037	Down
GO:0070372 regulation of ERK1 and ERK2 cascade	30	97	0.0038	Down
GO:0050671 positive regulation of lymphocyte proliferation	30	97	0.0040	Down

Set	n	Percentage	*p-value*	Status
GO:0032649 regulation of interferon-gamma production	30	97	0.0040	Down
GO:0002688 regulation of leukocyte chemotaxis	30	97	0.0045	Down
GO:0070665 positive regulation of leukocyte proliferation	30	97	0.0046	Down
GO:0050729 positive regulation of inflammatory response	30	97	0.0047	Down
GO:0032102 negative regulation of response to external stimulus	30	97	0.0047	Down
GO:0032946 positive regulation of mononuclear cell proliferation	30	97	0.0048	Down
GO:1903706 regulation of hemopoiesis	30	97	0.0049	Down
GO:0070371 ERK1 and ERK2 cascade	30	97	0.0051	Down
GO:0050730 regulation of peptidyl-tyrosine phosphorylation	30	97	0.0051	Down
GO:0002822 regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	30	97	0.0053	Down
GO:0002704 negative regulation of leukocyte mediated immunity	30	97	0.0054	Down
GO:0001910 regulation of leukocyte mediated cytotoxicity	30	97	0.0057	Down
GO:0150146 cell junction disassembly	30	97	0.0060	Down
GO:0046637 regulation of alpha-beta T cell differentiation	30	97	0.0061	Down
GO:0007249 I-kappaB kinase/NF-kappaB signaling	30	97	0.0064	Down
GO:0002699 positive regulation of immune effector process	30	97	0.0064	Down
GO:0050920 regulation of chemotaxis	30	97	0.0065	Down
GO:0050866 negative regulation of cell activation	30	97	0.0065	Down
GO:0050764 regulation of phagocytosis	30	97	0.0070	Down
GO:0006956 complement activation	30	97	0.0079	Down
GO:0010506 regulation of autophagy	30	97	0.0085	Down
GO:0018108 peptidyl-tyrosine phosphorylation	30	97	0.0085	Down
GO:0002755 MyD88-dependent toll-like receptor signaling pathway	30	97	0.0088	Down
GO:0032609 interferon-gamma production	30	97	0.0088	Down
GO:0002703 regulation of leukocyte mediated immunity	30	97	0.0088	Down
GO:0032729 positive regulation of interferon-gamma production	30	97	0.0089	Down
GO:0051250 negative regulation of lymphocyte activation	30	97	0.0089	Down
GO:0002455 humoral immune response mediated by circulating immunoglobulin	30	97	0.0091	Down
GO:0043542 endothelial cell migration	30	97	0.0092	Down
GO:0071706 tumor necrosis factor superfamily cytokine production	30	97	0.0093	Down
GO:0050663 cytokine secretion	30	97	0.0094	Down

Set	n	Percentage	*p-value*	Status
GO:1903555 regulation of tumor necrosis factor superfamily cytokine production	30	97	0.0097	Down
GO:0009615 response to virus	30	97	0.0099	Down
GO:0051767 nitric-oxide synthase biosynthetic process	30	97	0.0099	Down
GO:0051769 regulation of nitric-oxide synthase biosynthetic process	30	97	0.0099	Down
GO:0045582 positive regulation of T cell differentiation	30	97	0.0100	Down
GO:0042533 tumor necrosis factor biosynthetic process	30	97	0.0104	Down
GO:0042534 regulation of tumor necrosis factor biosynthetic process	30	97	0.0104	Down
GO:0030217 T cell differentiation	30	97	0.0104	Down
GO:0046635 positive regulation of alpha-beta T cell activation	30	97	0.0105	Down
GO:0002706 regulation of lymphocyte mediated immunity	30	97	0.0105	Down
GO:0001525 angiogenesis	30	97	0.0108	Down
GO:0032640 tumor necrosis factor production	30	97	0.0109	Down
GO:0032680 regulation of tumor necrosis factor production	30	97	0.0109	Down
GO:0002695 negative regulation of leukocyte activation	30	97	0.0109	Down
GO:0042107 cytokine metabolic process	30	97	0.0111	Down
GO:0018212 peptidyl-tyrosine modification	30	97	0.0111	Down
GO:0006958 complement activation, classical pathway	30	97	0.0112	Down
GO:0006874 cellular calcium ion homeostasis	30	97	0.0114	Down
GO:0002285 lymphocyte activation involved in immune response	30	97	0.0114	Down
GO:0043123 positive regulation of I-kappaB kinase/NF-kappaB signaling	30	97	0.0117	Down
GO:0035767 endothelial cell chemotaxis	30	97	0.0121	Down
GO:0051480 regulation of cytosolic calcium ion concentration	30	97	0.0122	Down
GO:0032092 positive regulation of protein binding	30	97	0.0123	Down
GO:0046632 alpha-beta T cell differentiation	30	97	0.0124	Down
GO:0051607 defense response to virus	30	97	0.0130	Down
GO:0071887 leukocyte apoptotic process	30	97	0.0132	Down
GO:0045621 positive regulation of lymphocyte differentiation	30	97	0.0136	Down
GO:0045619 regulation of lymphocyte differentiation	30	97	0.0139	Down
GO:0001818 negative regulation of cytokine production	30	97	0.0140	Down
GO:0042089 cytokine biosynthetic process	30	97	0.0140	Down
GO:0007204 positive regulation of cytosolic calcium ion concentration	30	97	0.0140	Down
GO:0055074 calcium ion homeostasis	30	97	0.0141	Down
GO:0001936 regulation of endothelial cell proliferation	30	97	0.0142	Down
GO:0072376 protein activation cascade	30	97	0.0152	Down
GO:0002286 T cell activation involved in immune response	30	97	0.0153	Down

Set	n	Percentage	*p-value*	Status
GO:0043122 regulation of I-kappaB kinase/NF-kappaB signaling	30	97	0.0153	Down
GO:0042035 regulation of cytokine biosynthetic process	30	97	0.0159	Down
GO:0009595 detection of biotic stimulus	30	97	0.0161	Down
GO:0098883 synapse pruning	30	97	0.0162	Down
GO:0002292 T cell differentiation involved in immune response	30	97	0.0169	Down
GO:0031348 negative regulation of defense response	30	97	0.0176	Down
GO:0070664 negative regulation of leukocyte proliferation	30	97	0.0182	Down
GO:0006914 autophagy	30	97	0.0182	Down
GO:0061919 process utilizing autophagic mechanism	30	97	0.0182	Down
GO:0002707 negative regulation of lymphocyte mediated immunity	30	97	0.0182	Down
GO:0031343 positive regulation of cell killing	30	97	0.0184	Down
GO:0002823 negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	30	97	0.0187	Down
GO:0030546 signaling receptor activator activity	30	97	0.0187	Down
GO:0043491 protein kinase B signaling	30	97	0.0195	Down
GO:0072503 cellular divalent inorganic cation homeostasis	30	97	0.0195	Down
GO:0097191 extrinsic apoptotic signaling pathway	30	97	0.0196	Down
GO:0002690 positive regulation of leukocyte chemotaxis	30	97	0.0202	Down
GO:0032606 type I interferon production	30	97	0.0203	Down
GO:0002820 negative regulation of adaptive immune response	30	97	0.0203	Down
GO:0009895 negative regulation of catabolic process	30	97	0.0204	Down
GO:1905897 regulation of response to endoplasmic reticulum stress	30	97	0.0207	Down
GO:0032615 interleukin-12 production	30	97	0.0207	Down
GO:0007033 vacuole organization	30	97	0.0208	Down
GO:0061097 regulation of protein tyrosine kinase activity	30	97	0.0212	Down
GO:0032655 regulation of interleukin-12 production	30	97	0.0214	Down
GO:0002291 T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	30	97	0.0215	Down
GO:0032479 regulation of type I interferon production	30	97	0.0217	Down
GO:0045730 respiratory burst	30	97	0.0221	Down
GO:0002431 Fc receptor mediated stimulatory signaling pathway	30	97	0.0223	Down
GO:0072507 divalent inorganic cation homeostasis	30	97	0.0236	Down
GO:0071622 regulation of granulocyte chemotaxis	30	97	0.0246	Down
GO:0001916 positive regulation of T cell mediated cytotoxicity	30	97	0.0247	Down

Set	n	Percentage	*p-value*	Status
GO:0070228 regulation of lymphocyte apoptotic process	30	97	0.0248	Down
GO:0019722 calcium-mediated signaling	30	97	0.0254	Down
GO:0051924 regulation of calcium ion transport	30	97	0.0254	Down
GO:0050688 regulation of defense response to virus	30	97	0.0261	Down
GO:0072148 epithelial cell fate commitment	30	97	0.0263	Down
GO:0051092 positive regulation of NF-kappaB transcription factor activity	30	97	0.0264	Down
GO:0045580 regulation of T cell differentiation	30	97	0.0270	Down
GO:0043370 regulation of CD4-positive, alpha-beta T cell differentiation	30	97	0.0272	Down
GO:2000146 negative regulation of cell motility	30	97	0.0273	Down
GO:2000516 positive regulation of CD4-positive, alpha-beta T cell activation	30	97	0.0274	Down
GO:0001914 regulation of T cell mediated cytotoxicity	30	97	0.0278	Down
GO:0051770 positive regulation of nitric-oxide synthase biosynthetic process	30	97	0.0282	Down
GO:0032945 negative regulation of mononuclear cell proliferation	30	97	0.0289	Down
GO:0050672 negative regulation of lymphocyte proliferation	30	97	0.0289	Down
GO:0002833 positive regulation of response to biotic stimulus	30	97	0.0292	Down
GO:0070997 neuron death	30	97	0.0292	Down
GO:0031330 negative regulation of cellular catabolic process	30	97	0.0297	Down
GO:0051271 negative regulation of cellular component movement	30	97	0.0301	Down
GO:0046677 response to antibiotic	30	97	0.0303	Down
GO:0002483 antigen processing and presentation of endogenous peptide antigen	30	97	0.0315	Down
GO:0019885 antigen processing and presentation of endogenous peptide antigen via MHC class I	30	97	0.0315	Down
GO:0046638 positive regulation of alpha-beta T cell differentiation	30	97	0.0316	Down
GO:0071624 positive regulation of granulocyte chemotaxis	30	97	0.0317	Down
GO:0002475 antigen processing and presentation via MHC class Ib	30	97	0.0320	Down
GO:1901214 regulation of neuron death	30	97	0.0320	Down
GO:0043524 negative regulation of neuron apoptotic process	30	97	0.0321	Down
GO:0090023 positive regulation of neutrophil chemotaxis	30	97	0.0330	Down
GO:0043410 positive regulation of MAPK cascade	30	97	0.0330	Down
GO:0071674 mononuclear cell migration	30	97	0.0336	Down
GO:2001233 regulation of apoptotic signaling pathway	30	97	0.0338	Down
GO:0033619 membrane protein proteolysis	30	97	0.0338	Down
GO:0042113 B cell activation	30	97	0.0342	Down

Set	n	Percentage	*p-value*	Status
GO:0050731 positive regulation of peptidyl-tyrosine phosphorylation	30	97	0.0345	Down
GO:0001935 endothelial cell proliferation	30	97	0.0346	Down
GO:1903573 negative regulation of response to endoplasmic reticulum stress	30	97	0.0346	Down
GO:0019883 antigen processing and presentation of endogenous antigen	30	97	0.0351	Down
GO:0001912 positive regulation of leukocyte mediated cytotoxicity	30	97	0.0353	Down
GO:0032720 negative regulation of tumor necrosis factor production	30	97	0.0354	Down
GO:0030336 negative regulation of cell migration	30	97	0.0357	Down
GO:0043393 regulation of protein binding	30	97	0.0374	Down
GO:2000514 regulation of CD4-positive, alpha-beta T cell activation	30	97	0.0386	Down
GO:0006509 membrane protein ectodomain proteolysis	30	97	0.0391	Down
GO:0040013 negative regulation of locomotion	30	97	0.0399	Down
GO:1903557 positive regulation of tumor necrosis factor superfamily cytokine production	30	97	0.0402	Down
GO:2001236 regulation of extrinsic apoptotic signaling pathway	30	97	0.0403	Down
GO:0002756 MyD88-independent toll-like receptor signaling pathway	30	97	0.0404	Down
GO:0030335 positive regulation of cell migration	30	97	0.0405	Down
GO:0045765 regulation of angiogenesis	30	97	0.0417	Down
GO:0030168 platelet activation	30	97	0.0420	Down
GO:0002040 sprouting angiogenesis	30	97	0.0421	Down
GO:0001938 positive regulation of endothelial cell proliferation	30	97	0.0422	Down
GO:0070838 divalent metal ion transport	30	97	0.0429	Down
GO:0002548 monocyte chemotaxis	30	97	0.0440	Down
GO:0042119 neutrophil activation	30	97	0.0443	Down
GO:0002861 regulation of inflammatory response to antigenic stimulus	30	97	0.0443	Down
GO:0032760 positive regulation of tumor necrosis factor production	30	97	0.0444	Down
GO:0097028 dendritic cell differentiation	30	97	0.0446	Down
GO:0097479 synaptic vesicle localization	30	97	0.0453	Down
GO:0007265 Ras protein signal transduction	30	97	0.0455	Down
GO:0051896 regulation of protein kinase B signaling	30	97	0.0456	Down
GO:0002921 negative regulation of humoral immune response	30	97	0.0461	Down
GO:0038094 Fc-gamma receptor signaling pathway	30	97	0.0465	Down
GO:0034113 heterotypic cell-cell adhesion	30	97	0.0471	Down
GO:0042176 regulation of protein catabolic process	30	97	0.0473	Down
GO:0045779 negative regulation of bone resorption	30	97	0.0477	Down
GO:0019932 second-messenger-mediated signaling	30	97	0.0479	Down

Set	n	Percentage	*p-value*	Status
GO:0002474 antigen processing and presentation of peptide antigen via MHC class I	30	97	0.0479	Down
GO:0050819 negative regulation of coagulation	30	97	0.0488	Down
GO:0045089 positive regulation of innate immune response	30	97	0.0492	Down
GO:0036230 granulocyte activation	30	97	0.0493	Down
GO:0046466 membrane lipid catabolic process	30	97	0.0494	Down
GO:0030641 regulation of cellular pH	30	97	0.0498	Down
GO:0032695 negative regulation of interleukin-12 production	30	97	0.0498	Down
GO:0033673 negative regulation of kinase activity	29	94	0.0053	Down
GO:0042326 negative regulation of phosphorylation	29	94	0.0081	Down
GO:0040017 positive regulation of locomotion	29	94	0.0084	Down
GO:0006469 negative regulation of protein kinase activity	29	94	0.0087	Down
GO:0051272 positive regulation of cellular component movement	29	94	0.0096	Down
GO:0002446 neutrophil mediated immunity	29	94	0.0107	Down
GO:2000147 positive regulation of cell motility	29	94	0.0109	Down
GO:0001933 negative regulation of protein phosphorylation	29	94	0.0110	Down
GO:0002283 neutrophil activation involved in immune response	29	94	0.0114	Down
GO:0050673 epithelial cell proliferation	29	94	0.0116	Down
GO:0019079 viral genome replication	29	94	0.0121	Down
GO:0002577 regulation of antigen processing and presentation	29	94	0.0132	Down
GO:0043312 neutrophil degranulation	29	94	0.0143	Down
GO:0010594 regulation of endothelial cell migration	29	94	0.0151	Down
GO:0048662 negative regulation of smooth muscle cell proliferation	29	94	0.0155	Down
GO:1903708 positive regulation of hemopoiesis	29	94	0.0165	Down
GO:0002287 alpha-beta T cell activation involved in immune response	29	94	0.0168	Down
GO:0002293 alpha-beta T cell differentiation involved in immune response	29	94	0.0168	Down
GO:0050678 regulation of epithelial cell proliferation	29	94	0.0170	Down
GO:0051348 negative regulation of transferase activity	29	94	0.0175	Down
GO:0002294 CD4-positive, alpha-beta T cell differentiation involved in immune response	29	94	0.0176	Down
GO:0043367 CD4-positive, alpha-beta T cell differentiation	29	94	0.0179	Down
GO:0031331 positive regulation of cellular catabolic process	29	94	0.0183	Down
GO:0071496 cellular response to external stimulus	29	94	0.0203	Down
GO:0031663 lipopolysaccharide-mediated signaling pathway	29	94	0.0208	Down
GO:0042130 negative regulation of T cell proliferation	29	94	0.0213	Down

Set	n	Percentage	*p-value*	Status
GO:0035924 cellular response to vascular endothelial growth factor stimulus	29	94	0.0214	Down
GO:1902622 regulation of neutrophil migration	29	94	0.0215	Down
GO:0010632 regulation of epithelial cell migration	29	94	0.0221	Down
GO:0001911 negative regulation of leukocyte mediated cytotoxicity	29	94	0.0221	Down
GO:0009896 positive regulation of catabolic process	29	94	0.0228	Down
GO:0043301 negative regulation of leukocyte degranulation	29	94	0.0233	Down
GO:1904706 negative regulation of vascular smooth muscle cell proliferation	29	94	0.0240	Down
GO:0002832 negative regulation of response to biotic stimulus	29	94	0.0242	Down
GO:0045351 type I interferon biosynthetic process	29	94	0.0248	Down
GO:0042093 T-helper cell differentiation	29	94	0.0276	Down
GO:0045078 positive regulation of interferon-gamma biosynthetic process	29	94	0.0284	Down
GO:2000108 positive regulation of leukocyte apoptotic process	29	94	0.0284	Down
GO:0002821 positive regulation of adaptive immune response	29	94	0.0299	Down
GO:1901342 regulation of vasculature development	29	94	0.0300	Down
GO:0002824 positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	29	94	0.0301	Down
GO:0002710 negative regulation of T cell mediated immunity	29	94	0.0315	Down
GO:0002708 positive regulation of lymphocyte mediated immunity	29	94	0.0326	Down
GO:0010508 positive regulation of autophagy	29	94	0.0352	Down
GO:0002763 positive regulation of myeloid leukocyte differentiation	29	94	0.0354	Down
GO:0060401 cytosolic calcium ion transport	29	94	0.0360	Down
GO:0098581 detection of external biotic stimulus	29	94	0.0364	Down
GO:1902235 regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	29	94	0.0365	Down
GO:1902236 negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	29	94	0.0372	Down
GO:0046636 negative regulation of alpha-beta T cell activation	29	94	0.0383	Down
GO:0045591 positive regulation of regulatory T cell differentiation	29	94	0.0383	Down
GO:0043372 positive regulation of CD4-positive, alpha-beta T cell differentiation	29	94	0.0389	Down
GO:1902106 negative regulation of leukocyte differentiation	29	94	0.0391	Down
GO:0060759 regulation of response to cytokine stimulus	29	94	0.0394	Down

Set	n	Percentage	*p-value*	Status
GO:0002456 T cell mediated immunity	29	94	0.0397	Down
GO:0001906 cell killing	29	94	0.0397	Down
GO:0030183 B cell differentiation	29	94	0.0397	Down
GO:0045058 T cell selection	29	94	0.0398	Down
GO:0035729 cellular response to hepatocyte growth factor stimulus	29	94	0.0400	Down
GO:0019058 viral life cycle	29	94	0.0412	Down
GO:0072511 divalent inorganic cation transport	29	94	0.0416	Down
GO:0003158 endothelium development	29	94	0.0418	Down
GO:0030195 negative regulation of blood coagulation	29	94	0.0419	Down
GO:0001909 leukocyte mediated cytotoxicity	29	94	0.0419	Down
GO:0051208 sequestering of calcium ion	29	94	0.0421	Down
GO:0002433 immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	29	94	0.0422	Down
GO:0038096 Fc-gamma receptor signaling pathway involved in phagocytosis	29	94	0.0422	Down
GO:0055067 monovalent inorganic cation homeostasis	29	94	0.0423	Down
GO:0061081 positive regulation of myeloid leukocyte cytokine production involved in immune response	29	94	0.0425	Down
GO:0042177 negative regulation of protein catabolic process	29	94	0.0429	Down
GO:0072539 T-helper 17 cell differentiation	29	94	0.0431	Down
GO:0002281 macrophage activation involved in immune response	29	94	0.0435	Down
GO:0002467 germinal center formation	29	94	0.0441	Down
GO:0070482 response to oxygen levels	29	94	0.0441	Down
GO:0050858 negative regulation of antigen receptor-mediated signaling pathway	29	94	0.0442	Down
GO:1904894 positive regulation of receptor signaling pathway via STAT	29	94	0.0442	Down
GO:0032703 negative regulation of interleukin-2 production	29	94	0.0448	Down
GO:0002685 regulation of leukocyte migration	29	94	0.0449	Down
GO:1900047 negative regulation of hemostasis	29	94	0.0450	Down
GO:0060337 type I interferon signaling pathway	29	94	0.0450	Down
GO:0071357 cellular response to type I interferon	29	94	0.0450	Down
GO:0050860 negative regulation of T cell receptor signaling pathway	29	94	0.0453	Down
GO:0010039 response to iron ion	29	94	0.0454	Down
GO:0010952 positive regulation of peptidase activity	29	94	0.0458	Down
GO:0002718 regulation of cytokine production involved in immune response	29	94	0.0459	Down
GO:0052548 regulation of endopeptidase activity	29	94	0.0460	Down
GO:0031342 negative regulation of cell killing	29	94	0.0467	Down
GO:0034340 response to type I interferon	29	94	0.0473	Down
GO:0010882 regulation of cardiac muscle contraction by calcium ion signaling	29	94	0.0476	Down
GO:0045342 MHC class II biosynthetic process	29	94	0.0480	Down

Set	n	Percentage	*p-value*	Status
GO:0060402 calcium ion transport into cytosol	29	94	0.0482	Down
GO:0002709 regulation of T cell mediated immunity	29	94	0.0492	Down
GO:1903556 negative regulation of tumor necrosis factor superfamily cytokine production	29	94	0.0493	Down
GO:0060627 regulation of vesicle-mediated transport	29	94	0.0493	Down
GO:0051282 regulation of sequestering of calcium ion	29	94	0.0493	Down
GO:1904892 regulation of receptor signaling pathway via STAT	29	94	0.0496	Down
GO:1905037 autophagosome organization	29	94	0.0498	Down
GO:0051051 negative regulation of transport	28	90	0.0035	Down
GO:0002791 regulation of peptide secretion	28	90	0.0062	Down
GO:0032623 interleukin-2 production	28	90	0.0062	Down
GO:0050707 regulation of cytokine secretion	28	90	0.0064	Down
GO:0050766 positive regulation of phagocytosis	28	90	0.0095	Down
GO:0050708 regulation of protein secretion	28	90	0.0100	Down
GO:0002544 chronic inflammatory response	28	90	0.0124	Down
GO:0008360 regulation of cell shape	28	90	0.0142	Down
GO:0002711 positive regulation of T cell mediated immunity	28	90	0.0163	Down
GO:0090066 regulation of anatomical structure size	28	90	0.0171	Down
GO:0002026 regulation of the force of heart contraction	28	90	0.0175	Down
GO:0042108 positive regulation of cytokine biosynthetic process	28	90	0.0184	Down
GO:0032663 regulation of interleukin-2 production	28	90	0.0186	Down
GO:0045744 negative regulation of G protein-coupled receptor signaling pathway	28	90	0.0215	Down
GO:0010522 regulation of calcium ion transport into cytosol	28	90	0.0229	Down
GO:0046850 regulation of bone remodeling	28	90	0.0232	Down
GO:0070099 regulation of chemokine-mediated signaling pathway	28	90	0.0233	Down
GO:0051897 positive regulation of protein kinase B signaling	28	90	0.0245	Down
GO:0000045 autophagosome assembly	28	90	0.0249	Down
GO:0016236 macroautophagy	28	90	0.0252	Down
GO:0050856 regulation of T cell receptor signaling pathway	28	90	0.0268	Down
GO:0035710 CD4-positive, alpha-beta T cell activation	28	90	0.0269	Down
GO:1904646 cellular response to amyloid-beta	28	90	0.0269	Down
GO:0032722 positive regulation of chemokine production	28	90	0.0275	Down
GO:0051580 regulation of neurotransmitter uptake	28	90	0.0279	Down
GO:0051283 negative regulation of sequestering of calcium ion	28	90	0.0287	Down
GO:2001024 negative regulation of response to drug	28	90	0.0288	Down
GO:0042542 response to hydrogen peroxide	28	90	0.0289	Down
GO:0030004 cellular monovalent inorganic cation homeostasis	28	90	0.0291	Down

Set	n	Percentage	*p-value*	Status
GO:0014909 smooth muscle cell migration	28	90	0.0293	Down
GO:0002705 positive regulation of leukocyte mediated immunity	28	90	0.0301	Down
GO:0001773 myeloid dendritic cell activation	28	90	0.0306	Down
GO:0001776 leukocyte homeostasis	28	90	0.0306	Down
GO:0051209 release of sequestered calcium ion into cytosol	28	90	0.0308	Down
GO:0045862 positive regulation of proteolysis	28	90	0.0309	Down
GO:0046629 gamma-delta T cell activation	28	90	0.0311	Down
GO:0050854 regulation of antigen receptor-mediated signaling pathway	28	90	0.0312	Down
GO:0010631 epithelial cell migration	28	90	0.0317	Down
GO:0045953 negative regulation of natural killer cell mediated cytotoxicity	28	90	0.0324	Down
GO:0032970 regulation of actin filament-based process	28	90	0.0325	Down
GO:0051817 modulation of process of other organism involved in symbiotic interaction	28	90	0.0325	Down
GO:2001185 regulation of CD8-positive, alpha-beta T cell activation	28	90	0.0338	Down
GO:0002573 myeloid leukocyte differentiation	28	90	0.0345	Down
GO:0002761 regulation of myeloid leukocyte differentiation	28	90	0.0347	Down
GO:1904950 negative regulation of establishment of protein localization	28	90	0.0351	Down
GO:0016241 regulation of macroautophagy	28	90	0.0352	Down
GO:0036037 CD8-positive, alpha-beta T cell activation	28	90	0.0353	Down
GO:0090130 tissue migration	28	90	0.0354	Down
GO:0051224 negative regulation of protein transport	28	90	0.0358	Down
GO:0042100 B cell proliferation	28	90	0.0359	Down
GO:0002228 natural killer cell mediated immunity	28	90	0.0361	Down
GO:0006885 regulation of pH	28	90	0.0365	Down
GO:0032648 regulation of interferon-beta production	28	90	0.0370	Down
GO:0090025 regulation of monocyte chemotaxis	28	90	0.0373	Down
GO:0090132 epithelium migration	28	90	0.0377	Down
GO:0042060 wound healing	28	90	0.0385	Down
GO:0030888 regulation of B cell proliferation	28	90	0.0385	Down
GO:0032608 interferon-beta production	28	90	0.0388	Down
GO:0042095 interferon-gamma biosynthetic process	28	90	0.0395	Down
GO:0032956 regulation of actin cytoskeleton organization	28	90	0.0405	Down
GO:0031668 cellular response to extracellular stimulus	28	90	0.0406	Down
GO:1901136 carbohydrate derivative catabolic process	28	90	0.0413	Down
GO:2000406 positive regulation of T cell migration	28	90	0.0413	Down
GO:0002701 negative regulation of production of molecular mediator of immune response	28	90	0.0414	Down
GO:0002700 regulation of production of molecular mediator of immune response	28	90	0.0415	Down

Set	n	Percentage	*p-value*	Status
GO:0045072 regulation of interferon-gamma biosynthetic process	28	90	0.0415	Down
GO:0045124 regulation of bone resorption	28	90	0.0418	Down
GO:0010507 negative regulation of autophagy	28	90	0.0420	Down
GO:0051259 protein complex oligomerization	28	90	0.0425	Down
GO:0051056 regulation of small GTPase mediated signal transduction	28	90	0.0431	Down
GO:0001504 neurotransmitter uptake	28	90	0.0440	Down
GO:0002686 negative regulation of leukocyte migration	28	90	0.0442	Down
GO:0009991 response to extracellular stimulus	28	90	0.0442	Down
GO:0051608 histamine transport	28	90	0.0442	Down
GO:0048489 synaptic vesicle transport	28	90	0.0444	Down
GO:0001959 regulation of cytokine-mediated signaling pathway	28	90	0.0446	Down
GO:0010881 regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	28	90	0.0450	Down
GO:0010633 negative regulation of epithelial cell migration	28	90	0.0450	Down
GO:0045824 negative regulation of innate immune response	28	90	0.0451	Down
GO:0034103 regulation of tissue remodeling	28	90	0.0456	Down
GO:0050857 positive regulation of antigen receptor-mediated signaling pathway	28	90	0.0456	Down
GO:0046427 positive regulation of receptor signaling pathway via JAK-STAT	28	90	0.0461	Down
GO:0032635 interleukin-6 production	28	90	0.0462	Down
GO:0034762 regulation of transmembrane transport	28	90	0.0467	Down
GO:2001238 positive regulation of extrinsic apoptotic signaling pathway	28	90	0.0472	Down
GO:0002715 regulation of natural killer cell mediated immunity	28	90	0.0472	Down
GO:0051043 regulation of membrane protein ectodomain proteolysis	28	90	0.0473	Down
GO:1900120 regulation of receptor binding	28	90	0.0476	Down
GO:0002863 positive regulation of inflammatory response to antigenic stimulus	28	90	0.0478	Down
GO:0060368 regulation of Fc receptor mediated stimulatory signaling pathway	28	90	0.0480	Down
GO:1903707 negative regulation of hemopoiesis	28	90	0.0483	Down
GO:0050864 regulation of B cell activation	28	90	0.0489	Down
GO:0019216 regulation of lipid metabolic process	28	90	0.0491	Down
GO:0046514 ceramide catabolic process	28	90	0.0494	Down
GO:0045453 bone resorption	28	90	0.0497	Down
GO:0051235 maintenance of location	28	90	0.0497	Down
GO:1902624 positive regulation of neutrophil migration	28	90	0.0498	Down

Annex XVIII The remaining 11 identified CpG sites whose DNA methylation were able to predict survival in patients with AML-M5 categorized in the intermediate prognostic risk group.

CpG sites	*p-value*	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (*p-value*)	gene	HR
cg03253268	0.0246	0.5579	8	8	0.4939	*CRYAA*	0.2543
cg18963509	0.0079	0.2779	7	9	0.5958	*WNK4*	0.1803
cg04556646	0.0079	0.4005	7	9	0.5958	*PHF21B*	0.1803
cg10626063	0.0079	0.415	7	9	0.5958	*SPRED3*	0.1803
cg00226822	0.0064	0.7251	9	6	0.9059	*SPON2*	0.1685
cg00678286	0.0057	0.7741	7	9	0.3961	*SHH*	0.1427
cg17683110	0.0038	0.3917	7	9	0.9155	*CBLN1*	0.1262
cg17534999	0.0012	0.3199	9	7	0.6331	*KIRREL3-AS3*	0.0997
cg23248910	0.0003	0.2599	9	6	0.5952	*FGFR2*	0.0793
cg16985667	0.0002	0.5046	9	7	0.4577	*KRTAP4-5*	0.0744
cg00754947	0.0008	0.7827	9	6	0.5546	*GRB10*	

Annex XIX Additional information about the 26 candidate biomarkers of prognostic of DNA methylation in patients with AML-M5 categorized in the intermediate prognostic risk group.

CpG sites	location	status	ratio	foldchange	*p-value*	gene	bibliographic
cg22212237	Promoter (<=1kb)	low	0.78	-0.23	0.000175	C1QL4	non-leukemia cancer types
cg20183094	Distal Intergenic	low	0.78	-0.22	0.000175	FEZF1	non-leukemia cancer types
cg08004278	Distal Intergenic	low	0.78	-0.20	0.000175	FEZF1	non-leukemia cancer types
cg05422647	Promoter (<=1kb)	low	0.78	-0.30	0.000175	GLRA1	non-AML leukemia types
cg17652792	Promoter (1-2kb)	low	1.29	-0.32	0.000175	PCDHB16	cited in PubMed
cg27462975	1st Intron	low	0.75	-0.24	0.000002	MIR573	non-leukemia cancer types
cg16759787	Distal Intergenic	low	1.14	-0.22	0.002402	RN7SK	non-leukemia cancer types
cg20362634	Promoter (<=1kb)	low	1.00	-0.23	0.001561	GABRG3	non-leukemia cancer types
cg03154226	Promoter (<=1kb)	low	1.29	-0.28	0.001024	OR5D14	never cited
cg11155432	Promoter (<=1kb)	low	1.29	-0.36	0.000175	CDH9	non-AML leukemia types
cg02171545	Other Intron	low	1.00	-0.37	0.000005	SNRPN	cited in AML
cg12436427	Distal Intergenic	low	1.00	-0.26	0.000155	WASHC2A	non-leukemia cancer types
cg18232125	Distal Intergenic	low	1.00	-0.22	0.000005	TENM2	non-leukemia cancer types
cg16368763	Promoter (2-3kb)	low	1.00	-0.21	0.000155	TRIM67	non-leukemia cancer types
cg26577836	Other Exon	high	1.00	-0.26	0.000032	TNXB	non-AML leukemia types
cg03253268	3' UTR	high	1.00	-0.28	0.000180	CRYAA	non-leukemia cancer types
cg18963509	Promoter (<=1kb)	high	0.78	-0.32	0.000000	WNK4	non-leukemia cancer types
cg04556646	Other Intron	high	0.78	-0.24	0.000157	PHF21B	non-leukemia cancer types
cg10626063	Promoter (<=1kb)	high	0.78	-0.39	0.000001	SPRED3	non-AML leukemia types

CpG sites	location	status	ratio	foldchange	*p-value*	gene	bibliographic
cg00226822	Distal Intergenic	high	1.50	-0.23	0.000167	SPON2	non-leukemia cancer types
cg00678286	Distal Intergenic	high	0.78	-0.28	0.000062	SHH	cited in AML
cg17683110	3' UTR	high	0.78	-0.38	0.000004	CBLN1	non-leukemia cancer types
cg17534999	Promoter (<=1kb)	high	1.29	-0.47	0.000017	KIRREL3-AS3	never cited
cg23248910	Other Intron	high	1.50	-0.21	0.000328	FGFR2	cited in AML
cg16985667	Promoter (<=1kb)	high	1.29	-0.31	0.000060	KRTAP4-5	non-leukemia cancer types
cg00754947	Promoter (<=1kb)	high	1.50	-0.21	0.000400	GRB10	cited in AML

Annex XX The remaining 161 identified genes whose gene expression were able to predict survival in patients with AML-M0-M1-M2-M4-M5 categorized in the intermediate prognostic risk group.

Gene	*p-value*	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (p-value)	HR
ANKEF1	0.001390	4.8568	53	33	0.876429	2.362363
NUDT5	0.000672	9.3438	34	55	0.120063	2.358147
REG4	0.001280	0	37	45	0.450132	2.357510
STK36	0.002397	8.7146	52	37	0.729602	2.220113
FOSL1	0.004470	7.2812	54	33	0.117200	2.211166
VPS33B	0.003160	8.3169	45	41	0.771955	2.207318
CEP89	0.003266	8.197	43	40	0.192296	2.183572
HAT1	0.002047	10.0544	38	51	0.718098	2.173449
ADK	0.002409	9.0034	39	49	0.791215	2.155982
COQ9	0.003112	9.0163	48	41	0.686555	2.131691
CSTB	0.003323	9.2987	39	49	0.070122	2.110184
GRHPR	0.006471	9.8666	37	51	0.869006	2.041174
MSMO1	0.006604	8.0439	45	42	0.203891	2.040044
AKIRIN2	0.007132	9.8579	41	44	0.083812	2.014150
SV2B	0.006619	5.745	43	46	0.856587	2.007315
SLC25A20	0.014782	9.4048	38	47	0.950635	1.919283
CINP	0.018024	8.1852	49	36	0.418055	1.898255
OCEL1	0.011821	7.0327	37	52	0.090876	1.896656
SNHG12	0.015181	8.9941	36	53	0.893543	1.862744
BCKDK	0.016351	9.8328	44	44	0.422795	1.841478
TOM1L1	0.017523	4.495	41	48	0.911475	1.839332
EBP	0.016520	8.363	39	48	0.144217	1.830974
NIT2	0.023562	8.8788	37	52	0.799468	1.796533
ARSD	0.028910	10.9881	36	50	0.551457	1.757749
LGI4	0.036721	2.8438	39	49	0.467244	0.578419
TSPAN33	0.034443	8.9687	37	49	0.077922	0.563952
PAWR	0.024020	2.1513	54	35	0.131440	0.561843
FCRL5	0.025023	7.2617	43	45	0.811857	0.557015
SH3RF1	0.022748	8.2421	48	38	0.137944	0.555232
PDZK1	0.025034	5.454	37	49	0.283068	0.551345
ZNF780B	0.018246	9.802	47	40	0.935479	0.548784
CNGA1	0.019576	2.3872	39	50	0.120843	0.545904
BCAR1	0.019114	1.9529	44	45	0.462443	0.544904
TRPC6	0.017186	0.9267	47	41	0.210863	0.543437
CACNA2D2	0.021770	4.7146	40	44	0.114746	0.542884
CEP68	0.015740	10.202	46	43	0.322246	0.541268
CCDC80	0.018401	4.033	38	51	0.666074	0.536875
PCDHGA9	0.013626	4.033	49	39	0.340144	0.530868
GLI3	0.016843	2.3489	39	46	0.821974	0.530679
LRRC2	0.014749	2.45	40	49	0.785374	0.529968

Gene	*p-value*	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (p-value)	HR
PLS3	0.010931	1.3466	52	36	0.598570	0.523826
MMRN2	0.010891	3.4267	43	46	0.500570	0.518965
FABP4	0.010925	2.4814	51	38	0.374551	0.515706
MCM9	0.010791	7.6216	47	38	0.922500	0.512015
FSTL1	0.008895	5.6949	55	34	0.839321	0.511612
WASL	0.009565	8.0565	49	35	0.342797	0.511566
BCAR3	0.008463	3.9799	53	36	0.424435	0.511229
MAMLD1	0.008158	4.3333	49	39	0.759030	0.510747
AGTPBP1	0.007057	10.8552	48	41	0.245565	0.504994
SULF1	0.007655	1.0169	48	41	0.704816	0.504636
NDEL1	0.007437	9.965	51	35	0.365004	0.503668
PLOD2	0.007422	1.3466	47	40	0.262499	0.501543
IGF2	0.007361	4.7413	46	43	0.289292	0.500307
AMOTL2	0.007099	3.1751	40	48	0.211558	0.497699
CCNJL	0.010409	2.8988	39	49	0.297353	0.497426
FAM171A1	0.006217	3.3341	48	37	0.814186	0.495873
ASIC4	0.007248	1.3487	39	49	0.239362	0.492441
S1PR2	0.006926	5.3641	40	48	0.483887	0.491915
CHRDL1	0.005739	2.8984	55	34	0.480534	0.491614
C12orf42	0.008432	2.4949	34	55	0.813001	0.489551
SORBS2	0.008179	0.851	39	47	0.804624	0.488332
VASH2	0.005631	4.8264	45	41	0.126784	0.487264
SHROOM3	0.006873	0.8251	39	49	0.480219	0.487250
ARHGAP35	0.006434	11.0511	39	44	0.967230	0.486807
FBXL7	0.004866	0	51	38	0.061867	0.482030
LDB2	0.003866	1.4717	50	39	0.943936	0.475076
GPX8	0.004278	1.6265	41	48	0.221346	0.474546
ADGRL1	0.004600	8.0903	40	49	0.177263	0.474134
WNT10A	0.005196	3.6729	38	51	0.730543	0.473652
CCBE1	0.003686	0.7979	45	44	0.519241	0.470515
CLDN5	0.003837	2.858	54	33	0.277781	0.469349
CALHM5	0.003083	0.9816	48	41	0.996715	0.469045
COL3A1	0.003120	2.9791	53	36	0.454118	0.468462
PODN	0.003022	1.737	49	40	0.704242	0.468360
GFRA1	0.004116	2.7741	37	52	0.404900	0.468204
TMEM56	0.003304	5.7681	47	42	0.201018	0.468057
CHSY3	0.003186	1.3487	49	39	0.444417	0.467786
LAMA4	0.003299	2.4828	46	43	0.342732	0.467676
POU2AF1	0.003196	7.4274	40	49	1.000000	0.462405
OLFM1	0.002104	0.9147	48	41	0.515307	0.461345
FAT4	0.002990	2.2909	52	36	0.779315	0.460730
NR2F1	0.002840	1.6664	40	49	0.324066	0.460592
CYGB	0.003731	3.2639	36	53	0.220459	0.458382

Gene	*p-value*	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (p-value)	HR
NMT2	0.002845	6.8006	40	49	0.134193	0.457015
TMEM132C	0.002206	1.3215	49	40	0.549651	0.456510
CHI3L2	0.006666	4.0398	33	54	0.360421	0.455723
C1orf21	0.001981	7.2828	47	42	0.905092	0.454781
DNAH9	0.001776	1.4278	51	38	0.923968	0.454584
NNMT	0.002010	2.8476	47	42	0.711361	0.454353
CYP46A1	0.002841	2.4644	45	38	0.247340	0.452669
BICC1	0.002627	1.7305	39	50	0.582199	0.452081
GEM	0.002091	1.946	39	50	0.967004	0.451753
TRH	0.002430	3.734	39	50	0.108489	0.450317
PCDH18	0.001924	2.9349	47	42	0.350667	0.450202
NFIB	0.002116	2.4398	49	40	0.077401	0.449754
SEMA6D	0.001777	1.6074	49	40	0.566288	0.449015
DCN	0.001507	3.145	51	38	0.227244	0.445507
APOD	0.002052	1.7462	45	41	0.893331	0.443363
LBR	0.002264	11.9283	39	46	0.575251	0.441290
EPAS1	0.001206	5.448	53	36	0.867152	0.440068
HSDL1	0.003211	8.7792	33	54	0.179104	0.437358
CXCL12	0.002077	9.5168	36	53	0.163745	0.436020
KDR	0.001451	2.8606	38	51	0.514748	0.435587
TMEM98	0.001382	0.9292	53	33	0.584779	0.434228
ADGRL4	0.001334	0.9398	51	38	0.525516	0.433533
FAM149A	0.001805	0.8465	40	49	0.695074	0.431690
SERAC1	0.001217	7.6025	51	35	0.509483	0.431687
AREL1	0.001634	10.5254	44	41	0.062718	0.430625
NTRK3	0.001016	0.6182	49	37	0.260252	0.428857
FBLN1	0.000939	2.3717	51	38	0.490944	0.427447
ALPL	0.001108	3.8456	52	37	0.190990	0.427015
MYT1	0.001094	1.4603	45	42	0.065769	0.426163
ATCAY	0.001618	1.6664	37	51	0.902398	0.426157
LTBP3	0.001187	9.7186	40	49	0.766407	0.425201
ST8SIA1	0.001641	3.7066	35	53	0.867891	0.423654
COL1A2	0.000669	3.0182	55	34	0.483166	0.418205
CPZ	0.001031	1.0888	39	48	0.068927	0.416727
CD160	0.000550	7.309	44	44	0.376114	0.414097
EFEMP1	0.000712	0.7768	49	38	0.169356	0.409557
CDH11	0.000486	3.601	45	44	0.125710	0.406818
LTBP2	0.000381	5.3125	53	35	0.391288	0.405443
VGLL3	0.000493	2.7043	48	40	0.205488	0.405306
FCHSD2	0.001518	11.0163	32	52	0.054091	0.405260
MXRA5	0.000383	2.3266	52	37	0.305613	0.402889
CTHRC1	0.000906	3.8462	39	42	0.639662	0.401971
CDH5	0.000526	3.3286	39	50	0.339291	0.400388

Gene	*p-value*	Optimal cutpoint	Group1 (n)	Group2 (n)	Age test (p-value)	HR
CD300LG	0.000980	1.3215	34	55	0.056218	0.399595
TJP1	0.000419	1.4864	54	35	0.159248	0.397900
SUCO	0.000372	10.4142	52	37	0.119345	0.397781
QSOX2	0.000528	9.6071	41	47	0.557985	0.396479
GJA1	0.000341	2.4606	49	39	0.170721	0.395150
GDF10	0.000439	1.0888	53	35	0.073240	0.393601
GABRE	0.000233	1.5542	48	38	0.365530	0.388315
FRZB	0.000574	2.8067	34	55	0.176456	0.387926
NLGN4X	0.000201	1.4442	50	39	0.103135	0.384189
MAP4K4	0.000259	11.4434	52	33	0.776273	0.381763
SELE	0.000122	0.9267	50	38	0.328218	0.380450
LYVE1	0.000260	2.3489	53	33	0.584753	0.377037
OSMR	0.000219	3.0146	50	38	0.177486	0.376739
NOL4L	0.000281	10.7633	37	51	0.260652	0.375099
DCLK1	0.000125	0.8301	50	39	0.172223	0.373177
CRIM1	0.000126	8.1774	42	45	0.782391	0.369971
PCDH17	0.000138	0.9462	47	42	0.154865	0.368110
SLC14A1	0.000069	6.5624	52	37	0.473808	0.367288
EYA1	0.000057	1.3865	54	34	0.395966	0.355724
PIMREG	0.000045	3.3832	54	35	0.550737	0.349571
ITGA8	0.000028	0	54	35	0.133603	0.343701
TSKU	0.000132	2.8832	36	53	0.241622	0.342914
IL33	0.000006	0.9267	52	37	0.134899	0.302496
ADAMTSL3	0.000001	0.9398	53	35	0.420204	0.262021
AWAT1	0.025321	1.0582	43	46	0.050093	
C16orf54	0.025321	11.0286	40	46	0.156660	
NDUFA12	0.000811	8.8284	41	47	0.516583	
ZNF433	0.020789	7.6258	42	47	0.268737	
SENP5	0.003716	10.2671	48	40	0.341276	
PSMA7	0.011657	10.3318	50	37	0.284874	
EVL	0.044814	10.6697	35	53	0.328716	
GALK1	0.022057	7.8817	36	52	0.935709	
JAK3	0.007906	11.2483	50	39	0.768985	
TOMM40L	0.000332	8.5908	51	34	0.332359	

Annex XXI Additional information about the 176 candidate biomarkers of prognostic of gene expression in patients with AML-M0-M1-M2-M4-M5 categorized in the intermediate prognostic risk group.

gene	Ratio	foldchange	*p-value*	status	bibliographic
CCT6B	0.62	0.43	0.0036825	low	non-leukemia cancer types
ITGB1BP1	0.93	0.34	0.0000001	low	non-AML leukemia types
PDE7B	1.54	0.39	0.0057739	low	cited in AML
ITGA11	0.74	0.32	0.0046237	low	non-leukemia cancer types
PBDC1	1.64	0.37	0.0354108	low	non-leukemia cancer types
NQO1	1.23	0.39	0.0001984	low	cited in AML
HSD17B7	0.62	0.38	0.0105473	low	non-leukemia cancer types
DRC7	1.17	0.27	0.0000000	low	cited in PubMed
TBC1D29P	0.62	0.34	0.0091614	low	never cited
ASCC1	0.93	0.35	0.0059529	low	non-leukemia cancer types
CCND3	1.17	0.30	0.0491560	low	cited in AML
IQCG	1.56	0.37	0.0008972	low	cited in AML
SH3TC2	1.02	0.35	0.0029086	low	non-AML leukemia types
S100A1	0.96	0.38	0.0000673	low	non-AML leukemia types
HIP1	0.69	0.30	0.0000025	low	cited in AML
ANKEF1	1.61	0.40	0.0010849	low	non-leukemia cancer types
NUDT5	0.62	0.34	0.0342869	low	non-leukemia cancer types
REG4	0.82	-1.48	0.0098793	low	non-AML leukemia types
STK36	1.41	0.34	0.0003672	low	non-leukemia cancer types
FOSL1	1.64	0.36	0.0023289	low	cited in AML
VPS33B	1.10	0.36	0.0132447	low	non-AML leukemia types
CEP89	1.08	0.36	0.0146579	low	non-leukemia cancer types
HAT1	0.75	0.33	0.0098708	low	non-AML leukemia types
ADK	0.80	0.35	0.0383823	low	cited in AML
COQ9	1.17	0.34	0.0103663	low	non-AML leukemia types
CSTB	0.80	0.34	0.0261336	low	cited in AML
GRHPR	0.73	0.33	0.0044511	low	non-leukemia cancer types
MSMO1	1.07	0.36	0.0349632	low	non-leukemia cancer types
AKIRIN2	0.93	0.33	0.0021630	low	non-leukemia cancer types
SV2B	0.93	0.38	0.0288494	low	non-AML leukemia types
SLC25A20	0.81	0.34	0.0138296	low	non-leukemia cancer types
CINP	1.36	0.36	0.0000000	low	non-AML leukemia types
OCEL1	0.71	0.38	0.0015659	low	non-leukemia cancer types
SNHG12	0.68	0.35	0.0483360	low	non-AML leukemia types
BCKDK	1.00	0.33	0.0025544	low	non-leukemia cancer types
TOM1L1	0.85	0.35	0.0071459	low	non-AML leukemia types
EBP	0.81	0.36	0.0039189	low	cited in AML
NIT2	0.71	0.35	0.0208930	low	non-leukemia cancer types
ARSD	0.72	0.31	0.0007807	low	non-AML leukemia types
LGI4	0.80	0.69	0.0070102	high	non-leukemia cancer types

gene	Ratio	foldchange	*p-value*	status	bibliographic
TSPAN33	0.76	0.37	0.0330537	high	cited in AML
PAWR	1.54	0.85	0.0000475	high	cited in AML
FCRL5	0.96	0.44	0.0059807	high	non-AML leukemia types
SH3RF1	1.26	0.38	0.0040728	high	non-leukemia cancer types
PDZK1	0.76	0.49	0.0032438	high	non-AML leukemia types
ZNF780B	1.18	0.34	0.0224013	high	non-leukemia cancer types
CNGA1	0.78	0.68	0.0224830	high	cited in PubMed
BCAR1	0.98	0.85	0.0037094	high	cited in AML
TRPC6	1.15	1.20	0.0006059	high	cited in AML
CACNA2D2	0.91	0.56	0.0002449	high	non-leukemia cancer types
CEP68	1.07	0.33	0.0223329	high	non-leukemia cancer types
CCDC80	0.75	0.76	0.0001815	high	non-leukemia cancer types
PCDHGA9	1.26	0.59	0.0027255	high	non-leukemia cancer types
GLI3	0.85	0.81	0.0045692	high	cited in AML
LRRC2	0.82	0.96	0.0021921	high	non-leukemia cancer types
PLS3	1.44	0.97	0.0002309	high	cited in AML
MMRN2	0.93	0.69	0.0171372	high	non-leukemia cancer types
FABP4	1.34	0.96	0.0003273	high	cited in AML
MCM9	1.24	0.39	0.0135093	high	non-leukemia cancer types
FSTL1	1.62	0.51	0.0017398	high	non-AML leukemia types
WASL	1.40	0.38	0.0177784	high	non-AML leukemia types
BCAR3	1.47	0.58	0.0112249	high	non-AML leukemia types
MAMLD1	1.26	0.57	0.0076265	high	non-leukemia cancer types
AGTPBP1	1.17	0.33	0.0011951	high	non-leukemia cancer types
SULF1	1.17	1.16	0.0004081	high	cited in AML
NDEL1	1.46	0.33	0.0436948	high	non-AML leukemia types
PLOD2	1.18	1.13	0.0004387	high	non-leukemia cancer types
IGF2	1.07	0.66	0.0000123	high	cited in AML
AMOTL2	0.83	0.77	0.0006208	high	non-leukemia cancer types
CCNJL	0.80	0.74	0.0078187	high	never cited
FAM171A1	1.30	0.73	0.0000253	high	non-leukemia cancer types
ASIC4	0.80	0.61	0.0380592	high	non-leukemia cancer types
S1PR2	0.83	0.51	0.0028484	high	non-AML leukemia types
CHRDL1	1.62	0.85	0.0000682	high	non-AML leukemia types
C12orf42	0.62	0.98	0.0001166	high	non-AML leukemia types
SORBS2	0.83	0.65	0.0041264	high	cited in AML
VASH2	1.10	0.52	0.0113074	high	non-leukemia cancer types
SHROOM3	0.80	0.60	0.0024588	high	non-leukemia cancer types
ARHGAP35	0.89	0.32	0.0000314	high	cited in AML
FBXL7	1.34	1.22	0.0001343	high	non-leukemia cancer types
LDB2	1.28	1.09	0.0000349	high	non-AML leukemia types
GPX8	0.85	0.97	0.0055510	high	non-leukemia cancer types
ADGRL1	0.82	0.40	0.0024922	high	cited in AML

gene	Ratio	foldchange	*p-value*	status	bibliographic
WNT10A	0.75	0.61	0.0462344	high	non-AML leukemia types
CCBE1	1.02	0.98	0.0012430	high	non-leukemia cancer types
CLDN5	1.64	0.69	0.0000594	high	non-AML leukemia types
CALHM5	1.17	1.25	0.0000064	high	never cited
COL3A1	1.47	0.87	0.0001025	high	cited in AML
PODN	1.23	0.89	0.0040495	high	non-leukemia cancer types
GFRA1	0.71	1.20	0.0000094	high	non-AML leukemia types
TMEM56	1.12	0.62	0.0000104	high	non-leukemia cancer types
CHSY3	1.26	0.82	0.0055629	high	non-leukemia cancer types
LAMA4	1.07	0.91	0.0006510	high	non-AML leukemia types
POU2AF1	0.82	0.43	0.0004058	high	cited in AML
OLFM1	1.17	0.99	0.0007294	high	non-leukemia cancer types
FAT4	1.44	0.85	0.0000195	high	cited in AML
NR2F1	0.82	1.28	0.0000357	high	non-AML leukemia types
CYGB	0.68	0.79	0.0010935	high	non-AML leukemia types
NMT2	0.82	0.46	0.0000017	high	non-AML leukemia types
TMEM132C	1.23	1.26	0.0000549	high	non-leukemia cancer types
CHI3L2	0.61	0.65	0.0043644	high	non-leukemia cancer types
C1orf21	1.12	0.45	0.0048230	high	cited in PubMed
DNAH9	1.34	0.71	0.0027938	high	cited in AML
NNMT	1.12	0.74	0.0044202	high	non-AML leukemia types
CYP46A1	1.18	0.81	0.0001470	high	non-leukemia cancer types
BICC1	0.78	0.91	0.0140329	high	non-leukemia cancer types
GEM	0.78	1.01	0.0003363	high	cited in AML
TRH	0.78	0.87	0.0001342	high	cited in AML
PCDH18	1.12	1.15	0.0000051	high	non-leukemia cancer types
NFIB	1.23	1.07	0.0000116	high	cited in AML
SEMA6D	1.23	1.17	0.0000106	high	non-leukemia cancer types
DCN	1.34	0.87	0.0000255	high	cited in AML
APOD	1.10	0.83	0.0069877	high	non-AML leukemia types
LBR	0.85	0.31	0.0212703	high	cited in AML
EPAS1	1.47	0.52	0.0001122	high	cited in AML
HSDL1	0.61	0.37	0.0125816	high	non-leukemia cancer types
CXCL12	0.68	0.52	0.0000045	high	cited in AML
KDR	0.75	1.10	0.0000096	high	cited in AML
TMEM98	1.61	1.06	0.0004171	high	non-leukemia cancer types
ADGRL4	1.34	1.11	0.0012319	high	non-leukemia cancer types
FAM149A	0.82	0.33	0.0039855	high	cited in PubMed
SERAC1	1.46	0.40	0.0028849	high	non-leukemia cancer types
AREL1	1.07	0.33	0.0001244	high	non-leukemia cancer types
NTRK3	1.32	0.49	0.0239769	high	cited in AML
FBLN1	1.34	0.87	0.0002876	high	non-AML leukemia types
ALPL	1.41	0.67	0.0042739	high	cited in AML

gene	Ratio	foldchange	*p-value*	status	bibliographic
MYT1	1.07	1.18	0.0001517	high	non-AML leukemia types
ATCAY	0.73	0.71	0.0294353	high	cited in AML
LTBP3	0.82	0.36	0.0437787	high	non-leukemia cancer types
ST8SIA1	0.66	0.78	0.0000294	high	non-AML leukemia types
COL1A2	1.62	0.82	0.0001951	high	cited in AML
CPZ	0.81	0.99	0.0012320	high	cited in AML
CD160	1.00	0.41	0.0007837	high	cited in AML
EFEMP1	1.29	0.90	0.0028682	high	non-leukemia cancer types
CDH11	1.02	0.89	0.0005113	high	cited in AML
LTBP2	1.51	0.51	0.0000054	high	non-AML leukemia types
VGLL3	1.20	0.94	0.0001051	high	non-leukemia cancer types
FCHSD2	0.62	0.32	0.0001775	high	cited in AML
MXRA5	1.41	1.00	0.0000969	high	non-leukemia cancer types
CTHRC1	0.93	0.58	0.0033507	high	non-leukemia cancer types
CDH5	0.78	1.01	0.0000028	high	non-leukemia cancer types
CD300LG	0.62	1.14	0.0004109	high	non-leukemia cancer types
TJP1	1.54	1.04	0.0000616	high	cited in AML
SUCO	1.41	0.33	0.0174382	high	non-leukemia cancer types
QSOX2	0.87	0.35	0.0075272	high	non-leukemia cancer types
GJA1	1.26	1.07	0.0000029	high	cited in AML
GDF10	1.51	0.80	0.0199014	high	non-leukemia cancer types
GABRE	1.26	0.80	0.0155091	high	cited in AML
FRZB	0.62	1.18	0.0001531	high	cited in AML
NLGN4X	1.28	0.97	0.0015786	high	non-AML leukemia types
MAP4K4	1.58	0.31	0.0001756	high	cited in AML
SELE	1.32	1.01	0.0005732	high	cited in AML
LYVE1	1.61	0.70	0.0182389	high	non-AML leukemia types
OSMR	1.32	0.77	0.0000126	high	non-AML leukemia types
NOL4L	0.73	0.33	0.0008201	high	cited in AML
DCLK1	1.28	1.10	0.0009695	high	non-AML leukemia types
CRIM1	0.93	0.40	0.0000870	high	non-AML leukemia types
PCDH17	1.12	1.17	0.0001171	high	cited in AML
SLC14A1	1.41	0.51	0.0000006	high	non-leukemia cancer types
EYA1	1.59	1.38	0.0000000	high	cited in AML
PIMREG	1.54	0.63	0.0357573	high	cited in AML
ITGA8	1.54	1.10	0.0017243	high	non-leukemia cancer types
TSKU	0.68	0.89	0.0004071	high	non-leukemia cancer types
IL33	1.41	1.40	0.0000078	high	cited in AML
ADAMTSL3	1.51	0.86	0.0022419	high	non-leukemia cancer types
AWAT1	0.93	0.41	0.0405402	high	cited in PubMed
C16orf54	0.87	0.31	0.0051232	low	never cited
NDUFA12	0.87	0.35	0.0002453	low	cited in PubMed
ZNF433	0.89	0.40	0.0106222	high	non-leukemia cancer types

gene	Ratio	foldchange	*p-value*	status	bibliographic
SENP5	1.20	0.33	0.0021849	high	cited in AML
PSMA7	1.35	0.32	0.0018333	low	non-AML leukemia types
EVL	0.66	0.33	0.0279061	high	cited in AML
GALK1	0.69	0.37	0.0099953	low	non-leukemia cancer types
JAK3	1.28	0.32	0.0001916	high	cited in AML
TOMM40L	1.50	0.35	0.0012764	low	non-leukemia cancer types

Annex XXII List of the gene sets shared by the majority of the intermediate-poor AML-M4 that were differentially enriched in comparison with the intermediate-favorable subgroups. For each gene set is represented the number and the percentage of intermediate-poor subgroups that have the gene sets enriched (n and percentage), a representative *p-value* and the status (upregulated (up) or downregulated (down)).

Set	n	Percentage	*p-value*	Status
GO:0043628 ncRNA 3'-end processing	170	98	0.0492	Up
GO:0006605 protein targeting	169	97	0.0276	Up
GO:0034472 snRNA 3'-end processing	167	96	0.0283	Up
GO:0016180 snRNA processing	167	96	0.0354	Up
GO:0046434 organophosphate catabolic process	166	95	0.0413	Up
GO:0016073 snRNA metabolic process	164	94	0.0466	Up
GO:0044282 small molecule catabolic process	159	91	0.0479	Up
GO:0007031 peroxisome organization	159	91	0.0480	Up
GO:0030534 adult behavior	172	99	0.0408	Down
GO:0048762 mesenchymal cell differentiation	169	97	0.0344	Down
GO:0048592 eye morphogenesis	168	97	0.0422	Down
GO:0048745 smooth muscle tissue development	167	96	0.0343	Down
GO:0003279 cardiac septum development	166	95	0.0374	Down
GO:0014065 phosphatidylinositol 3-kinase signaling	166	95	0.0463	Down
GO:0003272 endocardial cushion formation	166	95	0.0465	Down
GO:0048593 camera-type eye morphogenesis	166	95	0.0492	Down
GO:0043567 regulation of insulin-like growth factor receptor signaling pathway	165	95	0.0398	Down
GO:0060219 camera-type eye photoreceptor cell differentiation	165	95	0.0423	Down
GO:0060485 mesenchyme development	165	95	0.0467	Down
GO:2001026 regulation of endothelial cell chemotaxis	165	95	0.0469	Down
GO:0061564 axon development	165	95	0.0483	Down
GO:0060411 cardiac septum morphogenesis	164	94	0.0313	Down
GO:0021543 pallium development	164	94	0.0315	Down
GO:0021537 telencephalon development	164	94	0.0340	Down
GO:0043568 positive regulation of insulin-like growth factor receptor signaling pathway	164	94	0.0390	Down
GO:0021987 cerebral cortex development	164	94	0.0400	Down
GO:0007409 axonogenesis	164	94	0.0418	Down
GO:0072538 T-helper 17 type immune response	164	94	0.0453	Down
GO:0048286 lung alveolus development	164	94	0.0492	Down
GO:0090596 sensory organ morphogenesis	163	94	0.0404	Down
GO:0072539 T-helper 17 cell differentiation	163	94	0.0470	Down
GO:0003206 cardiac chamber morphogenesis	162	93	0.0338	Down
GO:0048009 insulin-like growth factor receptor signaling pathway	162	93	0.0456	Down
GO:0030900 forebrain development	162	93	0.0471	Down

Set	n	Percentage	*p-value*	Status
GO:0098815 modulation of excitatory postsynaptic potential	162	93	0.0479	Down
GO:0055023 positive regulation of cardiac muscle tissue growth	162	93	0.0490	Down
GO:0003007 heart morphogenesis	161	93	0.0412	Down
GO:2001028 positive regulation of endothelial cell chemotaxis	161	93	0.0427	Down
GO:0071772 response to BMP	161	93	0.0449	Down
GO:0071773 cellular response to BMP stimulus	161	93	0.0449	Down
GO:0070208 protein heterotrimerization	161	93	0.0453	Down
GO:0003323 type B pancreatic cell development	161	93	0.0497	Down
GO:0007423 sensory organ development	160	92	0.0438	Down
GO:0001764 neuron migration	160	92	0.0466	Down
GO:0003205 cardiac chamber development	160	92	0.0484	Down
GO:0001837 epithelial to mesenchymal transition	160	92	0.0488	Down
GO:0060317 cardiac epithelial to mesenchymal transition	160	92	0.0488	Down
GO:0014066 regulation of phosphatidylinositol 3-kinase signaling	160	92	0.0489	Down
GO:0048015 phosphatidylinositol-mediated signaling	160	92	0.0499	Down
GO:0007416 synapse assembly	159	91	0.0381	Down
GO:0030510 regulation of BMP signaling pathway	159	91	0.0482	Down
GO:0021536 diencephalon development	159	91	0.0495	Down
GO:0044331 cell-cell adhesion mediated by cadherin	158	91	0.0244	Down
GO:0051954 positive regulation of amine transport	158	91	0.0439	Down
GO:0085029 extracellular matrix assembly	158	91	0.0455	Down
GO:0098742 cell-cell adhesion via plasma-membrane adhesion molecules	158	91	0.0458	Down
GO:0007178 transmembrane receptor protein serine/threonine kinase signaling pathway	158	91	0.0469	Down
GO:0003198 epithelial to mesenchymal transition involved in endocardial cushion formation	158	91	0.0491	Down
GO:0007156 homophilic cell adhesion via plasma membrane adhesion molecules	158	91	0.0492	Down
GO:0097485 neuron projection guidance	158	91	0.0496	Down
GO:0007411 axon guidance	158	91	0.0500	Down
GO:0010717 regulation of epithelial to mesenchymal transition	157	90	0.0441	Down
GO:0021761 limbic system development	157	90	0.0452	Down
GO:0072578 neurotransmitter-gated ion channel clustering	157	90	0.0459	Down
GO:0015671 oxygen transport	157	90	0.0475	Down

Set	n	Percentage	*p-value*	Status
GO:0060079 excitatory postsynaptic potential	157	90	0.0487	Down
GO:0016339 calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	157	90	0.0492	Down
GO:0048863 stem cell differentiation	157	90	0.0497	Down
GO:0043518 negative regulation of DNA damage response, signal transduction by p53 class mediator	157	90	0.0497	Down

Annex XXIII The remaining 258 identified genes whose DNA methylation were able to predict survival in patients with AML-M0-M1-M2-M4-M5 categorized in the intermediate prognostic risk group.

CpG sites	*p-value*	Optimal cutpoint	Group1 (n)	Group 2 (n)	Age test (p-value)	HR	gene
cg19863563	0.0006	0.8924	47	38	0.1519	2.5269	*NTNG1*
cg18506679	0.0010	0.8841	48	35	0.0598	2.5185	*OLFML2A*
cg16114831	0.0023	0.7634	49	32	0.5235	2.5175	*ABLIM2*
cg16784198	0.0005	0.8751	46	39	0.0555	2.5160	*DNAJB6*
cg10516336	0.0003	0.0596	42	46	0.0946	2.5030	*ABCC5*
cg02486268	0.0008	0.8455	50	37	0.6801	2.5026	*FGF3*
cg03905134	0.0004	0.8782	45	40	0.4101	2.4935	*SNORA70*
cg11335960	0.0010	0.7567	51	35	0.1827	2.4873	*ISLR*
cg01042368	0.0006	0.8372	34	50	0.0840	2.4852	*GPR179*
cg11593247	0.0004	0.8057	34	52	0.1274	2.4830	*PYGM*
cg10259518	0.0010	0.8708	39	38	0.0778	2.4824	*NGEF*
cg03951153	0.0004	0.033	41	47	0.0984	2.4676	*CPOX*
cg13081014	0.0007	0.8394	45	40	0.2015	2.4559	*FMO1*
cg06866395	0.0026	0.8114	50	34	0.2719	2.4395	*TMEM266*
cg08756008	0.0006	0.7901	36	50	0.0556	2.4368	*BAG3*
cg02885428	0.0008	0.8165	41	44	0.1989	2.4311	*FRMD1*
cg12048341	0.0005	0.8775	37	50	0.8975	2.4241	*NAV1*
cg21901928	0.0030	0.8701	41	31	0.2721	2.4241	*EGFR*
cg10753636	0.0011	0.8721	40	43	0.0642	2.4181	*MIR520A*
cg17877470	0.0012	0.0702	40	40	0.0726	2.4158	*ZNF846*
cg21644914	0.0020	0.8333	49	35	0.0701	2.4144	*IGFBP5*
cg26884359	0.0013	0.8518	50	36	0.0821	2.4067	*DHX58*
cg05130129	0.0014	0.8249	46	38	0.0646	2.3771	*ENPP6*
cg11229160	0.0017	0.8694	43	41	0.1822	2.3714	*FARS2*
cg10054313	0.0008	0.0394	36	50	0.4005	2.3709	*MEGF8*
cg05576795	0.0016	0.8702	29	48	0.0976	2.3672	*NSG2*
cg09181104	0.0009	0.8699	34	51	0.2855	2.3657	*C1orf109*
cg09747891	0.0053	0.8286	45	30	0.1034	2.3626	*ADAMTS12*
cg19211186	0.0020	0.8457	45	35	0.0824	2.3529	*FAM241B*
cg00236601	0.0009	0.8896	37	49	0.1183	2.3286	*ZNF146*
cg01920182	0.0018	0.8706	35	50	0.1311	2.3268	*SOX5*
cg17154313	0.0020	0.0813	45	39	0.3021	2.3225	*COL13A1*
cg14403642	0.0009	0.8618	37	49	0.3900	2.3216	*CDK20*
cg19843449	0.0028	0.8819	28	46	0.1279	2.3063	*GABRG3*
cg14161159	0.0011	0.9141	40	49	0.4805	2.3012	*C2orf27A*
cg01483518	0.0037	0.8583	51	34	0.3235	2.2996	*OR2Y1*
cg03573068	0.0030	0.1169	55	34	0.3440	2.2890	*SLC6A5*
cg10020934	0.0015	0.8745	36	48	0.1454	2.2879	*CACNG5*

CpG sites	*p-value*	Optimal cutpoint	Group1 (n)	Group 2 (n)	Age test (p-value)	HR	gene
cg03465652	0.0011	0.5018	34	55	0.5319	2.2846	*GLI2*
cg13144594	0.0044	0.818	44	33	0.0892	2.2776	*TNFAIP2*
cg08109505	0.0021	0.0862	39	45	0.0817	2.2464	*SLC37A3*
cg13540805	0.0019	0.8367	36	50	0.4029	2.2429	*LMNTD1*
cg19707503	0.0028	0.8375	46	37	0.1706	2.2382	*NFKBIE*
cg22179256	0.0038	0.8761	47	36	0.3700	2.2375	*SLC5A5*
cg17529745	0.0038	0.8393	54	34	0.5174	2.2362	*EBF3*
cg22549339	0.0028	0.8948	36	45	0.8269	2.2314	*OCA2*
cg00615654	0.0019	0.8903	36	48	0.3090	2.2281	*ADARB2*
cg18547838	0.0053	0.8844	50	32	0.1392	2.2217	*ARID5B*
cg02027010	0.0024	0.0358	35	50	0.4136	2.2216	*ALAD*
cg07782808	0.0026	0.8825	38	48	0.1994	2.2210	*KRTAP17-1*
cg01100703	0.0041	0.8838	48	35	0.1064	2.2096	*ADAMTS8*
cg08907257	0.0022	0.8614	34	52	0.2434	2.2074	*TRAF7*
cg22675150	0.0027	0.8711	46	39	0.1541	2.2066	*TUBA3C*
cg03499905	0.0043	0.8701	47	36	0.3367	2.1998	*COL4A1*
cg06750076	0.0029	0.8315	34	52	0.1498	2.1982	*VOPP1*
cg25140133	0.0059	0.7995	53	33	0.1332	2.1958	*MIR4634*
cg03256601	0.0036	0.8624	44	37	0.2088	2.1883	*FAM53A*
cg19917720	0.0021	0.8639	37	49	0.1995	2.1881	*PLSCR2*
cg22264813	0.0029	0.7985	41	44	0.0878	2.1775	*WDR60*
cg04588710	0.0027	0.904	38	49	0.6905	2.1742	*OR4K17*
cg12060838	0.0034	0.8929	39	45	0.6732	2.1735	*KIRREL1*
cg25789216	0.0032	0.015	49	39	0.8897	2.1682	*CNIH2*
cg04476531	0.0035	0.8466	38	46	0.2846	2.1650	*MACROD2*
cg16025492	0.0031	0.8995	34	50	0.1076	2.1650	*FEM1C*
cg07903153	0.0039	0.3211	50	38	0.6765	2.1644	*SEPHS2*
cg24913110	0.0043	0.8783	45	39	0.1363	2.1600	*DEFA5*
cg01165355	0.0047	0.8607	35	44	0.8551	2.1509	*PRICKLE2*
cg07745344	0.0047	0.8677	44	36	0.1427	2.1432	*TDRP*
cg05919312	0.0060	0.8294	50	33	0.2208	2.1408	*CYB5R2*
cg03100044	0.0034	0.877	39	47	0.5875	2.1392	*CHN2*
cg01393841	0.0031	0.9014	33	52	0.2519	2.1366	*GPSM1*
cg21624165	0.0076	0.7173	49	35	0.9097	2.1262	*GRM6*
cg06810134	0.0051	0.8697	48	36	0.7792	2.1234	*BSG*
cg04743859	0.0062	0.8723	48	39	0.1442	2.1210	*TCIRG1*
cg04841371	0.0040	0.8554	35	52	0.0579	2.1179	*SPRR1A*
cg24893364	0.0063	0.0458	53	36	0.3982	2.1159	*METTL5*
cg15466245	0.0063	0.868	51	34	0.3213	2.1157	*ADAM15*
cg20584157	0.0061	0.8814	38	42	0.3598	2.1097	*PRICKLE2*
cg21497236	0.0060	0.8264	47	39	0.2761	2.1091	*SYNE4*

CpG sites	*p-value*	Optimal cutpoint	Group1 (n)	Group 2 (n)	Age test (p-value)	HR	gene
cg03033996	0.0065	0.852	41	41	0.0711	2.1089	*ABLIM2*
cg21986035	0.0049	0.8755	47	40	0.3918	2.1068	*MIR4655*
cg18770739	0.0061	0.7253	50	36	0.6457	2.1024	*OR10P1*
cg19472254	0.0045	0.887	38	47	0.1803	2.0998	*ATP8B3*
cg15638292	0.0044	0.8812	40	43	0.9600	2.0987	*MYO7A*
cg26113962	0.0085	0.888	43	40	0.0689	2.0983	*HTR1D*
cg02917889	0.0075	0.8233	34	39	0.0521	2.0975	*ARHGEF4*
cg14779404	0.0087	0.8825	45	36	0.5491	2.0920	*PITX1*
cg07394259	0.0082	0.8477	48	32	0.8327	2.0848	*FAM110B*
cg06201219	0.0044	0.7443	39	45	0.2257	2.0795	*ITIH5*
cg16912319	0.0092	0.8381	52	33	0.1044	2.0714	*KIAA2012*
cg09723488	0.0071	0.7891	50	36	0.1264	2.0694	*LHX6*
cg13710542	0.0075	0.8706	46	41	0.3949	2.0637	*EXD3*
cg17377797	0.0056	0.8764	34	49	0.3713	2.0599	*OR6C1*
cg10096321	0.0051	0.8631	35	50	1.0000	2.0558	*ZBTB16*
cg18499321	0.0103	0.8809	49	33	0.2388	2.0533	*RIMBP2*
cg06269928	0.0098	0.8699	38	37	0.5670	2.0512	*MAP1LC3C*
cg16999602	0.0054	0.7864	40	47	0.1560	2.0497	*SLC1A7*
cg02167753	0.0100	0.793	32	46	0.0778	2.0491	*TSPAN18*
cg14061609	0.0166	0.891	49	30	0.3498	2.0475	*TBX5*
cg22348356	0.0056	0.8972	35	53	0.9898	2.0431	*RASA3*
cg24655336	0.0063	0.8781	36	46	0.4920	2.0399	*GPRIN1*
cg02546490	0.0061	0.8621	39	46	0.0572	2.0395	*AATK*
cg26057765	0.0071	0.8692	41	43	0.2767	2.0354	*MTERF1*
cg27260984	0.0101	0.8778	50	33	0.6152	2.0251	*HS3ST3A1*
cg25368560	0.0099	0.8524	37	44	0.5757	2.0250	*PGBD5*
cg05719742	0.0065	0.8366	35	51	0.0956	2.0244	*ZNF503-AS1*
cg21785145	0.0111	0.8568	47	37	0.7319	2.0241	*CACNA1G*
cg04622024	0.0057	0.5749	40	49	0.6322	2.0211	*EPHA10*
cg20635409	0.0058	0.3655	38	51	0.4232	2.0150	*ASCL1*
cg10168419	0.0100	0.8453	51	37	0.1355	2.0083	*HGSNAT*
cg03705718	0.0069	0.3868	37	47	0.8428	2.0079	*SLC16A14*
cg10503007	0.0140	0.8696	39	34	0.1535	2.0071	*NTSR2*
cg00574639	0.0143	0.8869	43	35	0.1879	2.0063	*EFEMP1*
cg12622273	0.0066	0.8499	38	49	0.0900	1.9984	*LGI4*
cg03717414	0.0095	0.8528	36	47	0.2800	1.9929	*MAPK11*
cg26082023	0.0085	0.8869	45	43	0.0948	1.9887	*MUC4*
cg09664492	0.0068	0.8641	35	51	0.2697	1.9843	*PROM2*
cg07219227	0.0071	0.8203	38	51	0.1288	1.9786	*SMARCD3*
cg00372692	0.0119	0.8895	52	35	0.2987	1.9779	*ICOS*
cg27118986	0.0169	0.8813	52	32	0.9779	1.9752	*ZFHX2*

CpG sites	*p-value*	Optimal cutpoint	Group1 (n)	Group 2 (n)	Age test (p-value)	HR	gene
cg14592830	0.0222	0.0443	50	31	0.6688	1.9750	*BRINP1*
cg10721490	0.0083	0.0315	40	44	0.3027	1.9712	*TBC1D32*
cg24934400	0.0165	0.1129	55	34	0.3819	1.9626	*MSX1*
cg04235768	0.0081	0.6609	40	49	0.4577	1.9611	*PRDM8*
cg14246940	0.0131	0.8062	34	44	0.2361	1.9590	*LMX1B*
cg24768463	0.0107	0.8686	34	49	0.3059	1.9578	*ATN1*
cg10588720	0.0153	0.8797	48	35	0.7713	1.9553	*NRSN1*
cg20233228	0.0124	0.8955	48	38	0.1524	1.9435	*TEAD1*
cg02054568	0.0132	0.7888	45	41	0.1799	1.9397	*LCE3D*
cg00966557	0.0138	0.8596	46	41	0.0897	1.9393	*PPARGC1B*
cg16866892	0.0105	0.8575	41	46	0.1945	1.9293	*CACNA1C*
cg25940557	0.0159	0.8363	51	36	0.0918	1.9284	*OR10Z1*
cg22995904	0.0208	0.8811	51	34	0.0625	1.9232	*FGD5*
cg12631713	0.0191	0.8034	53	33	0.8173	1.9198	*AJAP1*
cg05808319	0.0221	0.0168	42	36	0.5440	1.9183	*MIR129-2*
cg19864941	0.0242	0.8827	54	33	0.6969	1.9172	*PITPNM1*
cg17188169	0.0200	0.8973	28	46	0.3814	1.9119	*DDX43*
cg00291877	0.0144	0.0297	42	43	0.0610	1.9103	*SNRPA1*
cg24312874	0.0206	0.8117	44	37	0.3985	1.9099	*TTC34*
cg02920178	0.0165	0.8574	44	42	0.2539	1.9079	*UBE2I*
cg07501052	0.0117	0.8604	37	48	0.0691	1.9072	*GLB1L2*
cg08400962	0.0101	0.4974	38	51	0.9570	1.9068	*CHST8*
cg12305870	0.0134	0.8754	47	40	0.5884	1.9052	*RBCK1*
cg02633600	0.0181	0.8817	32	46	0.2466	1.9033	*SOX8*
cg10988368	0.0146	0.8819	34	52	0.1412	1.9008	*ASCL2*
cg14538055	0.0204	0.0217	54	34	0.5258	1.8966	*RAB1B*
cg17923401	0.0144	0.9181	36	49	0.4876	1.8957	*SIGLEC7*
cg21291449	0.0228	0.8387	36	40	0.1044	1.8946	*C6orf136*
cg19201068	0.0138	0.8668	40	46	0.4695	1.8938	*NOG*
cg04274356	0.0165	0.9048	40	42	0.3855	1.8921	*TMEM72*
cg24258108	0.0130	0.909	37	49	0.8717	1.8906	*NSD3*
cg24645896	0.0160	0.8475	45	43	0.0725	1.8878	*BCL9*
cg10052687	0.0242	0.9076	52	34	0.8149	1.8854	*CLIP2*
cg07395930	0.0172	0.8705	45	41	0.0844	1.8827	*CLSTN1*
cg02471751	0.0168	0.8839	45	40	0.6218	1.8786	*SLC6A2*
cg05824973	0.0135	0.8103	40	47	0.4158	1.8779	*KRT6A*
cg04471045	0.0141	0.8688	36	50	0.1232	1.8759	*ADGRB1*
cg20715438	0.0198	0.8846	39	44	0.7425	1.8750	*RAP1GAP2*
cg17891088	0.0173	0.86	50	38	0.1568	1.8730	*KRT82*
cg18077580	0.0195	0.1102	41	40	0.9022	1.8631	*DLX5*
cg14564144	0.0242	0.886	48	38	0.0626	1.8550	*B4GALNT3*

CpG sites	*p-value*	Optimal cutpoint	Group1 (n)	Group 2 (n)	Age test (p-value)	HR	gene
cg27174861	0.0171	0.8767	36	51	0.3584	1.8529	*PTPRF*
cg13337064	0.0148	0.6273	36	53	0.2142	1.8486	*PCDHB15*
cg17614506	0.0176	0.8464	38	48	0.6261	1.8408	*LINC00525*
cg25042430	0.0167	0.203	41	48	0.1382	1.8367	*KIAA1217*
cg06676233	0.0223	0.0816	47	38	0.2028	1.8325	*NPL*
cg17453252	0.0175	0.7241	40	49	0.8982	1.8266	*COL4A2*
cg01737592	0.0291	0.8416	49	36	0.3366	1.8188	*MIR769*
cg01856384	0.0223	0.8767	33	51	0.4253	1.8137	*NCR2*
cg15261751	0.0246	0.8822	45	38	0.7111	1.8126	*PHACTR1*
cg12459514	0.0204	0.8751	35	49	0.2291	1.8118	*KLHL29*
cg13944644	0.0342	0.8922	45	35	0.2482	1.7982	*GULP1*
cg11647651	0.0246	0.017	46	40	0.9620	1.7916	*PLD2*
cg18854169	0.0386	0.7472	50	35	0.5465	1.7628	*RBP3*
cg20774846	0.0386	0.5486	52	37	0.4738	1.7292	*DPYS*
cg05246900	0.0384	0.8148	45	39	0.5124	1.7271	*UBE2I*
cg16010207	0.0461	0.8757	50	35	0.2330	1.7142	*PDE4DIP*
cg05935961	0.0404	0.8056	43	41	0.9038	1.7042	*WT1*
cg09263146	0.0437	0.8876	44	41	0.2067	1.6927	*SEMA6C*
cg07961456	0.0482	0.8897	44	43	0.2750	1.6679	*TEX35*
cg08229532	0.0270	0.4651	35	54	0.7719	0.5553	*TOPBP1*
cg07795968	0.0225	0.2845	40	49	0.3180	0.5512	*JPH2*
cg05004118	0.0198	0.0244	53	34	0.1288	0.5501	*VRK1*
cg02303801	0.0242	0.1535	49	30	0.2534	0.5449	*ARHGEF16*
cg17465930	0.0227	0.0231	37	47	0.6264	0.5396	*MATR3*
cg12346491	0.0195	0.0643	44	40	0.7812	0.5376	*GYPA*
cg10327067	0.0222	0.2451	32	53	0.7959	0.5368	*ZNF703*
cg02309627	0.0147	0.0463	49	40	0.8950	0.5367	*ZNF507*
cg08076125	0.0199	0.4059	37	52	0.4712	0.5350	*GRM1*
cg01229787	0.0217	0.0933	33	46	0.3272	0.5257	*MEF2A*
cg23698269	0.0128	0.073	44	41	0.3789	0.5247	*SBF2*
cg01319581	0.0131	0.878	41	45	0.4439	0.5229	*CTPS2*
cg15112395	0.0120	0.0235	48	34	0.5817	0.5215	*ZNF585B*
cg14686309	0.0173	0.044	37	45	0.5414	0.5208	*USP43*
cg21234506	0.0093	0.1444	52	37	0.7738	0.5197	*BCL2A1*
cg00459795	0.0126	0.0199	43	40	0.8624	0.5131	*ZNF514*
cg07567973	0.0116	0.014	33	52	0.4351	0.5011	*SRFBP1*
cg15736743	0.0059	0.3106	45	44	0.6369	0.4979	*KLHL29*
cg10402417	0.0140	0.0946	35	46	0.0583	0.4978	*TBC1D10C*
cg21793948	0.0088	0.0113	51	31	0.7449	0.4973	*BCL2*
cg17216243	0.0100	0.3022	34	55	0.7804	0.4964	*SSB*
cg25542319	0.0054	0.6596	52	37	0.8188	0.4954	*MCC*

CpG sites	*p-value*	Optimal cutpoint	Group1 (n)	Group 2 (n)	Age test (p-value)	HR	gene
cg18279337	0.0088	0.0747	38	46	0.6891	0.4933	*MYO5C*
cg00873517	0.0103	0.2918	37	42	0.2709	0.4905	*KHDRBS3*
cg06422694	0.0064	0.4317	37	52	0.2662	0.4902	*FLYWCH1*
cg09365677	0.0050	0.0266	54	33	0.7794	0.4857	*CHRM3*
cg04003903	0.0039	0.2095	52	37	0.5159	0.4843	*CPZ*
cg21761639	0.0040	0.3291	53	36	0.5781	0.4815	*ITPRID1*
cg01692379	0.0043	0.3286	43	46	0.8245	0.4769	*RNF39*
cg12843489	0.0034	0.3007	43	46	0.9574	0.4722	*RN7SK*
cg22698028	0.0043	0.1041	46	33	0.2548	0.4636	*AHRR*
cg26521139	0.0045	0.3368	34	55	0.9058	0.4616	*AGAP1*
cg01260103	0.0043	0.0156	35	52	0.0848	0.4517	*CPT1A*
cg04605617	0.0021	0.7684	51	35	0.3887	0.4451	*PLA2G2C*
cg13517138	0.0013	0.0204	52	35	0.3235	0.4388	*DLGAP5*
cg15590007	0.0008	0.2696	54	35	0.1094	0.4335	*ALOX5*
cg25639084	0.0009	0.193	47	42	0.6780	0.4332	*TNFRSF19*
cg15262954	0.0023	0.0137	39	37	0.5959	0.4291	*HELZ2*
cg02944084	0.0016	0.4351	36	53	0.8507	0.4287	*PNMT*
cg07020327	0.0006	0.027	49	40	0.6829	0.4197	*CDC23*
cg26294217	0.0015	0.0258	35	52	0.2566	0.4190	*PRKAA1*
cg11460820	0.0005	0.0169	47	39	0.4984	0.4124	*RPS24*
cg08999807	0.0007	0.0322	49	31	0.5467	0.4041	*GPC5*
cg03408904	0.0004	0.4948	36	53	0.2205	0.3862	*CECR2*
cg01529538	0.0001	0.0161	45	37	0.6278	0.3612	*RBM23*
cg23195687	0.0001	0.474	54	35	0.3132	0.3606	*MIR4679-2*
cg07380021	0.0002	0.1323	39	48	0.1431	0.3598	*RASSF5*
cg03074946	0.0255	0.831	47	36	0.5080		*PXN*
cg06623385	0.0022	0.0476	43	43	0.1832		*NPM3*
cg09277256	0.0270	0.7972	48	40	0.0565		*MIR4710*
cg01617933	0.0265	0.8747	48	37	0.0583		*CHN2*
cg16315582	0.0220	0.0556	34	46	0.4924		*CASP4*
cg22158547	0.0030	0.9345	51	32	1.0000		*SUSD4*
cg21101386	0.0267	0.8552	53	35	0.1300		*DLGAP4*
cg20079335	0.0281	0.8293	36	50	0.3647		*MAGEA2*
cg21304488	0.0215	0.8386	47	29	0.1502		*TIAF1*
cg08302300	0.0274	0.8314	50	35	0.1255		*ADARB2*
cg20960833	0.0290	0.8798	51	38	0.2590		*EN2*
cg15756928	0.0002	0.8851	42	36	0.3535		*GFRAL*
cg09044219	0.0422	0.0366	36	44	0.8808		*CCDC77*
cg03196437	0.0012	0.8778	40	47	0.0722		*FOXR1*
cg01118451	0.0335	0.0153	49	35	0.8275		*ENOX1*
cg13018793	0.0284	0.2814	36	53	0.5115		*LINC00242*

CpG sites	***p-value***	**Optimal cutpoint**	**Group1 (n)**	**Group 2 (n)**	**Age test (p-value)**	**HR**	**gene**
cg07615497	0.0382	0.4977	45	44	0.5993		*POU4F2*
cg16851924	0.0029	0.0321	36	38	0.8118		*CERKL*
cg11140606	0.0405	0.0216	48	38	0.5001		*PEF1*
cg02558162	0.0235	0.7988	45	28	0.1240		*CRABP1*
cg09950208	0.0052	0.2201	35	54	0.1180		*MGMT*
cg00073460	0.0186	0.2198	42	47	0.2039		*ZC3H12D*
cg19384717	0.0064	0.8861	34	51	0.0778		*NOTO*
cg01987224	0.0463	0.8608	46	31	0.1073		*CACNA1S*
cg11352369	0.0419	0.8775	47	37	0.7524		*SAMD1*
cg12439423	0.0107	0.8474	37	47	0.0765		*ANK1*
cg01023703	0.0162	0.4291	40	49	0.7790		*BAIAP3*
cg23222472	0.0182	0.203	35	46	0.7747		*LSMEM1*
cg04560098	0.0034	0.7457	33	52	0.2730		*TRIM10*
cg09633881	0.0157	0.1743	43	46	0.3365		*APTX*
cg25919979	0.0110	0.7786	34	54	0.0997		*GLI2*

Annex XXIV Additional information about the 273 candidate biomarkers of prognostic of DNA methylation in patients with AML-M0-M1-M2-M4-M5 categorized in the intermediate prognostic risk group.

CpG sites	CpG sites location	status	Ratio	delta beta	*p-value*	Bibliographic analysis
cg14469693	Other Intron	low	1.10	-0.14	7.20E-15	non-leukemia cancer types
cg25068253	Distal Intergenic	low	1.05	-0.09	1.46E-14	non-AML leukemia types
cg17755518	Promoter (1-2kb)	low	1.24	-0.06	9.06E-14	cited in AML
cg17572155	Promoter (2-3kb)	low	1.02	-0.25	4.66E-16	non-AML leukemia types
cg03841832	Other Intron	low	1.36	-0.14	1.61E-24	non-leukemia cancer types
cg14495958	1st Intron	low	1.39	-0.08	4.70E-14	non-leukemia cancer types
cg01918114	1st Intron	low	1.19	-0.06	1.23E-14	non-leukemia cancer types
cg13184077	Other Intron	low	1.08	-0.05	1.02E-14	non-leukemia cancer types
cg26118637	Distal Intergenic	low	0.89	-0.02	5.11E-15	non-leukemia cancer types
cg15596913	Promoter (1-2kb)	low	0.98	-0.03	9.95E-16	non-leukemia cancer types
cg15861089	Promoter (<=1kb)	low	1.36	-0.07	4.50E-15	cited in PubMed
cg26208930	Promoter (<=1kb)	low	1.18	-0.07	5.70E-15	cited in AML
cg10350957	Other Exon	low	0.80	-0.06	6.59E-15	cited in AML
cg22356541	3' UTR	low	1.10	-0.04	7.19E-15	non-AML leukemia types
cg03863069	Promoter (2-3kb)	low	0.67	-0.05	7.67E-15	non-leukemia cancer types
cg19863563	Other Intron	low	1.24	-0.05	3.05E-15	non-leukemia cancer types
cg18506679	Promoter (<=1kb)	low	1.37	-0.03	9.81E-15	cited in AML
cg16114831	Other Intron	low	1.53	-0.08	5.52E-23	non-leukemia cancer types
cg16784198	Distal Intergenic	low	1.18	-0.04	2.65E-15	non-AML leukemia types
cg10516336	Promoter (<=1kb)	low	0.91	-0.02	7.27E-16	cited in AML
cg02486268	Distal Intergenic	low	1.35	-0.04	2.06E-15	non-AML leukemia types
cg03905134	Distal Intergenic	low	1.13	-0.06	2.38E-15	cited in PubMed
cg11335960	Promoter (<=1kb)	low	1.46	-0.09	4.47E-15	non-leukemia cancer types
cg01042368	Promoter (<=1kb)	low	0.68	-0.04	9.83E-15	cited in PubMed
cg11593247	Other Exon	low	0.65	-0.04	6.01E-15	non-AML leukemia types
cg10259518	Promoter (<=1kb)	low	1.03	-0.04	4.53E-14	non-leukemia cancer types
cg03951153	Promoter (<=1kb)	low	0.87	-0.01	7.88E-16	cited in AML
cg13081014	Promoter (<=1kb)	low	1.13	-0.08	6.93E-25	non-AML leukemia types

CpG sites	CpG sites location	status	Ratio	delta beta	*p-value*	Bibliographic analysis
cg06866395	Other Intron	low	1.47	-0.06	9.83E-15	cited in PubMed
cg08756008	1st Intron	low	0.72	-0.07	3.43E-15	cited in AML
cg02885428	Promoter (<=1kb)	low	0.93	-0.05	2.22E-15	non-AML leukemia types
cg12048341	Other Intron	low	0.74	-0.08	2.06E-15	cited in AML
cg21901928	1st Intron	low	1.32	-0.09	5.14E-13	cited in AML
cg10753636	Promoter (1-2kb)	low	0.93	-0.06	4.76E-15	non-leukemia cancer types
cg17877470	Distal Intergenic	low	1.00	-0.06	1.43E-14	never cited
cg21644914	Distal Intergenic	low	1.40	-0.10	7.51E-15	non-AML leukemia types
cg26884359	Distal Intergenic	low	1.39	-0.07	3.43E-15	non-AML leukemia types
cg05130129	1st Intron	low	1.21	-0.03	4.14E-15	non-leukemia cancer types
cg11229160	Other Intron	low	1.05	-0.03	3.17E-15	non-AML leukemia types
cg10054313	Promoter (<=1kb)	low	0.72	-0.01	3.41E-15	non-leukemia cancer types
cg05576795	Distal Intergenic	low	0.60	-0.04	2.63E-13	non-AML leukemia types
cg09181104	Distal Intergenic	low	0.67	-0.05	7.66E-15	non-leukemia cancer types
cg09747891	Promoter (<=1kb)	low	1.50	-0.11	3.00E-13	non-AML leukemia types
cg19211186	Distal Intergenic	low	1.29	-0.04	2.29E-14	cited in PubMed
cg00236601	Distal Intergenic	low	0.76	-0.03	2.73E-15	non-leukemia cancer types
cg01920182	Promoter (<=1kb)	low	0.70	-0.16	5.77E-15	non-AML leukemia types
cg17154313	Promoter (<=1kb)	low	1.15	-0.03	3.66E-15	non-leukemia cancer types
cg14403642	Other Intron	low	0.76	-0.03	2.73E-15	non-leukemia cancer types
cg19843449	Promoter (<=1kb)	low	0.61	-0.06	7.38E-13	non-leukemia cancer types
cg14161159	Promoter (1-2kb)	low	0.82	-0.30	6.54E-16	cited in PubMed
cg01483518	Promoter (<=1kb)	low	1.50	-0.06	7.66E-15	cited in PubMed
cg03573068	Promoter (<=1kb)	low	1.62	-0.40	3.00E-15	cited in AML
cg10020934	Promoter (<=1kb)	low	0.75	-0.05	5.95E-15	non-leukemia cancer types
cg03465652	Other Intron	low	0.62	-0.34	3.00E-15	cited in AML
cg13144594	Promoter (1-2kb)	low	1.33	-0.08	3.18E-22	cited in AML
cg08109505	Promoter (<=1kb)	low	0.87	-0.03	3.66E-15	non-leukemia cancer types
cg13540805	Distal Intergenic	low	0.72	-0.06	3.43E-15	never cited

CpG sites	CpG sites location	status	Ratio	delta beta	*p-value*	Bibliographic analysis
cg19707503	Other Exon	low	1.24	-0.04	6.58E-15	non-AML leukemia types
cg22179256	Other Intron	low	1.31	-0.04	7.90E-15	non-AML leukemia types
cg17529745	Other Intron	low	1.59	-0.04	3.75E-15	cited in AML
cg22549339	Distal Intergenic	low	0.80	-0.07	1.43E-14	non-leukemia cancer types
cg00615654	Other Intron	low	0.75	-0.04	5.95E-15	non-AML leukemia types
cg18547838	Other Intron	low	1.56	-0.05	2.96E-14	cited in AML
cg02027010	Promoter (<=1kb)	low	0.70	-0.01	5.73E-15	cited in AML
cg07782808	Distal Intergenic	low	0.79	-0.06	2.26E-15	cited in PubMed
cg01100703	Other Exon	low	1.37	-0.03	9.82E-15	non-leukemia cancer types
cg08907257	Other Exon	low	0.65	-0.03	6.00E-15	cited in AML
cg22675150	Promoter (<=1kb)	low	1.18	-0.03	2.64E-15	non-leukemia cancer types
cg03499905	Other Intron	low	1.31	-0.06	7.90E-15	non-AML leukemia types
cg06750076	Promoter (1-2kb)	low	0.65	-0.05	6.01E-15	non-leukemia cancer types
cg25140133	Distal Intergenic	low	1.61	-0.07	8.39E-15	never cited
cg03256601	Other Intron	low	1.19	-0.02	1.23E-14	non-leukemia cancer types
cg19917720	1st Intron	low	0.76	-0.06	2.73E-15	non-leukemia cancer types
cg22264813	Other Intron	low	0.93	-0.03	2.21E-15	non-leukemia cancer types
cg04588710	Promoter (<=1kb)	low	0.78	-0.21	1.68E-15	never cited
cg12060838	1st Intron	low	0.87	-0.04	3.66E-15	non-leukemia cancer types
cg25789216	Promoter (<=1kb)	low	1.26	0.00	1.02E-15	cited in PubMed
cg04476531	Other Intron	low	0.83	-0.22	4.16E-15	non-AML leukemia types
cg16025492	Distal Intergenic	low	0.68	-0.05	9.82E-15	non-leukemia cancer types
cg07903153	Promoter (<=1kb)	low	1.32	-0.04	1.26E-15	cited in AML
cg24913110	Distal Intergenic	low	1.15	-0.07	3.66E-15	non-leukemia cancer types
cg01165355	Distal Intergenic	low	0.80	-0.09	3.09E-14	non-leukemia cancer types
cg07745344	Distal Intergenic	low	1.22	-0.04	1.94E-14	cited in AML
cg05919312	Promoter (<=1kb)	low	1.52	-0.04	1.69E-14	non-leukemia cancer types
cg03100044	Promoter (<=1kb)	low	0.83	-0.05	1.92E-15	non-AML leukemia types
cg01393841	Other Intron	low	0.63	-0.04	1.05E-14	non-leukemia cancer types
cg21624165	Promoter (<=1kb)	low	1.40	-0.12	3.79E-24	non-leukemia cancer types
cg06810134	Promoter (2-3kb)	low	1.33	-0.03	5.94E-15	cited in AML

CpG sites	CpG sites location	status	Ratio	delta beta	*p-value*	Bibliographic analysis
cg04743859	Promoter (<=1kb)	low	1.23	-0.04	1.41E-15	non-AML leukemia types
cg04841371	Promoter (1-2kb)	low	0.67	-0.09	3.47E-15	non-leukemia cancer types
cg24893364	Promoter (<=1kb)	low	1.47	-0.02	1.57E-15	non-leukemia cancer types
cg15466245	Other Intron	low	1.50	-0.03	7.66E-15	non-AML leukemia types
cg20584157	Other Intron	low	0.90	-0.08	1.55E-14	non-leukemia cancer types
cg21497236	3' UTR	low	1.21	-0.04	1.93E-15	cited in PubMed
cg03033996	Promoter (2-3kb)	low	1.00	-0.04	6.69E-15	non-leukemia cancer types
cg21986035	Distal Intergenic	low	1.18	-0.04	1.23E-15	never cited
cg18770739	Promoter (<=1kb)	low	1.39	-0.08	3.43E-15	cited in PubMed
cg19472254	Other Exon	low	0.81	-0.03	3.05E-15	non-leukemia cancer types
cg15638292	Other Intron	low	0.93	-0.21	4.76E-15	non-leukemia cancer types
cg26113962	Distal Intergenic	low	1.08	-0.05	4.76E-15	non-leukemia cancer types
cg02917889	Other Intron	low	0.87	-0.05	2.36E-13	non-AML leukemia types
cg14779404	Other Intron	low	1.25	-0.05	1.43E-14	cited in AML
cg07394259	Other Intron	low	1.50	-0.08	4.79E-14	non-leukemia cancer types
cg06201219	3' UTR	low	0.87	-0.04	3.66E-15	cited in AML
cg16912319	Other Intron	low	1.58	-0.05	1.05E-14	never cited
cg09723488	Promoter (1-2kb)	low	1.39	-0.07	3.43E-15	non-AML leukemia types
cg13710542	Promoter (<=1kb)	low	1.12	-0.05	1.11E-15	non-leukemia cancer types
cg17377797	Promoter (<=1kb)	low	0.69	-0.06	1.27E-14	non-leukemia cancer types
cg10096321	Other Exon	low	0.70	-0.03	5.76E-15	cited in AML
cg18499321	5' UTR	low	1.48	-0.04	2.17E-14	cited in PubMed
cg06269928	Distal Intergenic	low	1.03	-0.03	9.72E-14	cited in AML
cg16999602	Promoter (<=1kb)	low	0.85	-0.06	1.23E-15	non-leukemia cancer types
cg02167753	Distal Intergenic	low	0.70	-0.08	7.93E-14	non-leukemia cancer types
cg14061609	Distal Intergenic	low	1.63	-0.05	1.17E-13	non-AML leukemia types
cg22348356	1st Intron	low	0.66	-0.04	2.72E-15	cited in AML
cg24655336	3' UTR	low	0.78	-0.03	1.06E-14	non-leukemia cancer types
cg02546490	Promoter (<=1kb)	low	0.85	-0.04	2.65E-15	non-AML leukemia types
cg26057765	Distal Intergenic	low	0.95	-0.04	3.17E-15	non-leukemia cancer types
cg27260984	3' UTR	low	1.52	-0.06	1.69E-14	non-leukemia cancer types
cg25368560	1st Intron	low	0.84	-0.07	1.23E-14	non-leukemia cancer types

CpG sites	CpG sites location	status	Ratio	delta beta	*p-value*	Bibliographic analysis
cg05719742	Distal Intergenic	low	0.69	-0.03	4.46E-15	cited in PubMed
cg21785145	Promoter (2-3kb)	low	1.27	-0.04	4.88E-15	cited in AML
cg04622024	Other Exon	low	0.82	-0.30	6.01E-26	non-AML leukemia types
cg20635409	Distal Intergenic	low	0.75	-0.33	9.49E-16	non-AML leukemia types
cg10168419	Distal Intergenic	low	1.38	-0.03	1.57E-15	cited in PubMed
cg03705718	Promoter (<=1kb)	low	0.79	-0.04	4.88E-15	non-leukemia cancer types
cg10503007	Downstream (<=300)	low	1.15	-0.09	2.36E-13	non-AML leukemia types
cg00574639	Other Intron	low	1.23	-0.06	4.19E-14	non-leukemia cancer types
cg12622273	Promoter (<=1kb)	low	0.78	-0.04	1.68E-15	non-leukemia cancer types
cg03717414	Other Exon	low	0.77	-0.04	7.89E-15	non-AML leukemia types
cg26082023	Promoter (2-3kb)	low	1.05	-0.04	6.90E-16	cited in AML
cg09664492	Promoter (<=1kb)	low	0.69	-0.05	4.46E-15	non-leukemia cancer types
cg07219227	Distal Intergenic	low	0.75	-0.24	9.49E-16	non-AML leukemia types
cg00372692	Promoter (1-2kb)	low	1.49	-0.06	3.47E-15	cited in AML
cg27118986	Promoter (<=1kb)	low	1.63	-0.05	1.87E-14	cited in PubMed
cg14592830	Distal Intergenic	low	1.61	-0.03	5.24E-14	non-AML leukemia types
cg10721490	Promoter (<=1kb)	low	0.91	-0.01	3.32E-15	non-leukemia cancer types
cg24934400	Distal Intergenic	low	1.62	-0.52	3.00E-15	cited in AML
cg04235768	Promoter (<=1kb)	low	0.82	-0.37	6.54E-16	non-leukemia cancer types
cg14246940	Other Intron	low	0.77	-0.09	4.99E-14	non-AML leukemia types
cg24768463	Promoter (<=1kb)	low	0.69	-0.04	9.10E-24	non-AML leukemia types
cg10588720	Distal Intergenic	low	1.37	-0.06	9.83E-15	non-leukemia cancer types
cg20233228	Promoter (2-3kb)	low	1.26	-0.05	2.25E-15	non-AML leukemia types
cg02054568	Promoter (<=1kb)	low	1.10	-0.14	1.56E-15	non-leukemia cancer types
cg00966557	Other Intron	low	1.12	-0.05	1.11E-15	cited in AML
cg16866892	Other Intron	low	0.89	-0.06	1.11E-15	non-AML leukemia types
cg25940557	Promoter (1-2kb)	low	1.42	-0.04	2.62E-15	cited in PubMed
cg22995904	Promoter (<=1kb)	low	1.50	-0.05	7.65E-15	non-leukemia cancer types

CpG sites	CpG sites location	status	Ratio	delta beta	*p-value*	Bibliographic analysis
cg12631713	Other Exon	low	1.61	-0.22	8.38E-15	non-leukemia cancer types
cg05808319	Distal Intergenic	low	1.17	-0.01	3.64E-14	cited in AML
cg19864941	Other Exon	low	1.64	-0.03	6.69E-15	non-leukemia cancer types
cg17188169	Promoter (<=1kb)	low	0.61	-0.10	7.38E-13	cited in AML
cg00291877	Promoter (<=1kb)	low	0.98	-0.01	2.13E-15	non-AML leukemia types
cg24312874	Distal Intergenic	low	1.19	-0.12	1.23E-14	non-leukemia cancer types
cg02920178	Promoter (<=1kb)	low	1.05	-0.04	1.48E-15	cited in AML
cg07501052	1st Intron	low	0.77	-0.03	3.64E-15	non-leukemia cancer types
cg08400962	Promoter (<=1kb)	low	0.75	-0.39	9.49E-16	non-leukemia cancer types
cg12305870	5' UTR	low	1.18	-0.03	1.23E-15	non-AML leukemia types
cg02633600	Distal Intergenic	low	0.70	-0.04	7.92E-14	non-leukemia cancer types
cg10988368	Promoter (1-2kb)	low	0.65	-0.04	6.00E-15	non-AML leukemia types
cg14538055	Promoter (<=1kb)	low	1.59	-0.01	3.72E-15	cited in AML
cg17923401	Promoter (1-2kb)	low	0.73	-0.11	4.51E-15	cited in AML
cg21291449	Promoter (<=1kb)	low	0.90	-0.06	7.14E-14	non-leukemia cancer types
cg19201068	Distal Intergenic	low	0.87	-0.05	1.70E-15	cited in AML
cg04274356	Distal Intergenic	low	0.95	-0.07	6.80E-15	non-leukemia cancer types
cg24258108	1st Intron	low	0.76	-0.05	2.73E-15	cited in AML
cg24645896	Promoter (<=1kb)	low	1.05	-0.06	6.91E-16	cited in AML
cg10052687	Promoter (2-3kb)	low	1.53	-0.25	6.01E-15	non-AML leukemia types
cg07395930	Promoter (2-3kb)	low	1.10	-0.03	1.56E-15	non-AML leukemia types
cg02471751	Promoter (1-2kb)	low	1.13	-0.04	2.38E-15	non-AML leukemia types
cg05824973	3' UTR	low	0.85	-0.16	1.23E-15	non-leukemia cancer types
cg04471045	Other Intron	low	0.72	-0.03	3.43E-15	cited in AML
cg20715438	Other Intron	low	0.89	-0.09	2.75E-24	non-leukemia cancer types
cg17891088	Promoter (<=1kb)	low	1.32	-0.05	1.26E-15	non-leukemia cancer types
cg18077580	Promoter (1-2kb)	low	1.03	-0.03	9.82E-15	cited in AML
cg14564144	Promoter (1-2kb)	low	1.26	-0.05	2.25E-15	non-leukemia cancer types
cg27174861	Other Exon	low	0.71	-0.05	2.63E-15	non-leukemia cancer types

CpG sites	CpG sites location	status	Ratio	delta beta	*p-value*	Bibliographic analysis
cg13337064	Promoter (<=1kb)	low	0.68	-0.38	1.58E-15	non-leukemia cancer types
cg17614506	Promoter (1-2kb)	low	0.79	-0.13	5.36E-25	non-leukemia cancer types
cg25042430	Promoter (1-2kb)	low	0.85	-0.34	5.71E-16	non-leukemia cancer types
cg06676233	Promoter (<=1kb)	low	1.24	-0.02	3.04E-15	cited in AML
cg17453252	Other Intron	low	0.82	-0.26	6.54E-16	non-AML leukemia types
cg01737592	Promoter (<=1kb)	low	1.36	-0.04	4.50E-15	never cited
cg01856384	Distal Intergenic	low	0.65	-0.15	1.33E-14	cited in AML
cg15261751	Distal Intergenic	low	1.18	-0.05	5.70E-15	non-AML leukemia types
cg12459514	Other Intron	low	0.71	-0.03	7.51E-15	non-leukemia cancer types
cg13944644	Other Intron	low	1.29	-0.06	2.30E-14	non-AML leukemia types
cg11647651	Promoter (<=1kb)	low	1.15	0.00	1.68E-15	cited in AML
cg18854169	Promoter (1-2kb)	low	1.43	-0.09	5.78E-15	non-leukemia cancer types
cg20774846	Promoter (<=1kb)	low	1.41	-0.35	1.20E-15	non-AML leukemia types
cg05246900	Promoter (1-2kb)	low	1.15	-0.05	3.66E-15	cited in AML
cg16010207	Promoter (1-2kb)	low	1.43	-0.07	5.77E-15	non-leukemia cancer types
cg05935961	Distal Intergenic	low	1.05	-0.06	3.17E-15	cited in AML
cg09263146	Other Exon	low	1.07	-0.04	2.22E-15	non-leukemia cancer types
cg07961456	Other Intron	low	1.02	-0.03	9.98E-16	cited in PubMed
cg08229532	Promoter (<=1kb)	high	0.65	-0.28	2.14E-15	non-AML leukemia types
cg07795968	Promoter (1-2kb)	high	0.82	-0.47	6.01E-26	non-leukemia cancer types
cg05004118	Promoter (<=1kb)	high	1.56	-0.01	4.67E-15	non-AML leukemia types
cg02303801	Distal Intergenic	high	1.63	-0.16	3.61E-22	non-leukemia cancer types
cg17465930	Promoter (<=1kb)	high	0.79	-0.01	4.85E-15	cited in AML
cg12346491	Distal Intergenic	high	1.10	-0.25	1.31E-24	cited in AML
cg10327067	Distal Intergenic	high	0.60	-0.31	1.50E-14	non-AML leukemia types
cg02309627	Distal Intergenic	high	1.23	-0.01	6.51E-16	cited in PubMed
cg08076125	Promoter (<=1kb)	high	0.71	-0.46	1.20E-15	non-AML leukemia types
cg01229787	Distal Intergenic	high	0.72	-0.23	4.70E-14	cited in AML

CpG sites	CpG sites location	status	Ratio	delta beta	*p-value*	Bibliographic analysis
cg23698269	Promoter (1-2kb)	high	1.07	-0.03	2.22E-15	cited in AML
cg01319581	Promoter (<=1kb)	high	0.91	-0.06	1.56E-15	non-leukemia cancer types
cg15112395	Promoter (<=1kb)	high	1.41	-0.01	1.63E-14	never cited
cg14686309	Promoter (<=1kb)	high	0.82	-0.01	8.93E-15	non-leukemia cancer types
cg21234506	Promoter (<=1kb)	high	1.41	-0.56	1.20E-15	cited in AML
cg00459795	Promoter (<=1kb)	high	1.08	0.00	4.71E-15	never cited
cg07567973	Promoter (<=1kb)	high	0.63	0.00	1.03E-14	non-leukemia cancer types
cg15736743	Other Intron	high	1.02	-0.37	3.85E-26	non-leukemia cancer types
cg10402417	Promoter (<=1kb)	high	0.76	-0.03	1.72E-14	cited in AML
cg21793948	Promoter (1-2kb)	high	1.65	0.00	4.10E-14	cited in AML
cg17216243	Distal Intergenic	high	0.62	-0.47	3.00E-15	cited in AML
cg25542319	1st Intron	high	1.41	-0.46	1.20E-15	cited in AML
cg18279337	Promoter (<=1kb)	high	0.83	-0.03	7.89E-18	non-leukemia cancer types
cg00873517	1st Intron	high	0.88	-0.13	1.57E-17	non-leukemia cancer types
cg06422694	Distal Intergenic	high	0.71	-0.37	1.20E-15	cited in AML
cg09365677	Other Intron	high	1.64	-0.01	6.68E-15	non-leukemia cancer types
cg04003903	Other Intron	high	1.41	-0.23	1.20E-15	cited in AML
cg21761639	Distal Intergenic	high	1.47	-0.45	1.58E-15	never cited
cg01692379	Promoter (<=1kb)	high	0.93	-0.35	4.82E-16	non-leukemia cancer types
cg12843489	Distal Intergenic	high	0.93	-0.41	4.82E-16	non-leukemia cancer types
cg22698028	Other Intron	high	1.39	-0.07	4.70E-14	non-AML leukemia types
cg26521139	Other Intron	high	0.62	-0.44	3.00E-15	non-AML leukemia types
cg01260103	Promoter (<=1kb)	high	0.67	0.00	3.38E-15	cited in AML
cg04605617	Promoter (<=1kb)	high	1.46	-0.30	4.47E-15	non-leukemia cancer types
cg13517138	Promoter (<=1kb)	high	1.49	0.00	3.39E-15	cited in AML
cg15590007	Promoter (<=1kb)	high	1.54	-0.44	2.14E-15	cited in AML
cg25639084	Distal Intergenic	high	1.12	-0.53	5.16E-16	non-AML leukemia types
cg15262954	Promoter (<=1kb)	high	1.05	-0.01	6.67E-14	cited in AML

CpG sites	CpG sites location	status	Ratio	delta beta	*p-value*	Bibliographic analysis
cg02944084	Promoter (2-3kb)	high	0.68	-0.41	1.58E-15	non-leukemia cancer types
cg07020327	Promoter (<=1kb)	high	1.23	-0.01	6.51E-16	cited in AML
cg26294217	Promoter (<=1kb)	high	0.67	-0.01	3.44E-15	cited in AML
cg11460820	Promoter (<=1kb)	high	1.21	0.00	1.88E-15	cited in AML
cg08999807	Promoter (<=1kb)	high	1.58	-0.01	6.55E-14	non-leukemia cancer types
cg03408904	Promoter (<=1kb)	high	0.68	-0.43	1.58E-15	non-leukemia cancer types
cg01529538	Promoter (<=1kb)	high	1.22	0.00	8.83E-15	non-leukemia cancer types
cg23195687	Distal Intergenic	high	1.54	-0.51	2.14E-15	never cited
cg07380021	Promoter (1-2kb)	high	0.81	-0.12	1.41E-15	non-AML leukemia types
cg03074946	Promoter (<=1kb)	high	1.31	-0.10	7.91E-15	cited in AML
cg06623385	Promoter (<=1kb)	high	1.00	-0.01	1.45E-15	non-leukemia cancer types
cg09277256	Distal Intergenic	high	1.20	-0.08	8.93E-16	never cited
cg01617933	Other Intron	high	1.30	-0.05	3.64E-15	non-AML leukemia types
cg16315582	Promoter (<=1kb)	high	0.74	-0.02	2.82E-14	cited in AML
cg22158547	1st Intron	low	1.59	-0.16	2.35E-14	non-AML leukemia types
cg21101386	Promoter (<=1kb)	high	1.51	-0.05	2.72E-15	non-leukemia cancer types
cg20079335	Promoter (<=1kb)	low	0.72	-0.11	3.43E-15	non-AML leukemia types
cg21304488	Downstream (<=300)	low	1.62	-0.07	3.29E-13	cited in AML
cg08302300	Other Intron	high	1.43	-0.08	5.78E-15	non-AML leukemia types
cg20960833	Distal Intergenic	low	1.34	-0.19	9.49E-16	cited in AML
cg15756928	3' UTR	low	1.17	-0.05	9.23E-23	non-leukemia cancer types
cg09044219	Promoter (<=1kb)	high	0.82	-0.01	1.93E-14	cited in PubMed
cg03196437	Promoter (<=1kb)	low	0.85	-0.03	1.23E-15	non-leukemia cancer types
cg01118451	Promoter (<=1kb)	low	1.40	0.00	7.38E-15	non-leukemia cancer types
cg13018793	Distal Intergenic	low	0.68	-0.40	1.58E-15	cited in PubMed
cg07615497	Distal Intergenic	high	1.02	-0.45	4.66E-16	non-leukemia cancer types
cg16851924	Promoter (<=1kb)	high	0.95	-0.01	1.44E-13	non-leukemia cancer types

CpG sites	CpG sites location	status	Ratio	delta beta	*p-value*	Bibliographic analysis
cg11140606	Promoter (<=1kb)	low	1.26	0.00	2.23E-15	non-leukemia cancer types
cg02558162	Promoter (1-2kb)	low	1.61	-0.08	9.23E-13	cited in AML
cg09950208	Distal Intergenic	low	0.65	-0.41	2.14E-15	cited in AML
cg00073460	Promoter (<=1kb)	high	0.89	-0.49	4.40E-26	non-leukemia cancer types
cg19384717	Distal Intergenic	low	0.67	-0.04	7.67E-15	cited in AML
cg01987224	Promoter (<=1kb)	low	1.48	-0.07	6.23E-22	non-leukemia cancer types
cg11352369	Promoter (<=1kb)	low	1.27	-0.04	4.88E-15	non-leukemia cancer types
cg12439423	Promoter (<=1kb)	low	0.79	-0.04	4.88E-15	cited in AML
cg01023703	Other Intron	high	0.82	-0.35	6.01E-26	non-leukemia cancer types
cg23222472	Distal Intergenic	high	0.76	-0.16	1.72E-14	never cited
cg04560098	Promoter (<=1kb)	low	0.63	-0.16	1.05E-14	non-leukemia cancer types
cg09633881	Promoter (<=1kb)	high	0.93	-0.24	4.82E-16	cited in AML
cg25919979	Other Intron	low	0.63	-0.06	3.76E-15	cited in AML