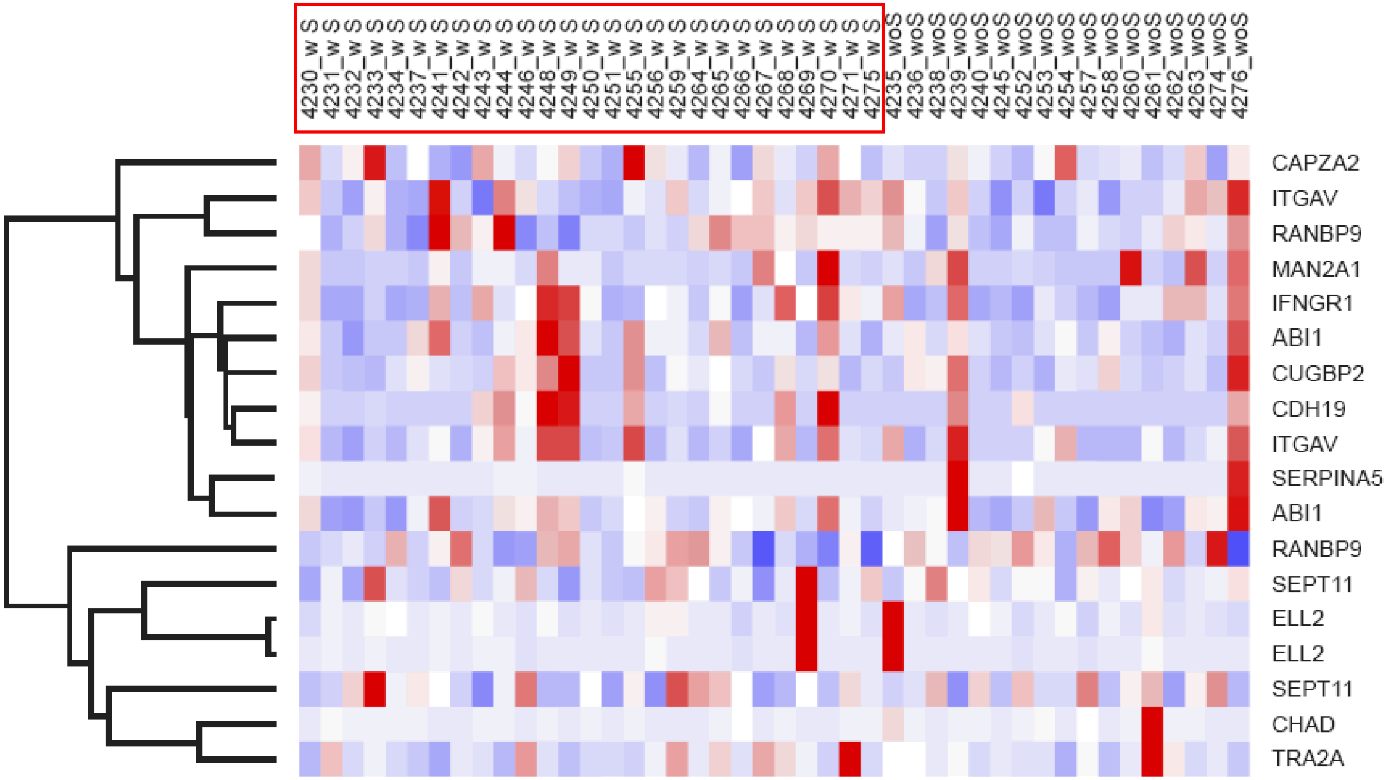
Supplementary Figure 1: The NF1-associated gene expression signature is specific to pilocytic astrocytoma. Heat map based on the top candidate genes differentially expressed in NF1-associated pilocytic astrocytomas with positive calls in a malignant peripheral nerve sheath tumor (MPNST) dataset. The genes are not differentially expressed in NF1-associated (red box) compared to sporadic MPNSTs.

Type of file: figure
Label: 8
Filename: Rays Supplementary figure 1.ppt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ITGAV
RANBP9
MAN2A1
IFNGR1
ABI1
CUGBP2
CDH19
ITGAV
SERPINA5
ABI1
RANBP9
SEPT11
ELL2
ELL2
SEPT11
CHAD
TRA2A

Type of file: table
Label: 5
Filename: Rays Supplementary Table

Supplementary Table 1. Transcripts with False Discovery Rate Less than 1

Transcript	UniGene ID	Gene Title	Gene Symbol	Fold Change (NF1-associated/ sporadic)
242232_at	Hs.497575	SLIT-ROBO Rho GTPase activating protein 2	SRGAP2	5.28
244357_at	Hs.15200	Stromal membrane-associated protein 1-like	SMAP1L	3.84
240665_at	Hs.309288	CUG triplet repeat, RNA binding protein 2	CUGBP2	3.43
232568_at	---	hypothetical protein MGC24103	MGC24103	3.41
242903_at	Hs.520414	interferon gamma receptor 1	IFNGR1	3.41
244358_at	---	---	---	3.17
1556323_at	Hs.309288	CUG triplet repeat, RNA binding protein 2	CUGBP2	3.03
233867_at	Hs.610960	CDNA FLJ20112 fis, clone COL05405	---	3.01
237018_at	Hs.459211	A kinase (PRKA) anchor protein 13	AKAP13	2.93
232670_at	Hs.636495	CDNA FLJ11735 fis, clone HEMBA1005447	---	2.91
233036_at	Hs.435309	Basonuclin 2	BNC2	2.87
242268_at	Hs.309288	CUG triplet repeat, RNA binding protein 2	CUGBP2	2.85
1569477_at	Hs.591328	Forkhead box O3A	FOXO3A	2.80
236781_at	Hs.544636	Ankyrin repeat and sterile alpha motif domain containing 1A	ANKS1A	2.80
240038_at	Hs.592742	Elongation factor, RNA polymerase II, 2	ELL2	2.74
231109_at	Hs.309288	CUG triplet repeat, RNA binding protein 2	CUGBP2	2.71
244508_at	Hs.191346	Septin 7	SEPT7	2.68
206140_at	Hs.445265	LIM homeobox 2	LHX2	2.68
242143_at	Hs.306242	RAN binding protein 9	RANBP9	2.67
214405_at	Hs.309288	CUG triplet repeat, RNA binding protein 2	CUGBP2	2.64
243450_at	Hs.459211	A kinase (PRKA) anchor protein 13	AKAP13	2.61
237849_at	Hs.102788	Mannosidase, alpha, class 1A, member 1	MAN1A1	2.60
219024_at	Hs.287830	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	PLEKHA1	2.60
205105_at	Hs.432822	mannosidase, alpha, class 2A, member 1	MAN2A1	2.57
233674_at	Hs.591328	Forkhead box O3A	FOXO3A	2.56
215574_at	Hs.591973	Hypothetical protein LOC646089	LOC646089	2.48
240865_at	---	---	---	2.46
243271_at	Hs.489118	Sterile alpha motif domain containing 9-like	SAMD9L	2.45
1560926_at	Hs.431092	Protein phosphatase 4, regulatory subunit 2	PPP4R2	2.43
237456_at	Hs.7910	RING1 and YY1 binding protein	RYBP	2.41
230892_at	Hs.39429	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	DERA	2.38
242320_at	Hs.591328	Forkhead box O3A	FOXO3A	2.32
237262_at	Hs.594689	Full length insert cDNA clone ZE05E03	---	2.30
216022_at	Hs.594024	Transcribed locus	---	2.30
241769_at	Hs.436873	Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	ITGAV	2.26
237026_at	Hs.38621	Sorbin and SH3 domain containing 1	SORBS1	2.26
238563_at	Hs.508148	Abl-interactor 1	ABI1	2.25
236512_at	Hs.591336	Sestrin 1	SESN1	2.22
240351_at	Hs.486228	Hypothetical protein LOC643749	LOC643749	2.20
230071_at	Hs.128199	Septin 11	SEPT11	2.19
243739_at	Hs.306242	RAN binding protein 9	RANBP9	2.18
220612_at	---	hypothetical protein LOC643328	LOC64332	2.18

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218876_at	Hs.534458	brain specific protein /// brain specific protein	CGI-38	2.12
213593_s_at	Hs.445652	transformer-2 alpha	TRA2A	2.11
207002_s_at	Hs.444975	pleiomorphic adenoma gene-like 1	PLAGL1	2.09
215147_at	Hs.309288	CUG triplet repeat, RNA binding protein 2	CUGBP2	2.07
240146_at	Hs.446123	Capping protein (actin filament) muscle Z-line, alpha 2	CAPZA2	2.04
232890_at	Hs.509499	Chromosome 14 open reading frame 135	C14orf135	2.04
240141_at	Hs.418198	PAP associated domain containing 4	PAPD4	2.03
205931_s_at	Hs.437075	cAMP responsive element binding protein 5	CREB5	2.02
229593_at	Hs.586218	H2A histone family, member Y	H2AFY	2.02
232929_at	Hs.122417	Zinc finger and BTB domain containing 20	ZBTB20	2.01
227405_s_at	Hs.302634	frizzled homolog 8 (Drosophila)	FZD8	2.01
232500_at	Hs.472285	chromosome 20 open reading frame 74	C20orf74	2.01
244801_at	Hs.213470	Proteasome (prosome, macropain) subunit, beta type, 7	PSMB7	1.96
216211_at	Hs.590989	Chromosome 10 open reading frame 18	C10orf18	1.95
240824_at	Hs.134491	Oligonucleotide/oligosaccharide-binding fold containing 1	OBFC1	1.94
235735_at	Hs.494901	Tumor necrosis factor (ligand) superfamily, member 8	TNFSF8	1.92
240829_at	Hs.7277	Peroxisomal biogenesis factor 3	PEX3	1.90
205145_s_at	Hs.410970	myosin, light polypeptide 5, regulatory /// similar to Superfast myosin regulatory light chain 2 (MyLC-2) (MYLC2) (Myosin regulatory light chain 5)	MYL5 /// LOC649851	1.88
242144_at	Hs.418198	PAP associated domain containing 4	PAPD4	1.85
239788_at	Hs.174021	Smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	SMU1	1.84
239597_at	Hs.369984	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	PAN3	1.83
235757_at	Hs.590989	Chromosome 10 open reading frame 18	C10orf18	1.82
1558842_at	---	---	---	1.79
212629_s_at	Hs.440833	protein kinase N2	PKN2	1.79
227948_at	Hs.117835	FYVE, RhoGEF and PH domain containing 4	FGD4	1.78
236841_at	---	---	---	1.76
210908_s_at	Hs.288856	prefoldin subunit 5	PFDN5	1.73
213156_at	Hs.592414	Homo sapiens, clone IMAGE:4214654, mRNA	---	1.70
240326_at	Hs.577252	SET binding factor 2	SBF2	1.69
236659_x_at	Hs.489722	Zinc finger protein 277	ZNF277	1.67
230375_at	Hs.591345	chromosome 6 open reading frame 111	C6orf111	1.66
232945_at	Hs.368348	Hypothetical protein FLJ32312	FLJ32312	1.66
215338_s_at	Hs.529509	natural killer-tumor recognition sequence	NKTR	1.65
237733_at	Hs.368282	KIAA0564 protein	RP11-125A7.3	1.65
207132_x_at	Hs.288856	prefoldin subunit 5	PFDN5	1.65
235652_at	Hs.109655	Sex comb on midleg-like 1 (Drosophila)	SCML1	1.64
243584_at	Hs.25338	Protease, serine, 23	PRSS23	1.60
242877_at	Hs.407368	LSM14 homolog A (SCD6, S. cerevisiae)	LSM14A	1.54
243240_at	Hs.21422	Neuronal cell adhesion molecule	NRCAM	1.52
226999_at	---	RNA-binding region (RNP1, RRM) containing 3	RNPC3	1.51
1555897_at	Hs.591518	amine oxidase (flavin containing) domain 2	AOF2	1.44
208646_at	Hs.592391	ribosomal protein S14 /// similar to ribosomal protein S14	RPS14 /// LOC644068	1.41
1558678_s_at	Hs.593060	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	MALAT1	1.39
219251_s_at	Hs.389945	WD repeat domain 60	WDR60	1.38

225563_at	Hs.369984	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	PAN3	1.32
223904_at	Hs.591634	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	PRKAG3	0.89
238724_at	Hs.198365	2,3-bisphosphoglycerate mutase	BPGM	0.89
214688_at	Hs.444213	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	TLE4	0.85
216561_x_at	---	---	---	0.85
1568923_at	Hs.488478	Hypothetical protein FLJ10099	FLJ10099	0.83
240300_at	Hs.512619	Thymidine kinase 2, mitochondrial	TK2	0.80
209128_s_at	Hs.584842	squamous cell carcinoma antigen recognised by T cells 3	SART3	0.78
1555947_at	Hs.372003	family with sequence similarity 120A	FAM120A	0.76
214228_x_at	Hs.129780	tumor necrosis factor receptor superfamily, member 4	TNFRSF4	0.76
201684_s_at	Hs.555910	chromosome 14 open reading frame 92	C14orf92	0.74
205252_at	Hs.155204	zinc finger protein 174	ZNF174	0.73
219928_s_at	Hs.511983	calcium binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	CABYR	0.72
201000_at	Hs.315137	alanyl-tRNA synthetase	AARS	0.72
1557581_x_at	Hs.517478	Calcineurin binding protein 1	CABIN1	0.71
1554311_a_at	Hs.250429	suppressor of Ty 6 homolog (S. cerevisiae)	SUPT6H	0.70
222911_s_at	Hs.98321	chromosome X open reading frame 36	CXorf36	0.70
239790_s_at	Hs.211973	Exosome component 2	EXOSC2	0.70
220607_x_at	Hs.517148	TH1-like (Drosophila)	TH1L	0.69
1552696_at	Hs.511797	non imprinted in Prader-Willi/Angelman syndrome 1	NIPA1	0.69
230822_at	Hs.568653	transmembrane protein 61	TMEM61	0.69
241813_at	Hs.405610	methyl-CpG binding domain protein 1	MBD1	0.69
226744_at	Hs.632237	methyltransferase 10 domain containing	METT10D	0.69
1554973_a_at	Hs.5638	zinc finger and BTB domain containing 26	ZBTB26	0.69
221064_s_at	Hs.161279	chromosome 16 open reading frame 28	C16orf28	0.68
208223_s_at	Hs.438918	activin A receptor, type IB	ACVR1B	0.67
212786_at	Hs.35490	KIAA0350 protein	KIAA0350	0.67
218023_s_at	Hs.54056	family with sequence similarity 53, member C	FAM53C	0.66
225755_at	Hs.13781	kelch domain containing 8B	KLHDC8B	0.66
209021_x_at	---	KIAA0652	KIAA0652	0.66
1554283_at	Hs.548091	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	CCRN4L	0.66
1559163_at	---	hypothetical protein LOC285954	LOC285954	0.63
1555904_at	Hs.594371	Homo sapiens, clone IMAGE:4779853, mRNA	---	0.62
203838_s_at	Hs.518513	tyrosine kinase, non-receptor, 2	TNK2	0.61
205436_s_at	Hs.477879	H2A histone family, member X	H2AFX	0.61
230764_at	Hs.308074	Chromosome 9 open reading frame 5	C9orf5	0.61
223852_s_at	Hs.471768	serine/threonine kinase 40	STK40	0.61
227234_at	Hs.535549	CDNA FLJ32177 fis, clone PLACE6001294	---	0.61
236537_at	Hs.596399	CDNA FLJ23896 fis, clone LNG15157	---	0.60
223575_at	Hs.490294	KIAA1549 protein	KIAA1549	0.59
223693_s_at	Hs.487409	hypothetical protein FLJ10324	FLJ10324	0.59
201673_s_at	Hs.386225	glycogen synthase 1 (muscle)	GYS1	0.58
215305_at	Hs.74615	platelet-derived growth factor receptor, alpha polypeptide /// tripartite motif-containing 6 and tripartite motif-containing 34	PDGFRA /// TRIM6-TRIM34	0.58
226531_at	Hs.55148	transmembrane protein 142A	TMEM142A	0.57
208289_s_at	Hs.591939	etoposide induced 2.4 mRNA	EI24	0.57
1438_at	Hs.2913	EPH receptor B3	EPHB3	0.57

203367_at	Hs.91448	dual specificity phosphatase 14	DUSP14	0.56
230659_at	Hs.224616	ER degradation enhancer, mannosidase alpha-like 1	EDEM1	0.56
221908_at	Hs.437195	Transmembrane protein 118	TMEM118	0.55
227574_at	Hs.526594	obscurin-like 1	OBSL1	0.54
204423_at	Hs.44693	muskelin 1, intracellular mediator containing kelch motifs	MKLN1	0.54
49051_g_at	Hs.32374	deltex 3 homolog (Drosophila)	DTX3	0.54
49049_at	Hs.32374	deltex 3 homolog (Drosophila)	DTX3	0.53
205807_s_at	Hs.489922	tuftelin 1	TUFT1	0.53
218086_at	Hs.105547	neural proliferation, differentiation and control, 1	NPDC1	0.53
219527_at	Hs.369042	MOCO sulphurase C-terminal domain containing 2	MOSC2	0.53
1553158_at	Hs.334526	chromosome 3 open reading frame 34	C3orf34	0.51
231737_at	Hs.514423	calcium channel, voltage-dependent, gamma subunit 4	CACNG4	0.51
220197_at	Hs.98967	ATPase, H+ transporting, lysosomal V0 subunit a4	ATP6V0A4	0.51
215847_at	Hs.510685	hypothetical protein LOC283755	LOC283755	0.51
224739_at	Hs.530381	pim-3 oncogene	PIM3	0.51
232226_at	Hs.135736	leucine rich repeat containing 4C	LRRC4C	0.51
226056_at	Hs.477278	Cdc42 GTPase-activating protein	CDGAP	0.47
209736_at	Hs.201671	SRY (sex determining region Y)-box 13	SOX13	0.44
205392_s_at	Hs.272493	chemokine (C-C motif) ligand 14 /// chemokine (C-C motif) ligand 15	CCL14 /// CCL15	0.43
218574_s_at	Hs.475353	LIM and cysteine-rich domains 1	LMCD1	0.43
222723_at	Hs.449009	von Willebrand factor A domain containing 1	VWA1	0.43
205535_s_at	Hs.570785	BH-protocadherin (brain-heart)	PCDH7	0.42
205286_at	Hs.473152	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	TFAP2C	0.40
206329_at	Hs.150956	exostoses (multiple)-like 1	EXTL1	0.40
1555962_at	Hs.299329	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	B3GNT7	0.37
38918_at	Hs.201671	SRY (sex determining region Y)-box 13	SOX13	0.37
229655_at	Hs.436854	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	FAM19A5	0.36
228770_at	Hs.585007	G protein-coupled receptor 146	GPR146	0.35
208065_at	Hs.23172	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	ST8SIA3	0.34
226499_at	Hs.535075	similar to ankyrin-repeat protein Nrarp	MGC61598	0.34
221585_at	Hs.514423	calcium channel, voltage-dependent, gamma subunit 4	CACNG4	0.33
214761_at	Hs.530930	zinc finger protein 423	ZNF423	0.32
202022_at	Hs.155247	aldolase C, fructose-bisphosphate	ALDOC	0.32
1554281_at	---	---	---	0.32
206645_s_at	Hs.268490	nuclear receptor subfamily 0, group B, member 1	NR0B1	0.31
1569879_a_at	Hs.438250	multiple EGF-like-domains 11	MEGF11	0.31
237268_at	Hs.397800	Down syndrome cell adhesion molecule	DSCAM	0.29
1569481_s_at	Hs.599195	sorting nexin 22	SNX22	0.28
219010_at	Hs.518997	chromosome 1 open reading frame 106	C1orf106	0.27
213768_s_at	Hs.524672	achaete-scute complex-like 1 (Drosophila)	ASCL1	0.27
205208_at	Hs.434435	aldehyde dehydrogenase 1 family, member L1	ALDH1L1	0.27
236034_at	---	---	---	0.27
226913_s_at	Hs.243678	SRY (sex determining region Y)-box 8	SOX8	0.27
228307_at	Hs.25897	elastin microfibril interfacer 3	EMILIN3	0.27
240218_at	Hs.160418	Transcribed locus	---	0.26
225777_at	Hs.19322	chromosome 9 open reading frame 140	C9orf140	0.26
227703_s_at	Hs.592224	synaptotagmin-like 4 (granuphilin-a)	SYTL4	0.26

220595_at	Hs.380044	PDZ domain containing RING finger 4	PDZRN4	0.26
234472_at	Hs.470277	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	GALNT13	0.25
214038_at	Hs.271387	chemokine (C-C motif) ligand 8	CCL8	0.24
231798_at	Hs.248201	Noggin	NOG	0.23
232054_at	Hs.391781	protocadherin 20	PCDH20	0.21
209443_at	Hs.510334	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	SERPINA5	0.19
206243_at	Hs.591665	TIMP metallopeptidase inhibitor 4	TIMP4	0.18
219197_s_at	Hs.523468	signal peptide, CUB domain, EGF-like 2	SCUBE2	0.16
235639_at	Hs.594900	Transcribed locus	---	0.13
206869_at	Hs.97220	chondroadherin	CHAD	0.11
205229_s_at	Hs.21016	coagulation factor C homolog, cochlin (Limulus polyphemus)	COCH	0.07
1555403_a_at	Hs.42771	cadherin 19, type 2	CDH19	0.07