

RUNX1 mutations in cytogenetically normal acute myeloid leukemia are associated with a poor prognosis and up-regulation of lymphoid genes

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Online Supplementary Table S1. Primers targeting the coding exons of RUNX1.

cDNA sequence: uc010gmu.1 (NM_001754.4)

Genomic sequence: hg18_chr21:35080967-35344437_rev

NAME	LEFT PRIMER	NAME	RIGHT PRIMER	PRODUCT SIZE
RUNX1-exon 2F	GTCTTGTTTTTCGCTCCG	RUNX1-exon 2R	CATTTTCATTACAGGCAAAGCTG	197
RUNX1-exon 3F	AACCACGTGCATAAGGAACAG	RUNX1-exon 3R	GCAGAAACAGCCTTAATTATTGG	363
RUNX1-exon 4F	TGGTAGGAGCTGTTGCAGG	RUNX1-exon 4R	CATCCCAAGCTAGGAAGACC	459
RUNX1-exon 5F	TCACTACACAAATGCCCTAAAAG	RUNX1-exon 5R	TTGAAATGTGGGTTTGTTC	292
RUNX1-exon 6F	AGATATGTTTCAGGCCACCAAC	RUNX1-exon 6R	TCTGAGACATGGTCCCTGAG	243
RUNX1-exon 7F	AAGAAAAGCCCAAGTTTTAGG	RUNX1-exon 7R	AGTTGGTCTGGGAAGGTGTG	387
RUNX1-exon 8F	GAACAAGGGCCACTCATTTTC	RUNX1-exon 8R	TGGACCTTCCACCCAG	301
RUNX1-exon 9F	CTCCGCAACCTCCTACTCAC	RUNX1-exon 9Ra	CCCACCATGGAGAACTGGTA	342
RUNX1_exon_9Fa	CACGCGCTACCACACCTAC	RUNX1-exon_9R	CCTGACCTACAGCGAGATCC	484

Online Supplementary Table S2. List of probe sets differentially expressed in *RUNX1*-mutated (n=15) versus *RUNX1*-wild-type (n=26) CN-AML patients. The analysis was restricted to *NPM1*-wild-type patients. 85 probe sets out of 17109 were significant (q value<0.05). The P value of a global test for difference between the two groups was 0.03.

Microarray probe set	Gene symbol	Gene name	Fold change: <i>RUNX1</i> -mutated vs. <i>RUNX1</i> -wild type	q value
GC04M057210_at	HOPX	HOP homeobox	4,10	0,0079
GC10P098054_at	DNTT	deoxynucleotidyltransferase, terminal	3,38	0,0231
GC08P026491_at	DPYSL2	dihydropyrimidinase-like 2	2,71	0,0122
GC01P026516_at	CD52	CD52 molecule	2,67	0,0114
GC14P105461_at	KIAA0125	KIAA0125	2,65	0,0079
GC01P078858_at	IFI44L	interferon-induced protein 44-like	2,63	0,0301
GC10M097941_at	BLNK	B-cell linker	2,58	0,0151
GC06M006089_at	F13A1	coagulation factor XIII, A1 polypeptide	2,51	0,0182
GC07M047281_at	TNS3	tensin 3	2,46	0,0079
GC12P092466_at	SOC52	suppressor of cytokine signaling 2	2,40	0,0127
GC04M122868_at	ANXA5	annexin A5	2,39	0,0315
GC05P135392_at	TGFB1	transforming growth factor, beta-induced, 68kDa	2,29	0,0273
GC10M015294_at	FAM171A1	family with sequence similarity 171, member A1	2,23	0,0079
GC21P041720_at	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	2,14	0,0278
GC08P104222_at	BAALC	brain and acute leukemia, cytoplasmic	2,14	0,0122
GC11M000602_at	IRF7	interferon regulatory factor 7	2,13	0,0231
GC07P093388_at	NGG11	guanine nucleotide binding protein (G protein), gamma 11	2,09	0,0118
GC11P000303_at	IFITM1	interferon induced transmembrane protein 1 (9-27)	2,09	0,0262
GC12M044867_at	SLC38A1	solute carrier family 38, member 1	2,08	0,0251
GC07P079602_at	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	2,07	0,0231
GC01M152220_at	RAB13	RAB13, member RAS oncogene family	2,01	0,0452
GC18M051045_at	TCF4	transcription factor 4	2,00	0,0120
GC04P110700_at	CCDC109B	coiled-coil domain containing 109B	1,99	0,0150
GC07P150015_at	GIMAP2	GTPase, IMAP family member 2	1,99	0,0164
GC03M152412_at	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	1,96	0,0216
GC04P156807_at	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	1,96	0,0153
GC03M015700_at	ANKRD28	ankyrin repeat domain 28	1,93	0,0251
GC01M089345_at	GBP2	guanylate binding protein 2, interferon-inducible	1,93	0,0158
GC07M149953_at	GIMAP6	GTPase, IMAP family member 6	1,92	0,0315
GC18M020895_at	ZNF521	zinc finger protein 521	1,91	0,0496
GC10U900364_at	LOC283070	hypothetical LOC283070	1,89	0,0153
GC15P020444_at	CYFIP1	cytoplasmic FMR1 interacting protein 1	1,87	0,0301
GC07M139370_at	PARP12	poly (ADP-ribose) polymerase family, member 12	1,84	0,0114
GC13M042358_at	EPSTI1	epithelial stromal interaction 1 (breast)	1,83	0,0496
GC01P012161_at	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	1,81	0,0493
GC06P116708_at	DSE	dermatan sulfate epimerase	1,79	0,0153
GC09M025668_at	TUSC1	tumor suppressor candidate 1	1,79	0,0150
GC02P237143_at	CXCR7	chemokine (C-X-C motif) receptor 7	1,77	0,0122
GC15P086983_at	ISG20	interferon stimulated exonuclease gene 20kDa	1,77	0,0363
GC18P040535_at	SETBP1	SET binding protein 1	1,76	0,0079
GC22P049402_at	SHANK3	SH3 and multiple ankyrin repeat domains 3	1,76	0,0150
GC02M165652_at	SCN3A	sodium channel, voltage-gated, type III, alpha subunit	1,76	0,0311
GC14M105389_at	IGHM	immunoglobulin heavy constant mu	1,75	0,0394
GC01M089290_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	1,75	0,0466
GC14M094943_at	C14orf139	chromosome 14 open reading frame 139	1,74	0,0127
GC06P032649_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	1,74	0,0420
GC05M088051_at	MEF2C	myocyte enhancer factor 2C	1,71	0,0153
GC0XP135057_at	FHL1	four and a half LIM domains 1	1,71	0,0114
GC08P030361_at	RBPMS	RNA binding protein with multiple splicing	1,70	0,0122
GC21P041655_at	MX2	myxovirus (influenza virus) resistance 2 (mouse)	1,69	0,0390
GC05M149413_at	CSF1R	colony stimulating factor 1 receptor	1,69	0,0479
GC22M026704_at	TTC28	tetratricopeptide repeat domain 28	1,69	0,0079
GC16M087468_at	CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	1,66	0,0284
GC04M025425_at	KIAA0746	KIAA0746 protein	1,64	0,0301
GC07P043764_at	BLVRA	biliverdin reductase A	1,64	0,0301
GC07M149094_at	ZNF467	zinc finger protein 467	1,64	0,0280
GC07P149842_at	GIMAP7	GTPase, IMAP family member 7	1,62	0,0311
GC04P113286_at	C4orf32	chromosome 4 open reading frame 32	1,61	0,0479
GC02M037389_at	PRKD3	protein kinase D3	1,59	0,0448
GC10P114700_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	1,59	0,0273
GC08M141737_at	PTK2	PTK2 protein tyrosine kinase 2	1,58	0,0079
GC09M138039_at	NACC2	NACC family member 2, BEN and BTB (POZ) domain containing	1,58	0,0388
GC04M140646_at	SETD7	SET domain containing (lysine methyltransferase) 7	1,57	0,0270
GC07M076779_at	PION	pigeon homolog (Drosophila)	1,57	0,0264
GC02M060589_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	1,56	0,0210
GC01P221966_at	CAPN2	calpain 2, (m/II) large subunit	1,55	0,0301
GC18P027332_at	DSG2	desmoglein 2	1,54	0,0420
GC0XM109724_at	CHRD1L	chordin-like 1	1,53	0,0401
GC02M001606_at	PXDN	peroxidasin homolog (Drosophila)	1,53	0,0374
GC07M150272_at	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	0,65	0,0420
GC12M000543_at	NINJ2	ninjurin 2	0,65	0,0231
GC16M019422_at	GDE1	glycerophosphodiester phosphodiesterase 1	0,64	0,0479
GC13M102219_at	C13orf27	chromosome 13 open reading frame 27	0,63	0,0463
GC10M119033_at	PDZD8	PDZ domain containing 8	0,60	0,0322
GC02P047425_at	EPCAM	epithelial cell adhesion molecule	0,57	0,0394
GC01P117860_at	FAM46C	family with sequence similarity 46, member C	0,56	0,0278
GC11P034417_at	CAT	catalase	0,52	0,0153
GC12M115961_at	TESC	tescalcin	0,52	0,0122
GC03P112743_at	CD96	CD96 molecule	0,52	0,0311
GC11P017255_at	NUCB2	nucleobindin 2	0,45	0,0122
GC11P065405_at	CTSW	cathepsin W	0,41	0,0114
GC14P020429_at	RNASE3	ribonuclease, RNase A family, 3 (eosinophil cationic protein)	0,37	0,0432
GC22M022239_at	IGLL1	immunoglobulin lambda-like polypeptide 1	0,36	0,0311
GC14M024112_at	CTSG	cathepsin G	0,30	0,0231
GC17M053702_at	MPO	myeloperoxidase	0,29	0,0127

Online Supplementary Table S3. Gene set enrichment analysis, identifying sets of functionally related genes that are enriched in CN-AML patients with (n=15) or without (n=26) *RUNX1* mutations.

This analysis used the curated 'canonical pathways' (c2:cp) collection of the Molecular Signatures Database, version 3.0, available online at <http://www.broadinstitute.org/gsea/msig>. Only gene sets comprising between 15 and 200 individual genes (654 of the 880 total gene sets) were included in the analysis. Gene sets were considered significant at a false discover 128 gene sets were significant: 71 were enriched in *RUNX1*-mut patients and 51 in *RUNX1*-wt patients.

A) Gene sets enriched in *RUNX1*-mut patients compared to *RUNX1*-wt

Gene Set Name	No. of Genes in Gene Set	Normalized Enrichment Score	Nominal p Value	FDR q Value
BIOCARTA_EDG1_PATHWAY	27	1,97	<.0001	0,057
BIOCARTA_BCR_PATHWAY	34	1,96	0,001	0,034
REACTOME_TOLL_LIKE_RECEPTOR_4_CASCADE	28	1,95	0,001	0,025
REACTOME_TOLL_RECEPTOR_CASCADES	83	1,94	<.0001	0,022
BIOCARTA_CALCINEURIN_PATHWAY	18	1,94	<.0001	0,018
REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEINS	15	1,94	<.0001	0,015
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	38	1,89	<.0001	0,026
REACTOME_MYD88_CASCADE	19	1,89	0,001	0,025
REACTOME_SIGNALING_BY_BMP	22	1,89	0,003	0,023
REACTOME_INNATE_IMMUNITY_SIGNALING	103	1,89	<.0001	0,021
REACTOME_BOTULINIUM_NEUROTOXICITY	17	1,88	0,002	0,019
REACTOME_TOLL_LIKE_RECEPTOR_9_CASCADE	23	1,88	<.0001	0,018
BIOCARTA_MEF2D_PATHWAY	18	1,87	0,002	0,020
KEGG_GAP_JUNCTION	84	1,86	0,0004	0,022
ST_GA12_PATHWAY	22	1,85	<.0001	0,021
REACTOME_PLATELET_ACTIVATION_TRIGGERS	56	1,85	0,0005	0,020
BIOCARTA_CXCR4_PATHWAY	24	1,84	0,002	0,023
SA_B_CELL_RECEPTOR_COMPLEXES	24	1,81	0,002	0,030
BIOCARTA_PAR1_PATHWAY	37	1,81	0,002	0,031
KEGG_TIGHT_JUNCTION	127	1,81	<.0001	0,029
BIOCARTA_VEGF_PATHWAY	28	1,80	0,003	0,029
BIOCARTA_TH1TH2_PATHWAY	18	1,79	0,002	0,031
BIOCARTA_PGC1A_PATHWAY	22	1,79	0,003	0,030
KEGG_ALLOGRAFT_REJECTION	25	1,79	0,003	0,030
BIOCARTA_BIOPEPTIDES_PATHWAY	42	1,78	0,001	0,032
BIOCARTA_CCR3_PATHWAY	23	1,78	0,004	0,032
KEGG_NOTCH_SIGNALING_PATHWAY	46	1,78	0,002	0,032
KEGG_GRAFT_VERSUS_HOST_DISEASE	23	1,77	0,002	0,032
BIOCARTA_SPPA_PATHWAY	21	1,77	0,002	0,033
REACTOME_ERK_MAPK_TARGETS	21	1,77	0,003	0,032
BIOCARTA_MYOSIN_PATHWAY	31	1,75	0,002	0,037
KEGG_DORSO_VENTRAL_AXIS_FORMATION	23	1,75	0,003	0,038
BIOCARTA_HDAC_PATHWAY	28	1,74	0,003	0,039
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	25	1,73	0,004	0,041
KEGG_LEISHMANIA_INFECTION	59	1,72	0,002	0,046
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	74	1,72	0,0004	0,045
REACTOME_THROMBIN_SIGNALING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS	25	1,71	0,006	0,047
REACTOME_PLC_BETA_MEDIATED_EVENTS	38	1,71	0,006	0,048
REACTOME_ACTIVATED_TLR4_SIGNALLING	24	1,71	0,010	0,047
BIOCARTA_AT1R_PATHWAY	32	1,71	0,005	0,047
KEGG_CHEMOKINE_SIGNALING_PATHWAY	173	1,70	<.0001	0,048
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_Glutamate_BINDING	30	1,69	0,006	0,053
KEGG_WNT_SIGNALING_PATHWAY	144	1,66	0,001	0,067
BIOCARTA_NFKB_PATHWAY	22	1,66	0,010	0,068
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	24	1,65	0,006	0,074
BIOCARTA_FCER1_PATHWAY	38	1,65	0,010	0,072
BIOCARTA_AGR_PATHWAY	35	1,65	0,009	0,071
KEGG_AXON_GUIDANCE	128	1,65	0,001	0,072
REACTOME_G_ALPHA_12_13_SIGNALLING_EVENTS	53	1,65	0,005	0,071
BIOCARTA_TOLL_PATHWAY	35	1,65	0,006	0,070
BIOCARTA_ERK5_PATHWAY	17	1,64	0,017	0,070
BIOCARTA_NTH1_PATHWAY	24	1,64	0,018	0,072
KEGG_MELANOGENESIS	97	1,64	0,002	0,071
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	74	1,64	0,002	0,070
REACTOME_CRMP5_IN_SEMA3A_SIGNALING	16	1,62	0,017	0,078
REACTOME_SEMAPHORIN_INTERACTIONS	65	1,62	0,007	0,081
REACTOME_SIGNAL_AMPLIFICATION	29	1,61	0,017	0,083
ST_WNT_BETA_CATENIN_PATHWAY	30	1,61	0,016	0,083
BIOCARTA_CDMAC_PATHWAY	16	1,61	0,022	0,084
REACTOME_TCR_SIGNALING	49	1,60	0,009	0,088
REACTOME_REGULATION_OF_LIPID_METABOLISM_BY_PEROXISOME_PROLIFERATOR_ACTIVATED_	55	1,60	0,008	0,091
REACTOME_OPIOID_SIGNALLING	81	1,59	0,005	0,090
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	25	1,59	0,021	0,091
REACTOME_AXON_GUIDANCE	158	1,59	0,001	0,092
BIOCARTA_RARRXR_PATHWAY	15	1,58	0,031	0,100
BIOCARTA_CD40_PATHWAY	15	1,57	0,034	0,100
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	20	1,57	0,031	0,099

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KEGG_TYPE_I_DIABETES_MELLITUS	29	1,57	0,018	0,098
REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_ACETYLCHOLINE	20	1,57	0,036	0,097
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	30	1,57	0,019	0,098
KEGG_LONG_TERM_DEPRESSION	66	1,57	0,011	0,099

B) Gene sets enriched in *RUNX1*-wt patients compared to *RUNX1*-mut

Gene Set Name	No. of Genes in Gene Set	Normalized Enrichment Score	Nominal <i>p</i> Value	FDR <i>q</i> Value
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	29	-2,45	<.0001	<.0001
REACTOME_DNA_REPLICATION_PRE_INITIATION	68	-2,44	<.0001	<.0001
KEGG_DNA_REPLICATION	36	-2,43	<.0001	<.0001
REACTOME_DNA_STRAND_ELONGATION	30	-2,38	<.0001	<.0001
REACTOME_G1_S_TRANSITION	90	-2,33	<.0001	0,0002
REACTOME_SYNTHESIS_OF_DNA	81	-2,31	<.0001	0,0002
REACTOME_S_PHASE	93	-2,25	<.0001	0,001
REACTOME_MITOTIC_M_M_G1_PHASES	144	-2,19	<.0001	0,001
REACTOME_M_G1_TRANSITION	54	-2,17	<.0001	0,002
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	34	-2,16	<.0001	0,002
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	30	-2,15	<.0001	0,002
REACTOME_EXTENSION_OF_TELOMERES	28	-2,11	<.0001	0,003
REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S	19	-2,11	0,001	0,003
REACTOME_G2_M_CHECKPOINTS	39	-2,09	<.0001	0,003
REACTOME_LAGGING_STRAND_SYNTHESIS	20	-2,07	0,001	0,004
REACTOME_REPAIR_SYNTHESIS_OF_PATCH_27_30_BASES_LONG_BY_DNA_POLYMERASE	15	-2,02	0,003	0,007
KEGG_CELL_CYCLE	115	-2,02	<.0001	0,007
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	56	-1,99	<.0001	0,008
BIOCARTA_MCM_PATHWAY	18	-1,99	<.0001	0,007
REACTOME_TRANSCRIPTION_COUPLED_NER	38	-1,99	0,001	0,007
REACTOME_CELL_CYCLE_CHECKPOINTS	97	-1,98	<.0001	0,008
KEGG_NUCLEOTIDE_EXCISION_REPAIR	40	-1,93	0,002	0,012
KEGG_BASE_EXCISION_REPAIR	31	-1,92	0,002	0,013
KEGG_MISMATCH_REPAIR	22	-1,87	0,003	0,021
REACTOME_ELECTRON_TRANSPORT_CHAIN	57	-1,87	<.0001	0,021
REACTOME_GLUCOSE_TRANSPORT	38	-1,86	0,002	0,022
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	28	-1,86	0,003	0,021
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	45	-1,84	0,001	0,023
BIOCARTA_MITOCHONDRIA_PATHWAY	21	-1,77	0,010	0,042
REACTOME_GLOBAL_GENOMIC_NER	30	-1,77	0,003	0,042
REACTOME_MITOTIC_PROMETAPHASE	86	-1,77	0,001	0,041
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	43	-1,75	0,001	0,048
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	31	-1,74	0,003	0,047
REACTOME_METABOLISM_OF_CARBOHYDRATES	113	-1,74	<.0001	0,048
REACTOME_REGULATION_OF_APC_ACTIVATORS_BETWEEN_G1_S_AND_EARLY_ANAPHASE	61	-1,72	0,001	0,055
KEGG_TYROSINE_METABOLISM	38	-1,70	0,007	0,062
REACTOME_TRANSPORT_OF_THE_SLBP_INDEPENDENT_MATURE_MRNA	31	-1,69	0,007	0,066
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE	40	-1,69	0,007	0,064
REACTOME_INFLUENZA_LIFE_CYCLE	85	-1,66	<.0001	0,076
REACTOME_TAT_MEDIATED_HIV1_ELONGATION_ARREST_AND_RECOVERY	27	-1,66	0,011	0,077
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	82	-1,65	0,001	0,077
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	29	-1,65	0,011	0,078
REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21	44	-1,65	0,006	0,077
REACTOME_HIV_LIFE_CYCLE	94	-1,63	0,003	0,086
REACTOME_GLYCOLYSIS	21	-1,63	0,023	0,084
REACTOME_P53_INDEPENDENT_DNA_DAMAGE_RESPONSE	36	-1,62	0,011	0,087
REACTOME_MTOR_SIGNALLING	25	-1,61	0,014	0,089
REACTOME_CDC20_PHOSPHO_APC_MEDIATED_DEGRADATION_OF_CYCLIN_A	53	-1,61	0,003	0,088
KEGG_RNA_POLYMERASE	26	-1,60	0,019	0,093
REACTOME_HIV1_TRANSCRIPTION_ELONGATION	35	-1,60	0,015	0,095
REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT	21	-1,59	0,026	0,099
REACTOME_VPR_MEDIATED_NUCLEAR_IMPORT_OF_PICS	31	-1,58	0,015	0,098
KEGG_PHENYLALANINE_METABOLISM	18	-1,58	0,032	0,097
REACTOME_IRS_RELATED_EVENTS	75	-1,58	0,004	0,096
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION	49	-1,58	0,011	0,097
REACTOME_GLUCOSE_REGULATION_OF_INSULIN_SECRETION	135	-1,58	0,000	0,096
REACTOME_FRS2MEDIATED_CASCADE	25	-1,56	0,027	0,100

Online Supplementary Figure S1. Enrichment of gene sets differentially expressed between *RUNX1*-mutated and *RUNX1*-wild-type patients.

