

## Supplemental data 1.

### Supervised analysis of $\Delta^{13+}$ versus $\Delta^{13-}$ patients.

Symbols, names, locations, GO biological processes and supervised analysis scores for the selected 67 genes.

Gene	Name	Location	Biological Process	SAM Score( <i>d</i> )
AKAP11	A kinase (PRKA) anchor protein 11	13q14.11	protein kinase cascade	-4.70686
ALG5	asparagine-linked glycosylation 5 homolog (yeast)	13q13.3	protein amino acid glycosylation	-5.96108
ANKRD10	ankyrin repeat domain 10	13q34	---	-5.98148
APRIN	androgen-induced proliferation inhibitor	13q12.3	regulation of cell proliferation	-5.10322
ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	13q34	signal transduction	-5.03077
C13orf22	chromosome 13 open reading frame 22	13q12-q14	ubiquitin-dependent protein catabolism	-6.66435
C13orf23	chromosome 13 open reading frame 23	13q13.3	---	-5.21658
CDC16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	13q34	ubiquitin cycle	-6.23328
CUL4A	cullin 4A	13q34	G1/S transition of mitotic cell cycle	-5.36472
DHPS	deoxyhypusine synthase	19p13.2-p13.1	protein biosynthesis	-4.42392
DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	13q14.1	protein folding	-4.73397
EFHA1	EF-hand domain family, member A1	13q12.11	---	-4.59565
EIF3S7	eukaryotic translation initiation factor 3, subunit 7 zeta, 66/67kDa	22q13.1	protein biosynthesis	-4.64042
ELF1	E74-like factor 1 (ets domain transcription factor)	13q13	transcription	-5.61399
ERCC5	excision repair cross-complementing rodent repair deficiency, complementation group 5	13q22 13q33	transcription-coupled nucleotide-excision repair	-5.70894
ESD	esterase D/formylglutathione hydrolase	13q14.1-q14.2	---	-6.00023
FAM48A	family with sequence similarity 48, member A	13q13.3	---	-5.23514
FAU	ribosomal protein S30	11q13	protein biosynthesis	-5.59644
FLJ10154	hypothetical protein FLJ10154	13q33.3	---	-5.5216
FLJ11305	hypothetical protein FLJ11305	13q34	---	-6.66769
FLJ12118	hypothetical protein FLJ12118	13q34	cysteinyl-tRNA aminoacylation	-4.47185
FNBP4	formin binding protein 4	11p11.2	cell adhesion	-4.62567
GLTSCR2	glioma tumor suppressor candidate region gene 2	19q13.3	---	-4.57567
GMFG	glia maturation factor, gamma	19q13.2	protein amino acid phosphorylation	-4.68745
GTF2F2	general transcription factor IIF, polypeptide 2, 30kDa	13q14	transcription	-4.46879
GTF3A	general transcription factor IIIA	13q12.3-q13.1	transcription	-5.16331
HMGB1	high-mobility group box 1	13q12	DNA unwinding during replication	-6.19893
HSMPP8	M-phase phosphoprotein, mpp8	13q12.11	chromatin assembly or disassembly	-5.16761

ITM2B	integral membrane protein 2B	13q14.3	nervous system development	-4.54652
KIAA0999	KIAA0999 protein	11q23.3	protein amino acid phosphorylation	-4.95433
KPNA3	karyopherin alpha 3 (importin alpha 4)	13q14.3	protein complex assembly	-4.6382
LBA1	lupus brain antigen 1	3p22.3	---	-4.82455
LOC143941	Similar to CDNA sequence BC021608	11q23.3	---	-4.51701
MED4	mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)	13q14.2	transcription	-4.62922
METTL3	methyltransferase like 3	14q11.1	RNA methylation	-4.42514
MRPS31	mitochondrial ribosomal protein S31	13q14.11	---	-5.96495
MYCBP2	MYC binding protein 2	13q22	transcription	-6.40204
NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	13q14.2	---	-5.28421
NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	13q14	RNA processing	-5.36429
PARP4	poly (ADP-ribose) polymerase family, member 4	13q11	DNA repair	-5.01428
PDLIM1	PDZ and LIM domain 1 (elfin)	10q22-q26.3	response to oxidative stress	-4.72994
PDLIM2	PDZ and LIM domain 2 (mystique)	8p21.2	---	-4.67977
PFAAP5	phosphonoformate immuno-associated protein 5	13q12-q13	---	-4.78301
PHF11	PHD finger protein 11	13q14.2	regulation of transcription, DNA-dependent	-7.53685
POLR1D	polymerase (RNA) I polypeptide D, 16kDa	13q12.2	transcription	-8.35806
PORIMIN	pro-oncosis receptor inducing membrane injury gene	11q22.1	---	-4.81275
PSPC1	paraspeckle component 1	13q12.11	nuclear mRNA splicing, via spliceosome	-4.68219
RANBP5	RAN binding protein 5	13q32.2	protein import into nucleus, docking	-6.2302
RFP2	ret finger protein 2	13q14	cell cycle	-5.85865
RNF6	ring finger protein (C3H2C3 type) 6	13q12.2	protein ubiquitination	-5.27923
RPL21	ribosomal protein L21	13q12.2	protein biosynthesis	-7.88347
RPL22	ribosomal protein L22	1p36.3-p36.2	protein biosynthesis	-4.49204
RPL24	ribosomal protein L24 /// ribosomal protein L24	3q12	protein biosynthesis	-4.47322
RPL31	ribosomal protein L31	2q11.2	protein biosynthesis	-5.47384
RPL36AL	ribosomal protein L36a-like	14q21	protein biosynthesis	-4.57951
RPLP2	ribosomal protein, large, P2	11p15.5-p15.4	protein biosynthesis	-4.49725
RPS2	ribosomal protein S2	16p13.3	protein biosynthesis	-4.91708
RPS29	ribosomal protein S29	14q	protein biosynthesis	-4.89471
SAP18	sin3-associated polypeptide, 18kDa	13q12.11	transcription	-6.80756
SLC35F2	solute carrier family 35, member F2	11q22.3	---	-4.4704
STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	13q31.2-q32.3	protein amino acid phosphorylation	-5.81955
TGDS	TDP-glucose 4,6-dehydratase	13q32.1	nucleotide-sugar metabolism	-5.07744
TM2D3	TM2 domain containing 3	15q26.3	---	-4.42628

TPP2	tripeptidyl peptidase II	13q32-q33	proteolysis	-5.57549
TPT1	tumor protein, translationally-controlled 1	13q12-q14	---	-5.28998
TUBGCP3	tubulin, gamma complex associated protein 3	13q34	microtubule nucleation	-4.46882
UCHL3	ubiquitin carboxyl-terminal esterase L3	13q22.2	ubiquitin- dependent protein catabolism	-8.41433