

# **The pan-cancer pathological regulatory landscape**

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## **Supplementary Material**

## Supplementary Table 2.

List of p-values of the Kaplan-Meier test that relates TF with survival, along with hazard ratios and the number of patients with high and low TF activity.

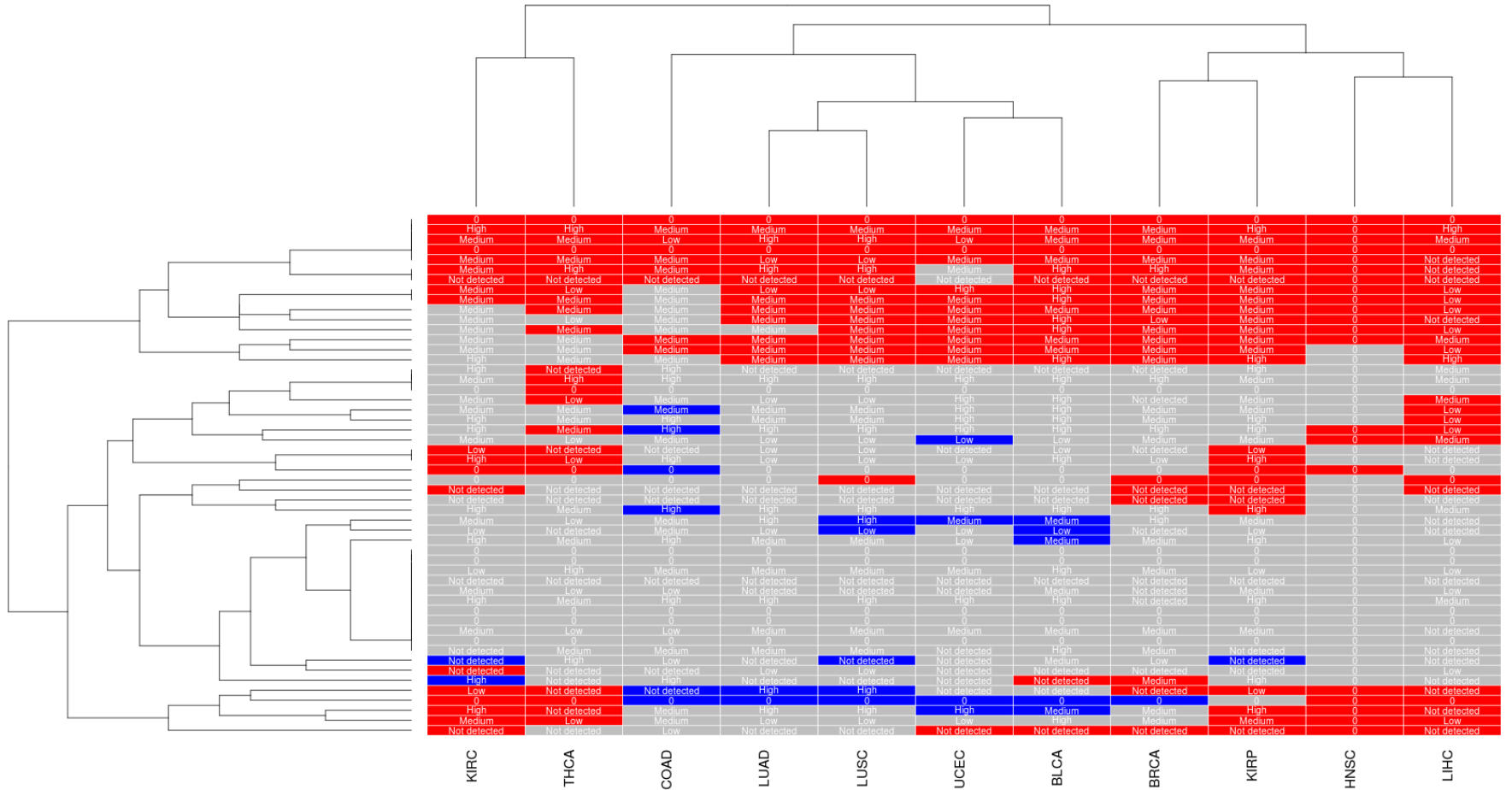
Cancer	Transcription Factor	Kaplan-Meier p-value	Hazard ratio (confidence interval)	Patients high TF activity	Patients low TF activity
BLCA	EBF1	0.0421115	0.475 (0.228-0.99)	61	233
BLCA	MEF2C	0.0373213	6.508 (0.853-49.628)	9	285
BLCA	PAX5	0.0201307	0.277 (0.087-0.883)	35	259
BLCA	SRF	0.0074854	4.375 (1.34-14.281)	13	281
BRCA	EBF1	0.000572921	0.467 (0.299-0.728)	443	592
BRCA	FOSL1	0.0357151	0.582 (0.349-0.971)	270	765
BRCA	GATA2	0.0268621	0.639 (0.428-0.953)	540	495
BRCA	TAL1_GATA1	0.0168877	0.578 (0.367-0.911)	383	652
BRCA	ZBTB33	0.0254967	1.619 (1.056-2.481)	533	502
COAD	MYC	0.0149399	0.491 (0.275-0.88)	193	233
COAD	E2F6	0.00313592	0.415 (0.228-0.756)	196	230
COAD	EBF1	0.035267	0.154 (0.021-1.129)	24	402
COAD	FOXA1	0.0498402	0.467 (0.215-1.016)	65	361
COAD	FOXA2	0.0211085	0.216 (0.052-0.9)	42	384
COAD	HNF4G	0.0214298	0.351 (0.138-0.891)	61	365
COAD	MAX	0.0463207	0.547 (0.3-0.997)	149	277
HNSC	FOS	0.0408123	1.434 (1.013-2.031)	126	352
HNSC	JUN	0.00226654	1.636 (1.189-2.252)	232	246
HNSC	MYC	0.00494556	1.575 (1.144-2.167)	250	228
HNSC	CTCF	0.00401685	1.626 (1.164-2.273)	268	210
HNSC	CTCFL	0.0168626	1.513 (1.075-2.129)	293	185
HNSC	ELF1	1.95045e-05	1.987 (1.442-2.74)	233	245
HNSC	ETS1	0.0146949	1.479 (1.078-2.031)	160	318
HNSC	FOSL1	0.0364771	1.41 (1.02-1.949)	155	323
HNSC	FOSL2	0.0261911	1.435 (1.042-1.977)	162	316
HNSC	JUN_FOS	0.0132304	1.482 (1.084-2.027)	220	258
HNSC	JUND	3.41571e-05	1.946 (1.412-2.682)	227	251
HNSC	NRF1	0.00226138	1.624 (1.186-2.223)	208	270
HNSC	RXR_RAR_DR5	0.020795	1.448 (1.056-1.986)	183	295
HNSC	SP1	0.0168308	1.464 (1.069-2.005)	203	275
HNSC	SP2	0.0281694	1.418 (1.037-1.941)	196	282
HNSC	NR2C2	0.00135607	1.741 (1.235-2.455)	117	361
HNSC	YY1	0.0109523	1.522 (1.099-2.108)	122	356
KIRC	FOS	0.00545171	0.645 (0.472-0.881)	305	212
KIRC	JUN	5.34566e-09	0.382 (0.273-0.534)	263	254
KIRC	MYC	0.00405561	0.57 (0.386-0.84)	442	75
KIRC	CTCF	0.000280997	0.563 (0.411-0.771)	357	160
KIRC	CTCFL	0.00925749	0.638 (0.453-0.897)	400	117
KIRC	E2F4	0.0253689	0.638 (0.428-0.949)	125	392

KIRC	E2F6	0.00626335	0.616 (0.434-0.875)	190	327
KIRC	EGR1	2.10067e-05	0.444 (0.302-0.652)	178	339
KIRC	ELF1	0.00159433	0.584 (0.417-0.819)	205	312
KIRC	ETS1	0.000242133	0.561 (0.41-0.767)	330	187
KIRC	FOSL1	0.000396099	0.54 (0.382-0.764)	416	101
KIRC	FOXA2	0.0215194	1.61 (1.069-2.424)	71	446
KIRC	HNF4G	0.000911417	0.594 (0.435-0.811)	332	185
KIRC	IRF4	0.000802979	0.559 (0.396-0.789)	404	113
KIRC	JUN_FOS	1.13106e-06	0.467 (0.342-0.64)	311	206
KIRC	JUNB	0.00204717	0.601 (0.433-0.834)	394	123
KIRC	JUND	0.0005622	0.58 (0.424-0.794)	296	221
KIRC	MAX	0.000286817	0.562 (0.41-0.771)	357	160
KIRC	MEF2A	2.17395e-08	0.379 (0.266-0.54)	239	278
KIRC	MEF2C	1.84387e-05	0.341 (0.203-0.571)	125	392
KIRC	MYC_MAX	0.0410002	0.724 (0.53-0.988)	290	227
KIRC	NRF1	1.92972e-06	0.4 (0.271-0.591)	174	343
KIRC	REST	0.0488188	0.668 (0.446-1.001)	442	75
KIRC	PAX5	0.00315687	0.626 (0.458-0.857)	277	240
KIRC	PBX3	0.00198271	0.59 (0.421-0.827)	390	127
KIRC	SPI1	2.09049e-06	0.46 (0.331-0.639)	403	114
KIRC	RXR_RAR_DR5	0.00711851	0.643 (0.465-0.889)	242	275
KIRC	RXRA_VDR	0.00158299	0.609 (0.446-0.831)	309	208
KIRC	SP1	0.0121442	0.531 (0.321-0.878)	81	436
KIRC	SP2	0.00902423	0.575 (0.377-0.876)	117	400
KIRC	SRF	6.57821e-08	0.289 (0.178-0.466)	153	364
KIRC	TCF12	0.0190257	0.69 (0.505-0.942)	277	240
KIRC	NR2C2	0.00215925	0.609 (0.442-0.839)	241	276
KIRC	USF1	8.99021e-06	0.44 (0.303-0.639)	199	318
KIRC	YY1	3.34266e-05	0.265 (0.135-0.52)	83	434
KIRC	ZBTB33	0.0084004	0.113 (0.016-0.805)	24	493
KIRC	ZEB1	5.97385e-05	2.142 (1.463-3.134)	68	449
KIRC	ZNF263	0.00801888	0.601 (0.411-0.879)	434	83
KIRP	RXRA	0.0372079	2.343 (1.027-5.346)	56	166
LIHC	EGR1	0.0129996	0.506 (0.293-0.875)	103	191
LUAD	JUND	0.00948775	1.635 (1.123-2.378)	232	241
LUAD	MEF2C	0.000982058	13.464 (1.777-102.048)	3	470
LUAD	TAL1_GATA1	0.0206886	1.537 (1.065-2.22)	225	248
LUAD	TCF12	0.037926	1.723 (1.025-2.897)	59	414
LUSC	FOS	0.0155074	0.61 (0.408-0.914)	130	296
LUSC	ELF1	0.0227034	3.518 (1.107-11.175)	6	420
LUSC	NRF1	0.0448748	3.057 (0.967-9.665)	6	420
LUSC	REST	0.0149819	0.651 (0.459-0.922)	278	148
THCA	EBF1	0.0420116	0.239 (0.053-1.07)	223	272
THCA	ECR_USP	0.0100013	0.216 (0.06-0.779)	458	37
THCA	HNF4A	0.0499348	0.357 (0.122-1.044)	361	134
THCA	PAX5	0.0399298	0.156 (0.02-1.196)	180	315
THCA	RXRA	0.0239565	0.247 (0.067-0.918)	447	48
THCA	RXRA_VDR	0.00828255	0.266 (0.093-0.763)	376	119
UCEC	E2F4	0.00221894	0.401 (0.218-0.734)	323	184
UCEC	E2F6	0.035514	0.487 (0.245-0.966)	211	296
UCEC	ELF1	0.0113017	0.319 (0.126-0.811)	153	354
UCEC	GATA2	0.017712	0.469 (0.248-0.89)	240	267
UCEC	HNF4G	0.041277	0.529 (0.285-0.985)	264	243

UCEC	NR1H3_RXRA	0.0386898	0.526 (0.283-0.977)	247	260
UCEC	PAX5	0.0111818	0.366 (0.163-0.822)	176	331

### **Supplementary Figure 1.**

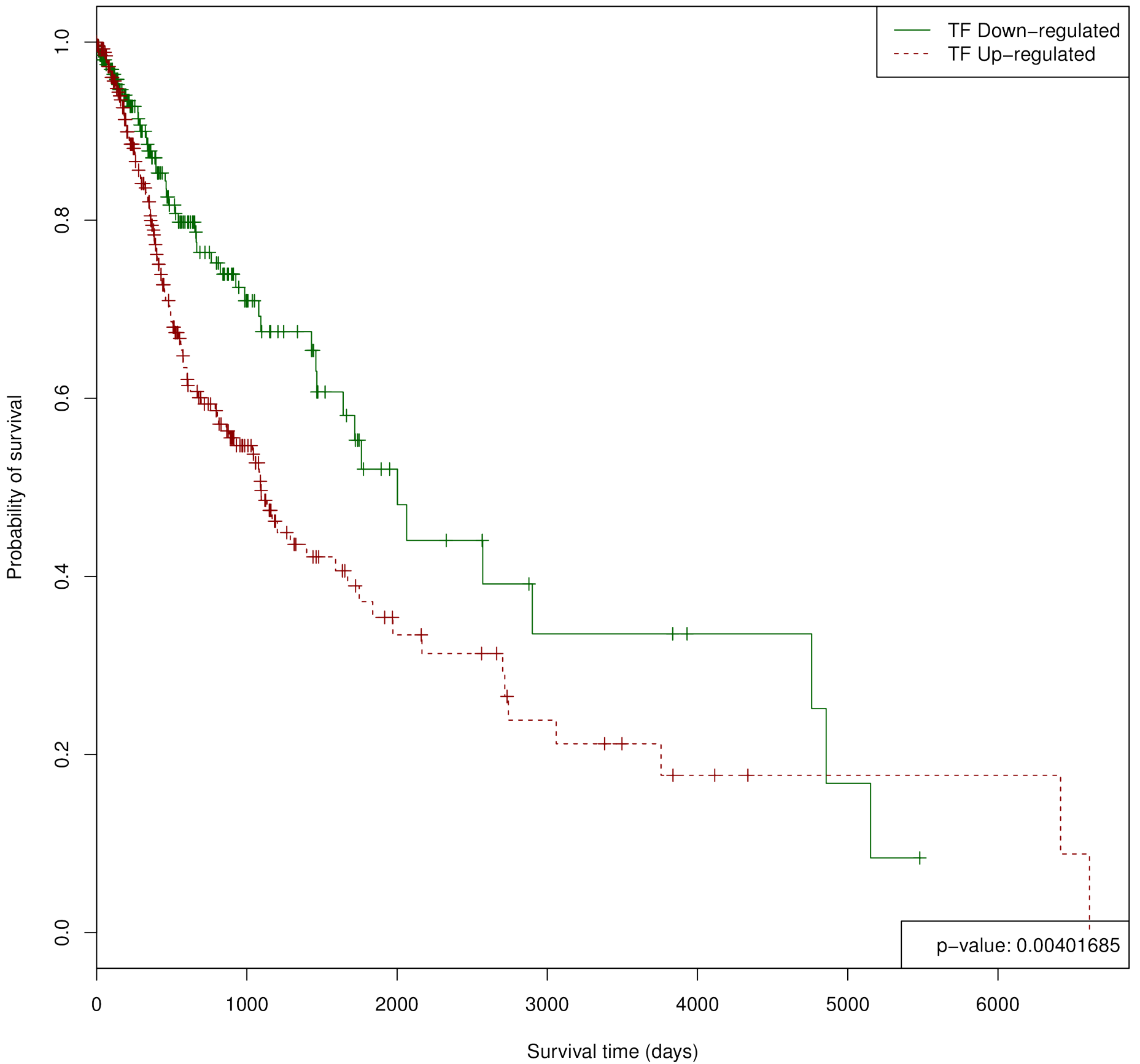
Change of TF activity in the different cancers studied. Cells in red indicate increased activity of the TF in the cancer with respect to the corresponding normal tissue, according to the TFTEA, cells in blue indicate a decreased activity and cells in grey indicate that no significant change in activity was detected. In addition, cells contain the discretized (Not detected / low / medium / high) protein expression value, according to the Human Proteome Atlas <sup>57</sup> of the TF in the healthy tissue in which the cancer originated, when available, otherwise a “0” appears. Columns correspond to cancers and rows to TFs.



**Supplementary Figure 2.**

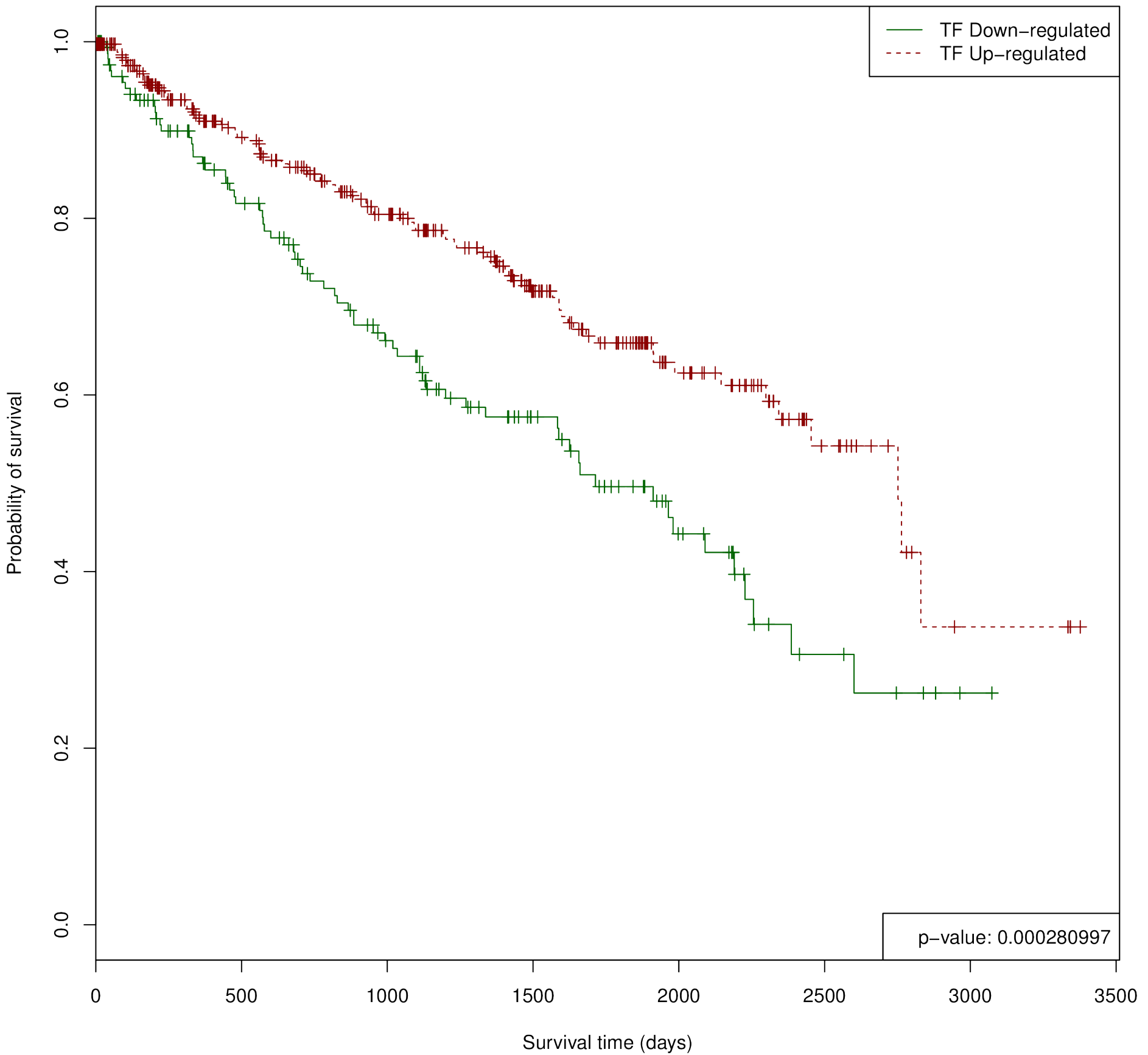
K-M detailed plots representing TF activities significantly associated to patient survival in all the cancers analysed from Figure 3.

# CTCF in HNSC

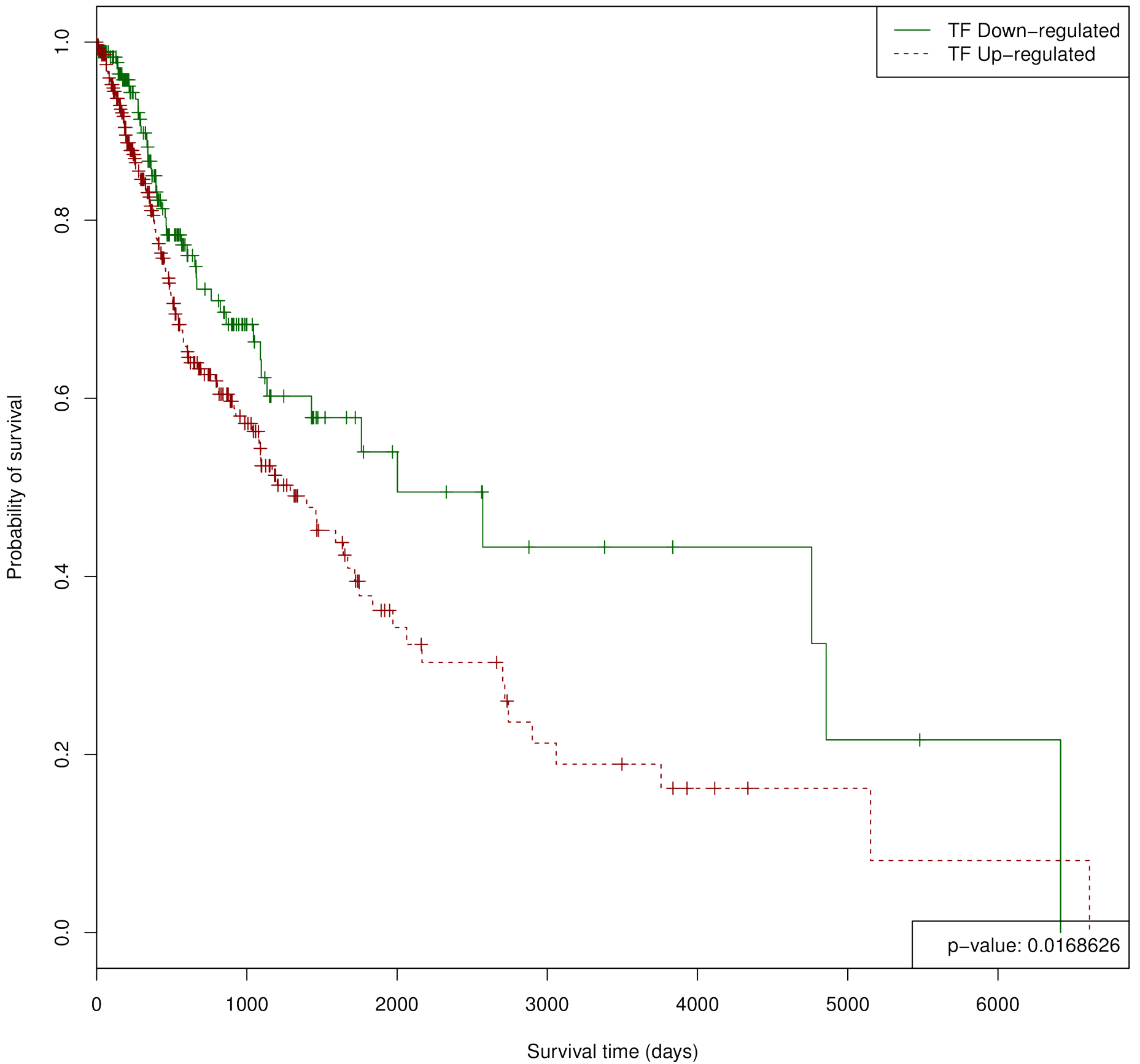




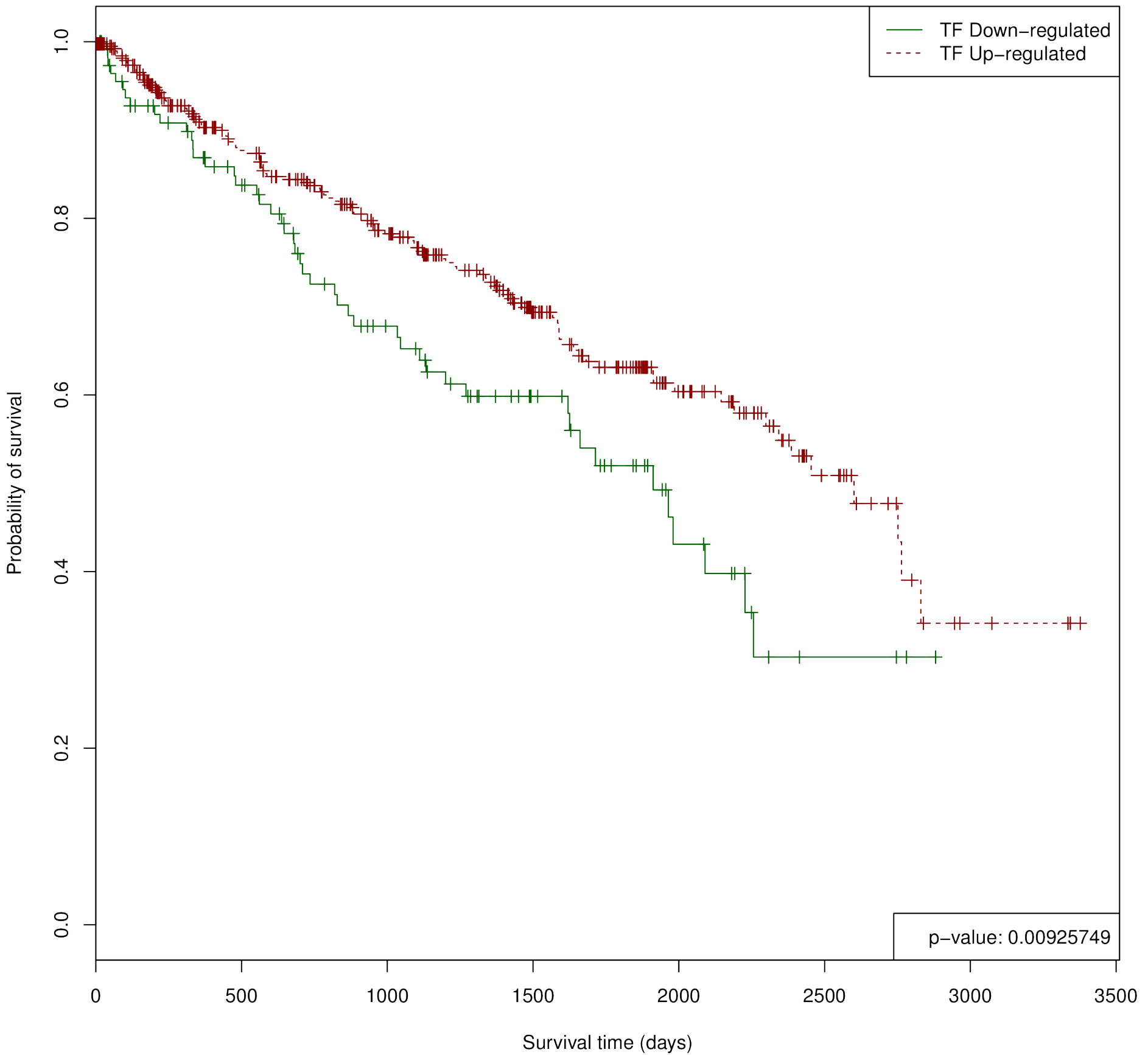
# CTCF in KIRC



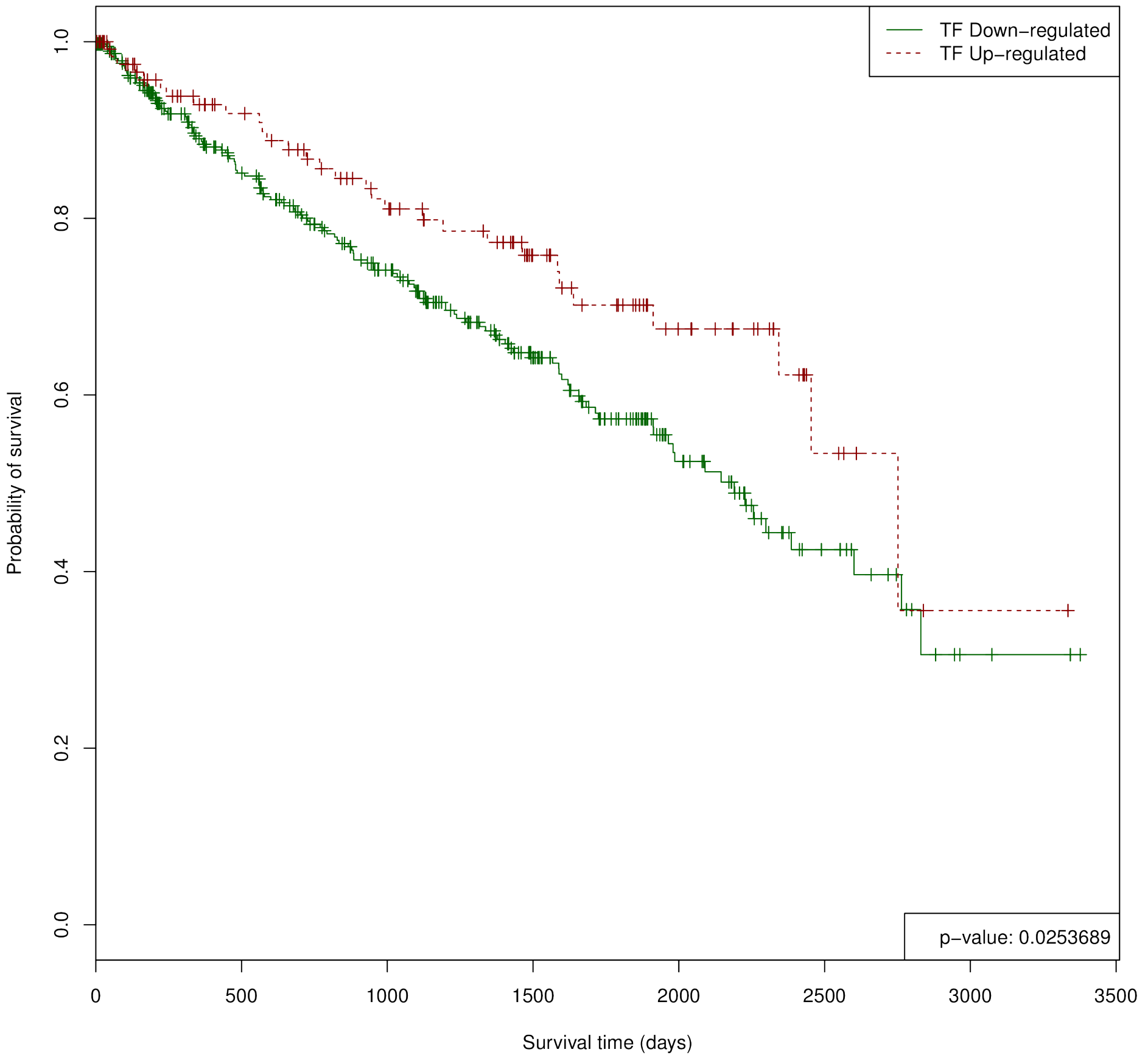
# CTCFL in HNSC



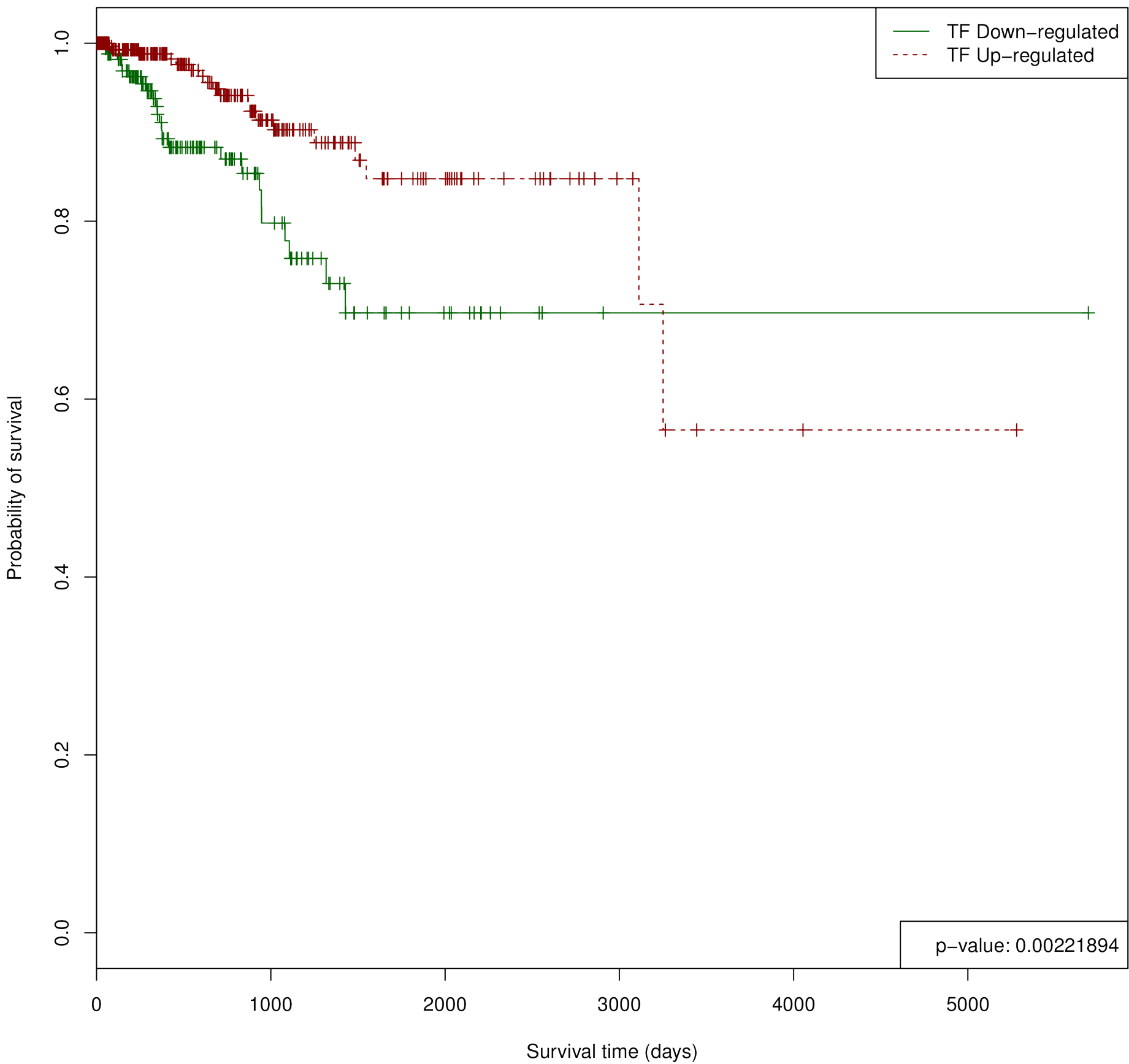
# CTCFL in KIRC



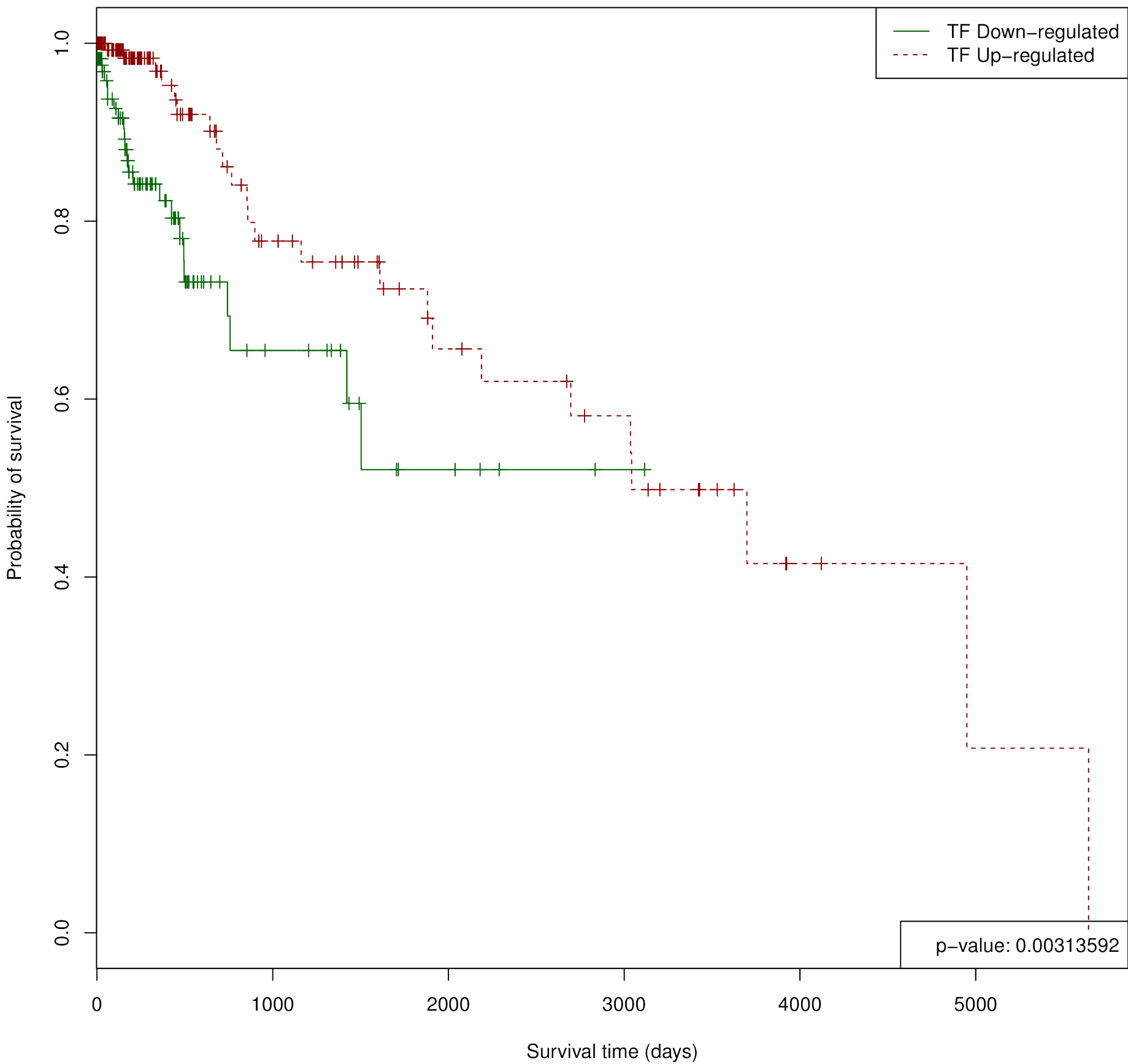
# E2F4 in KIRC



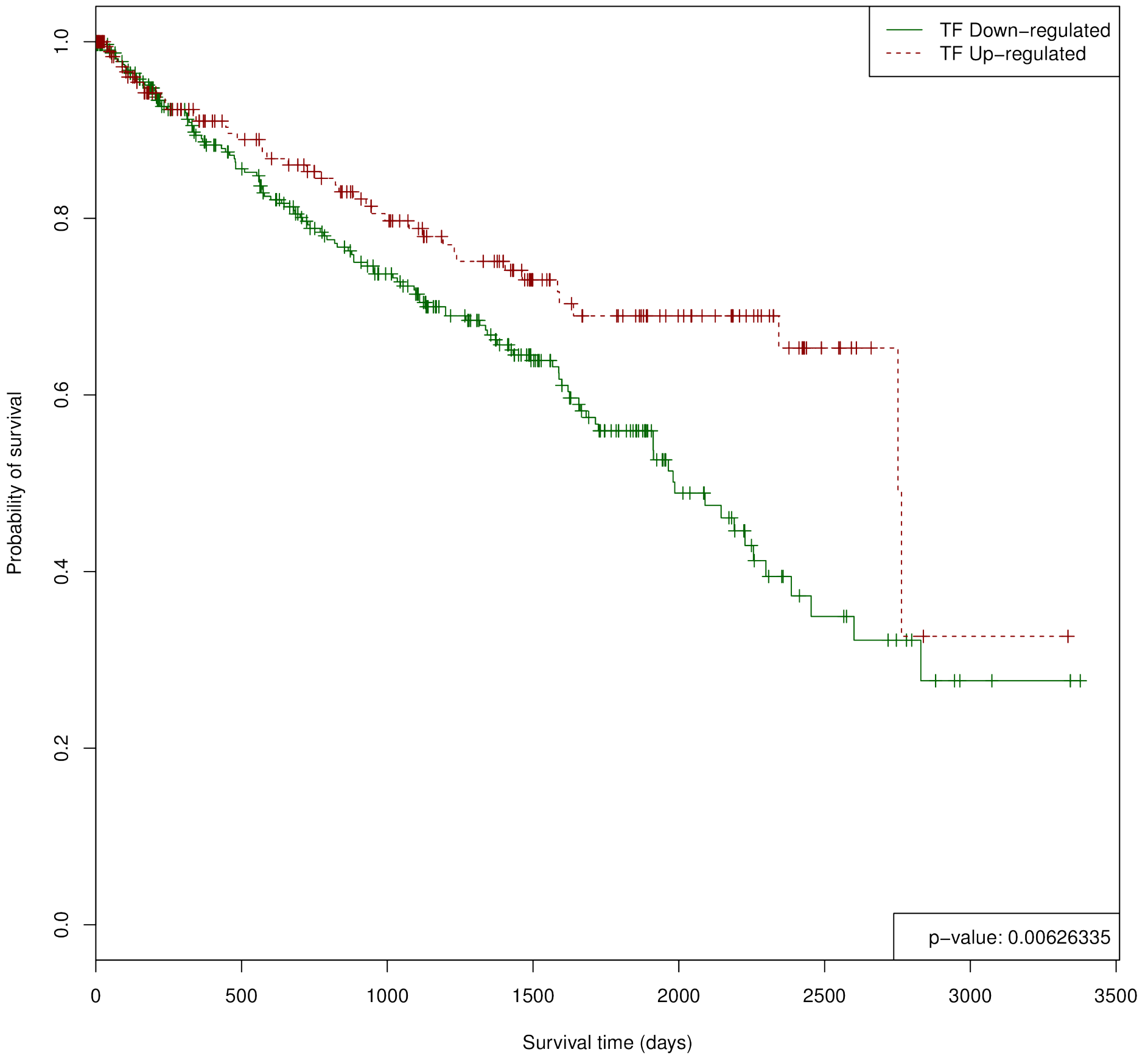
# E2F4 in UCEC



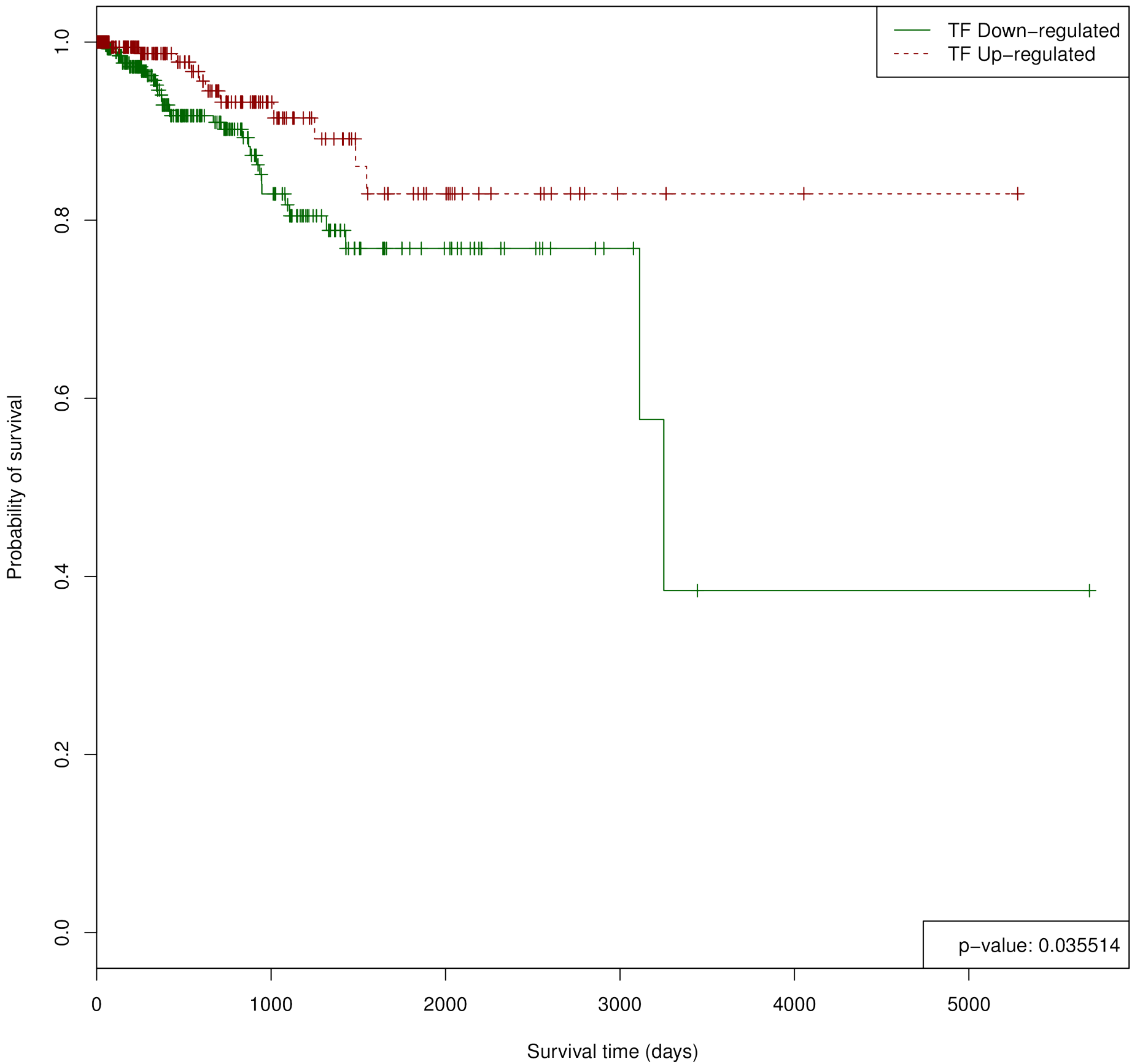
# E2F6 in COAD



# E2F6 in KIRC

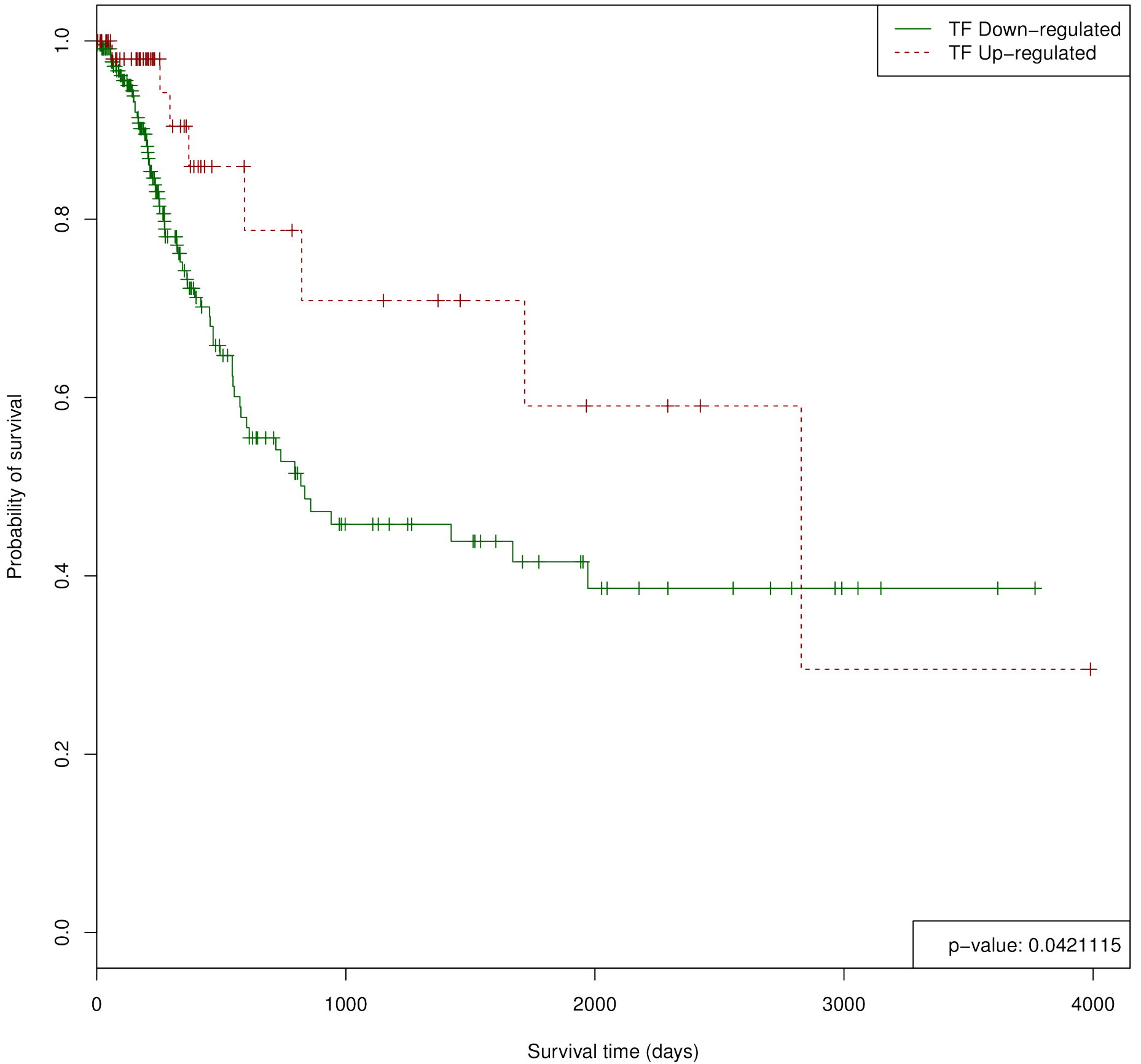


# E2F6 in UCEC

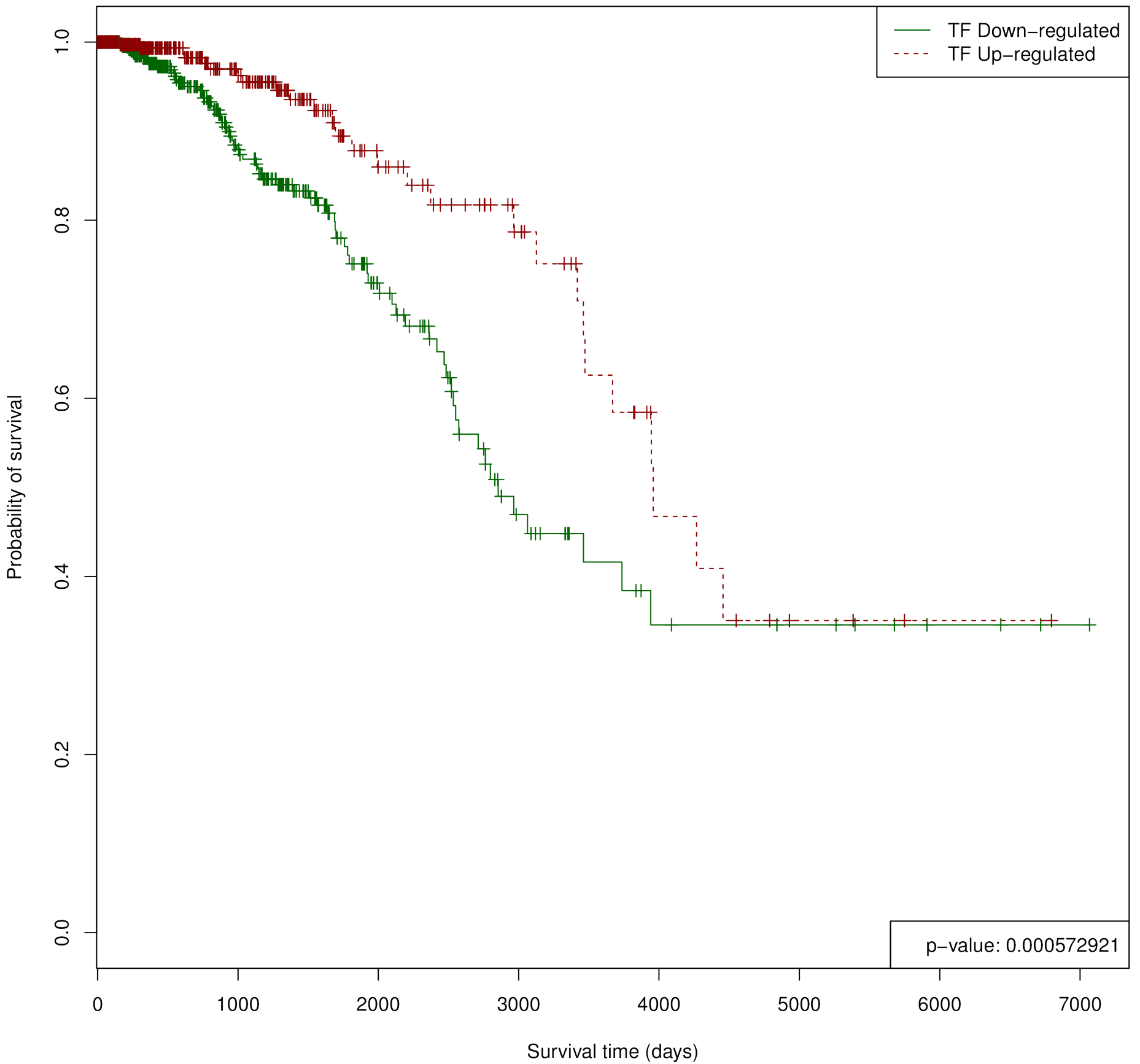




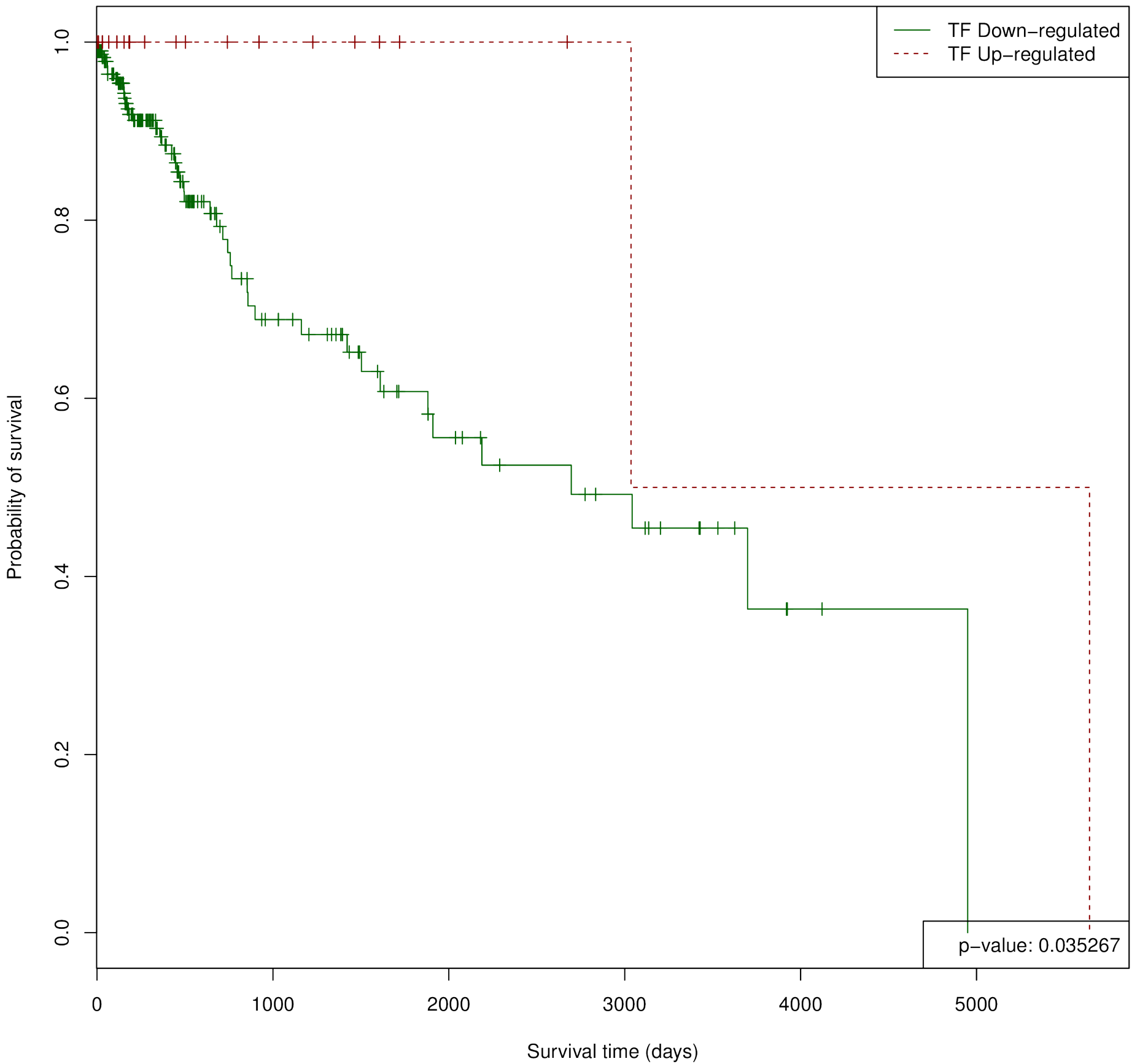
# EBF1 in BLCA



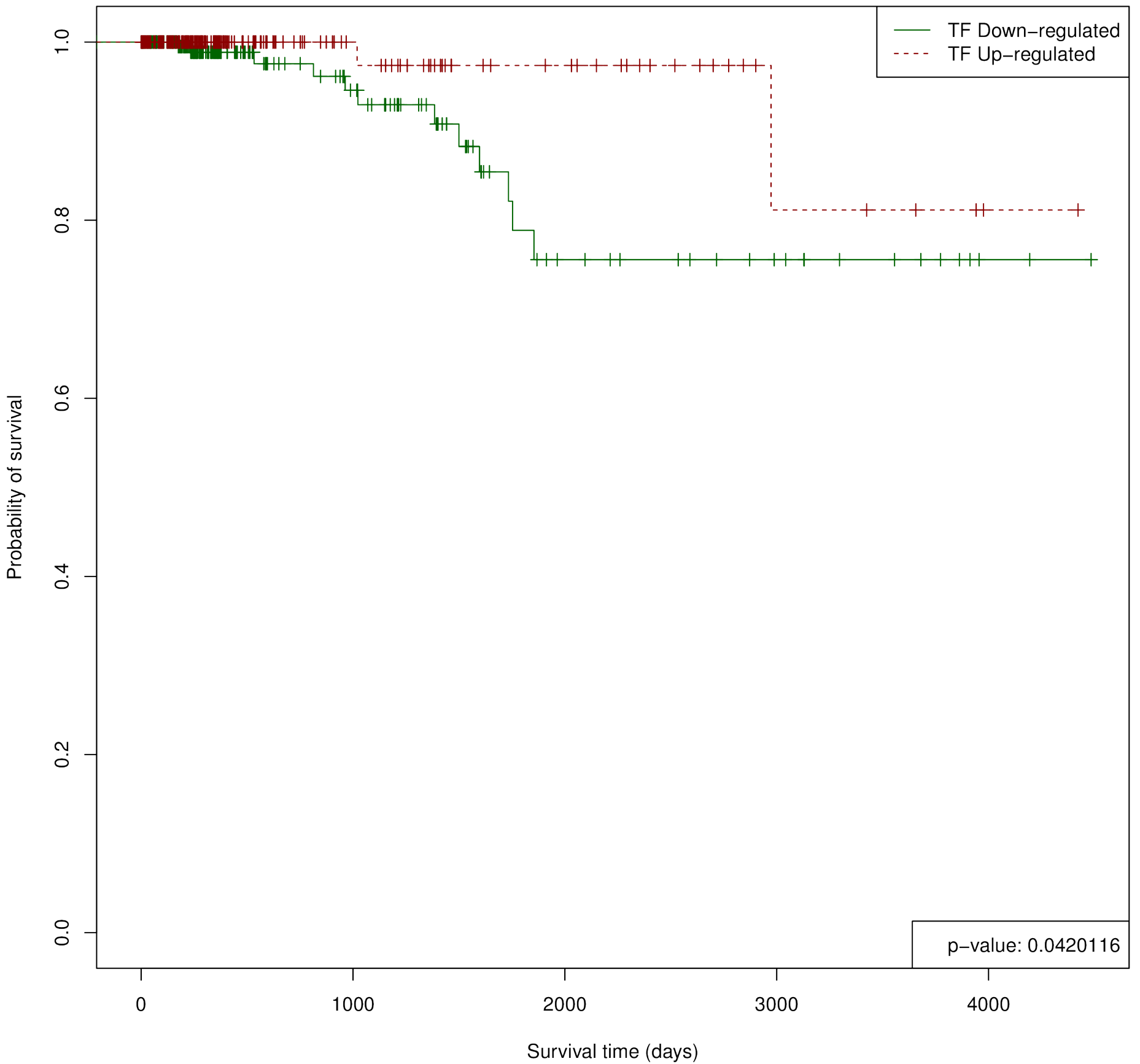
# EBF1 in BRCA



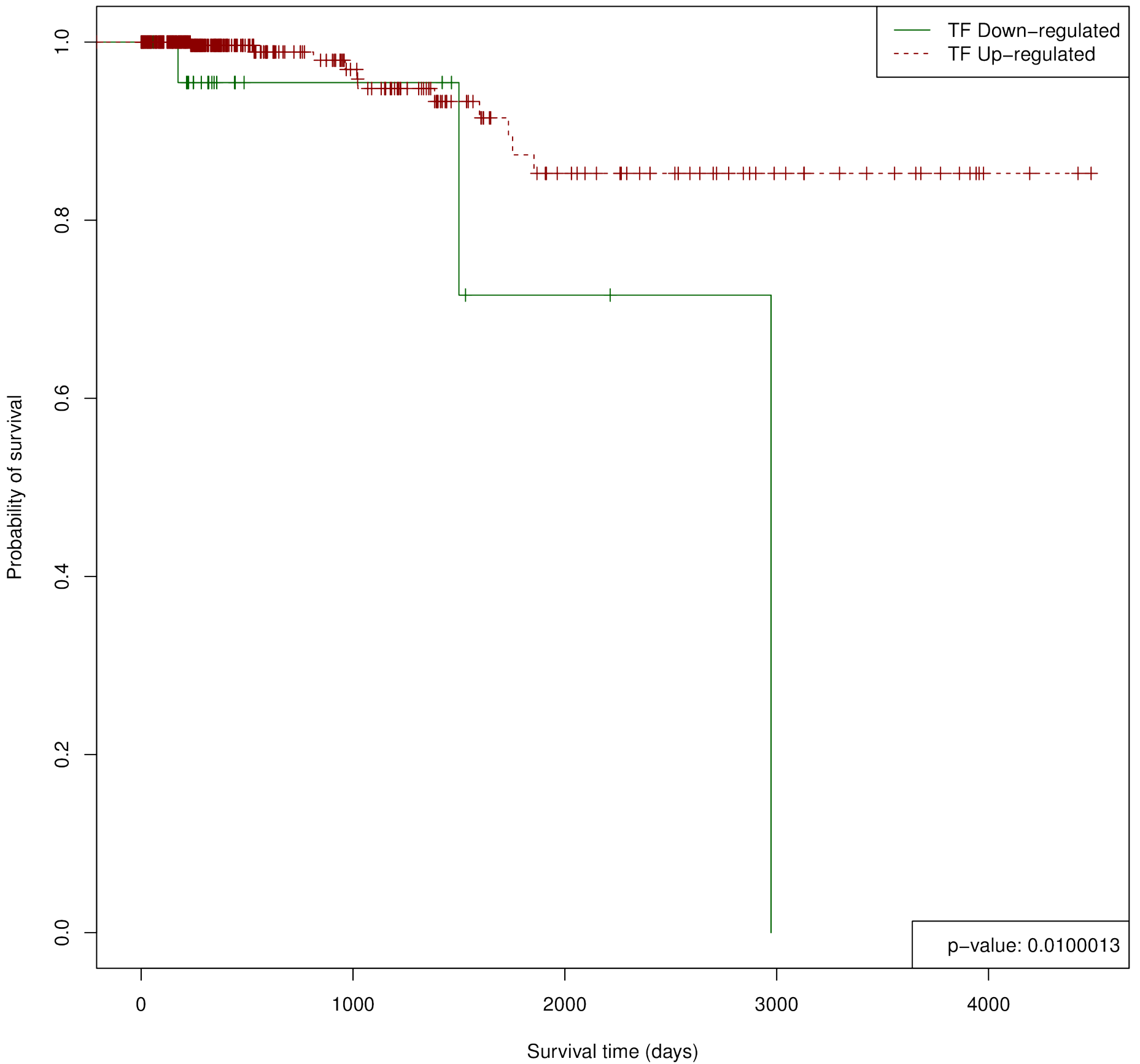
# EBF1 in COAD



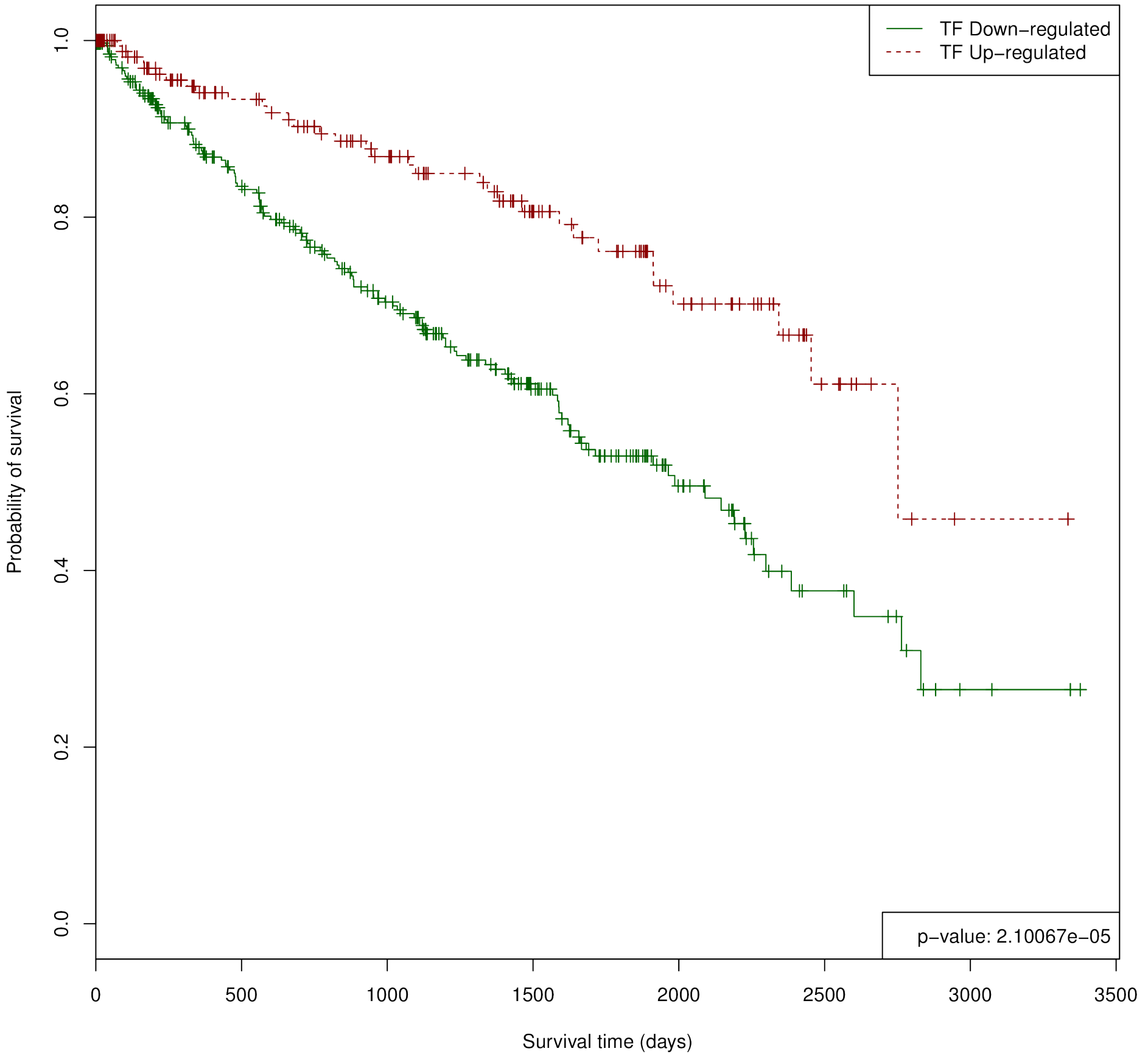
# EBF1 in THCA



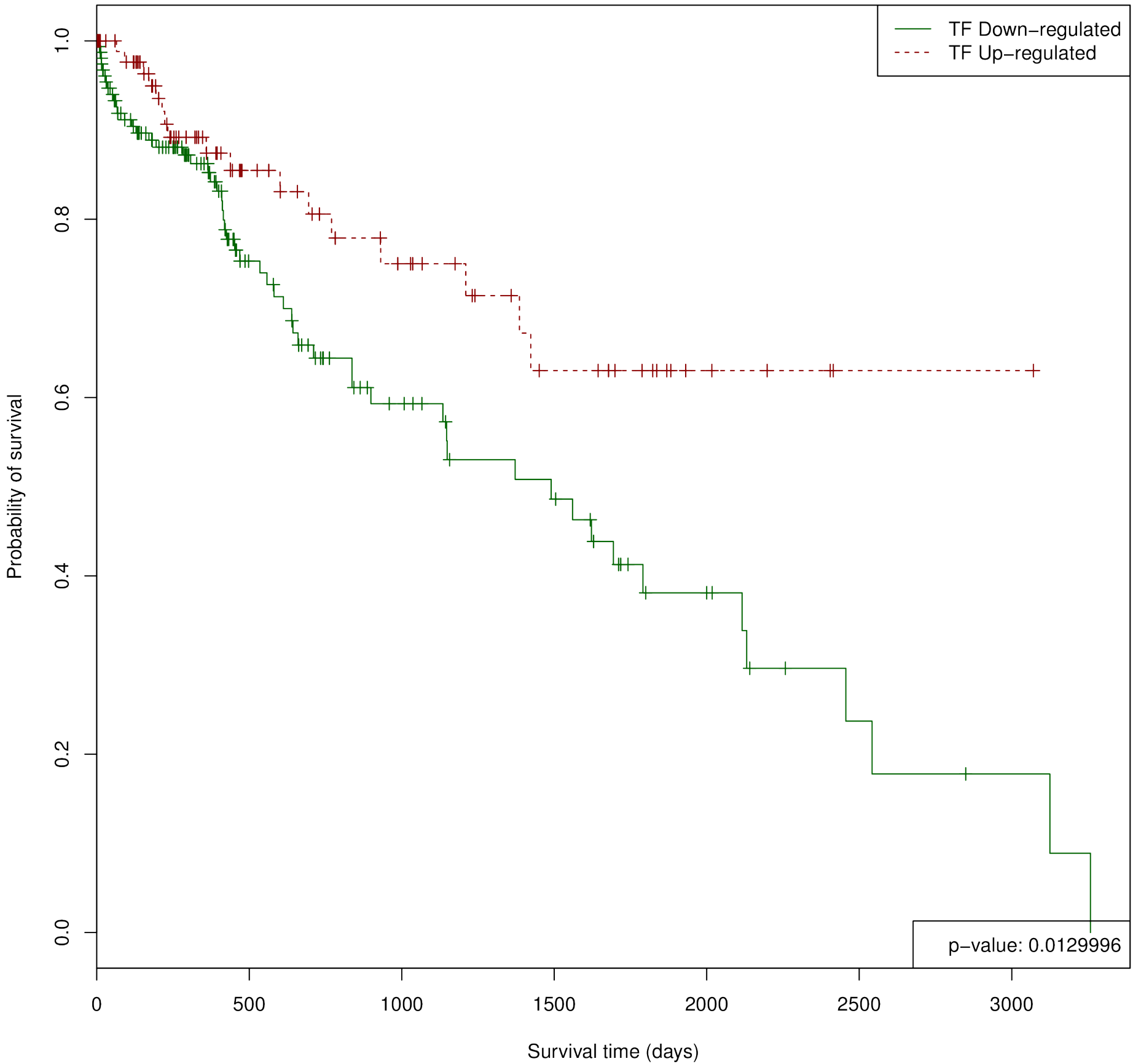
# ECR::USP in THCA



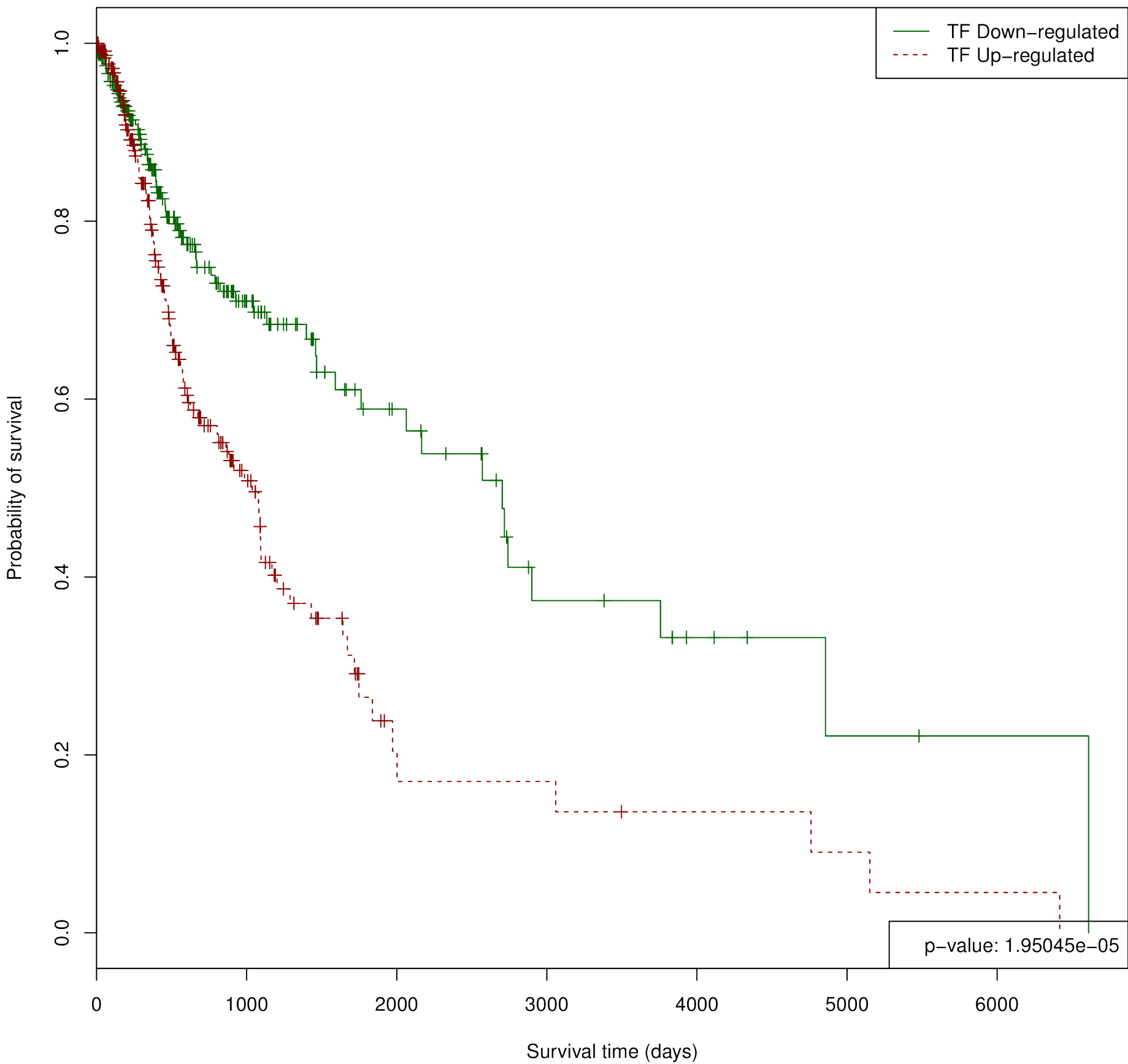
# EGR1 in KIRC



# EGR1 in LIHC

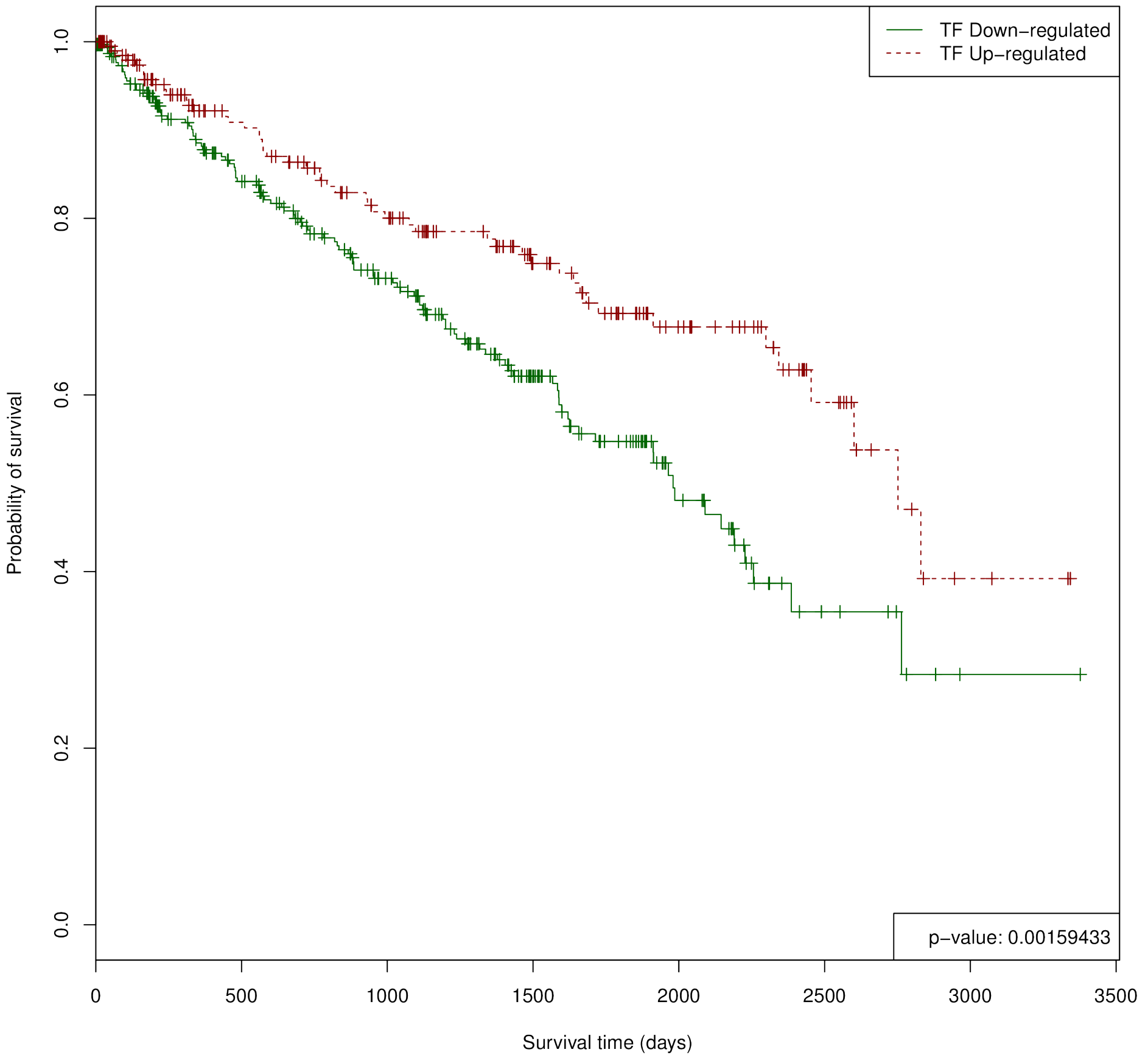


# ELF1 in HNSC

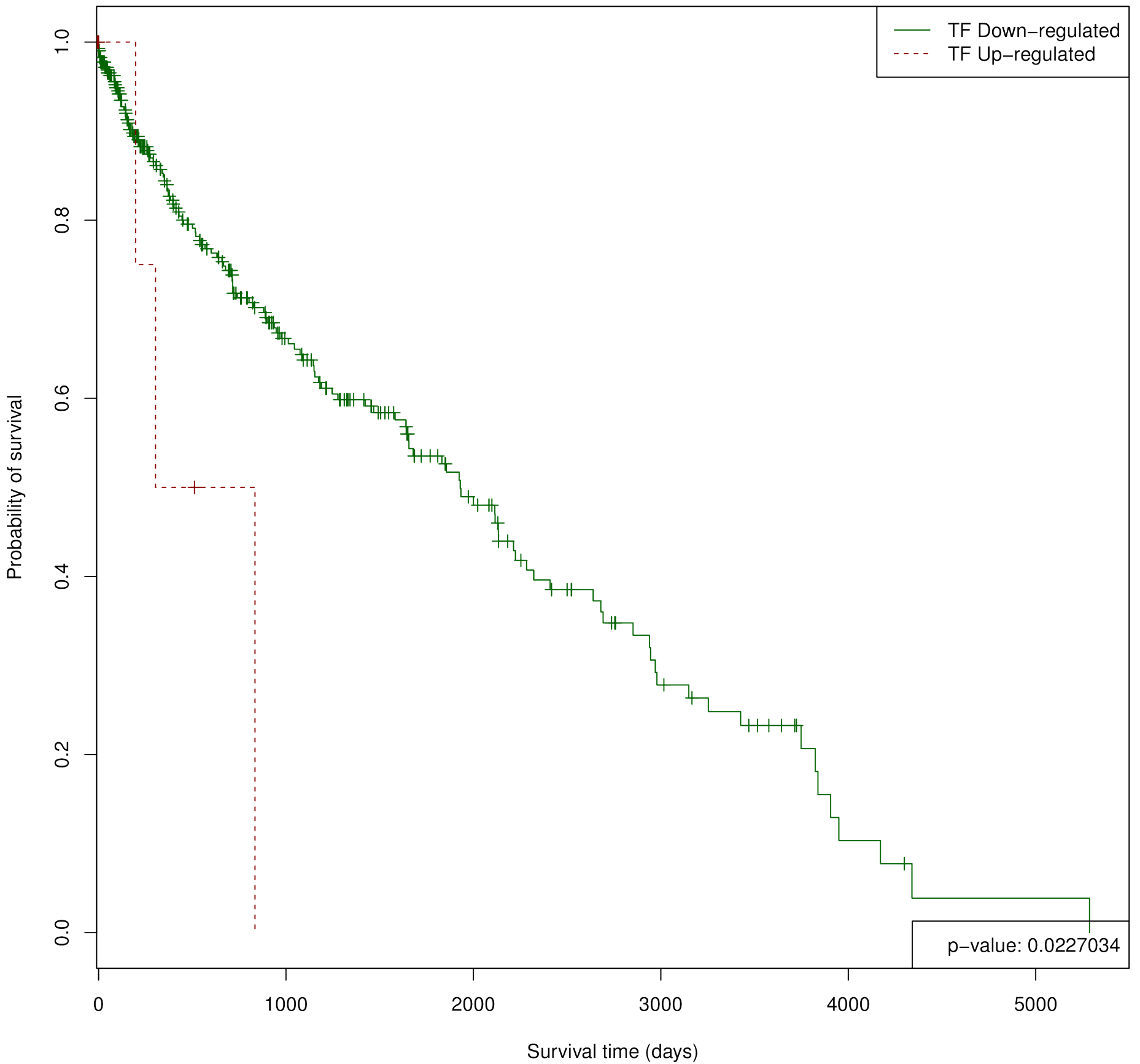




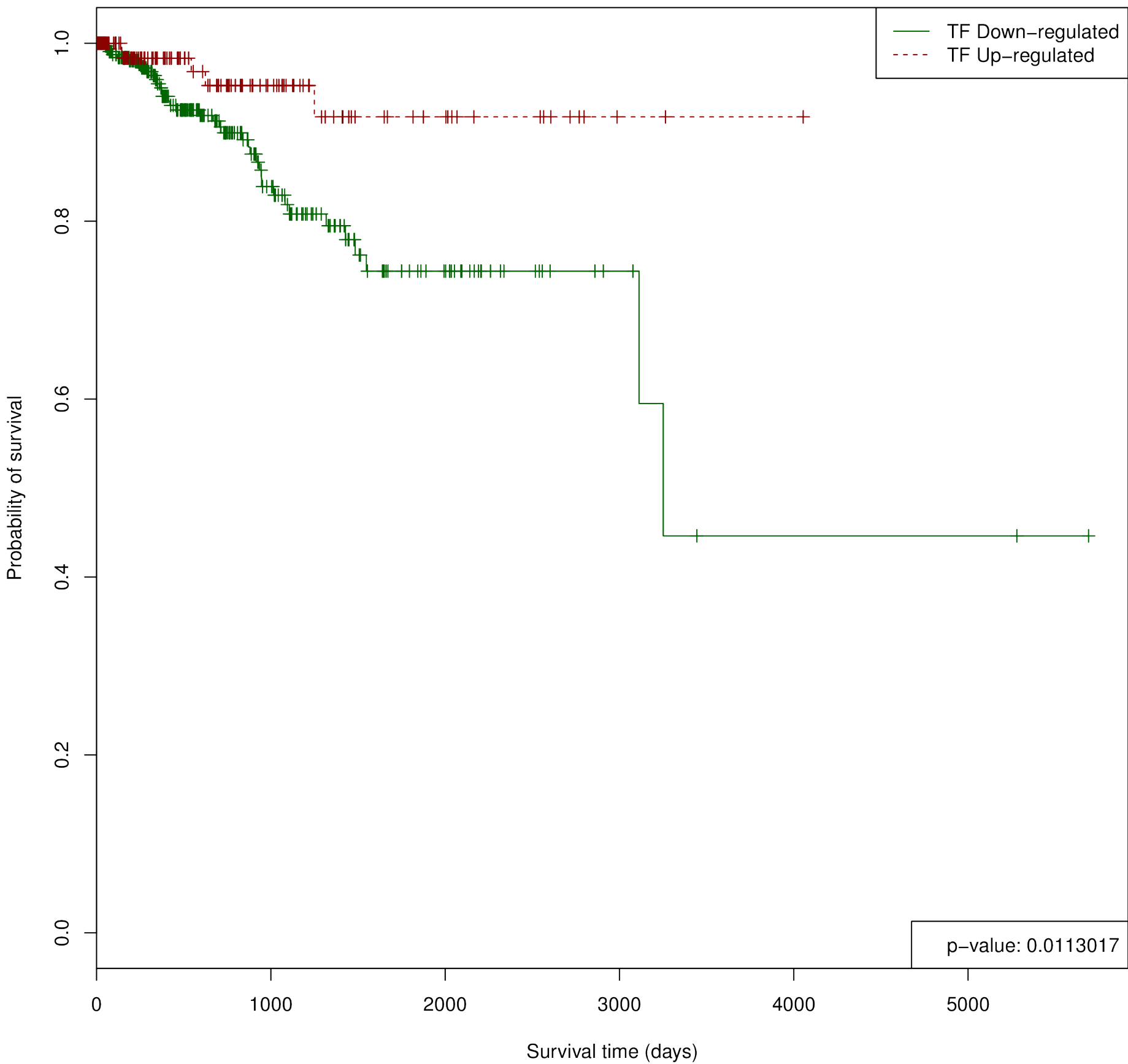
# ELF1 in KIRC



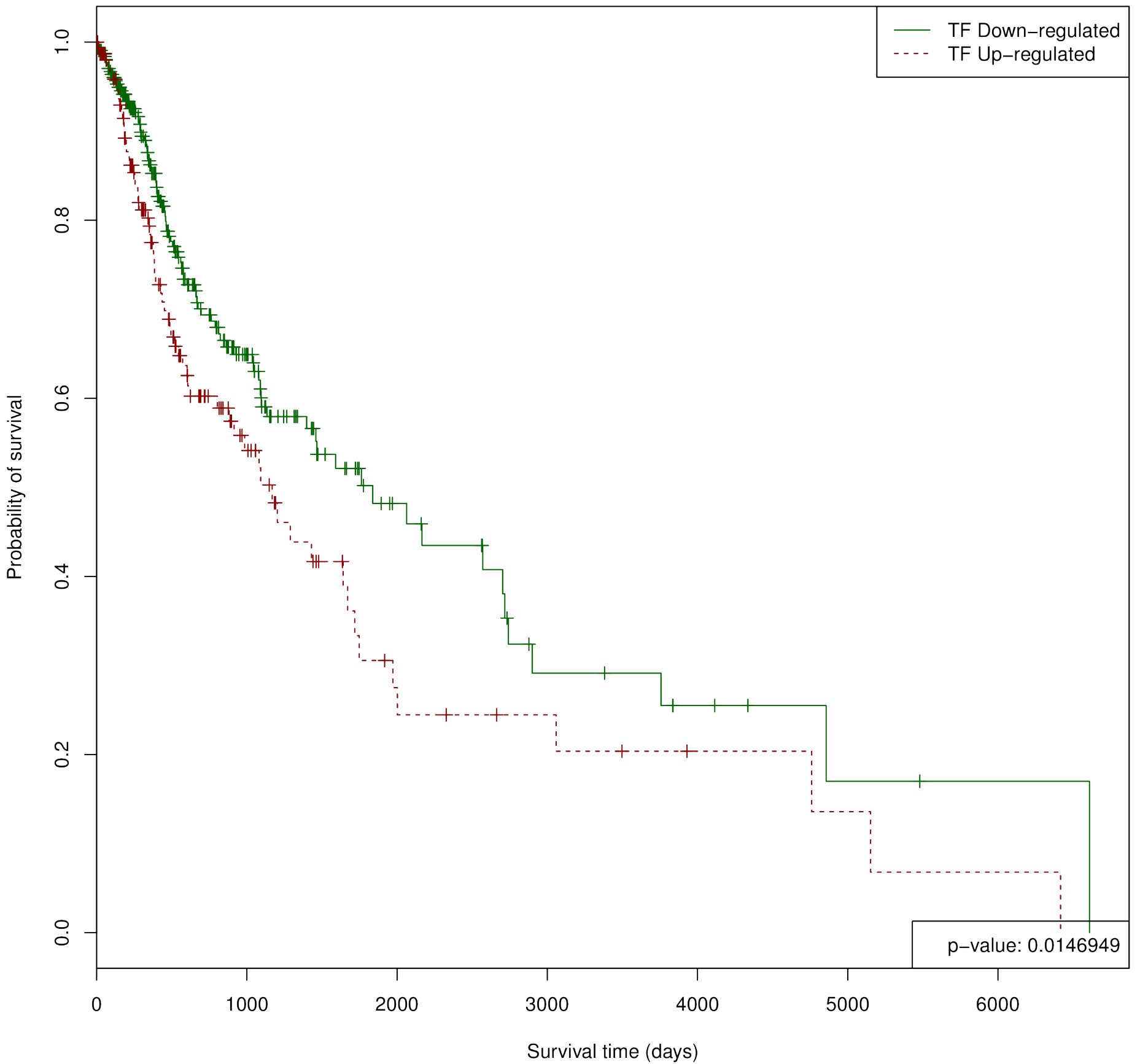
# ELF1 in LUSC



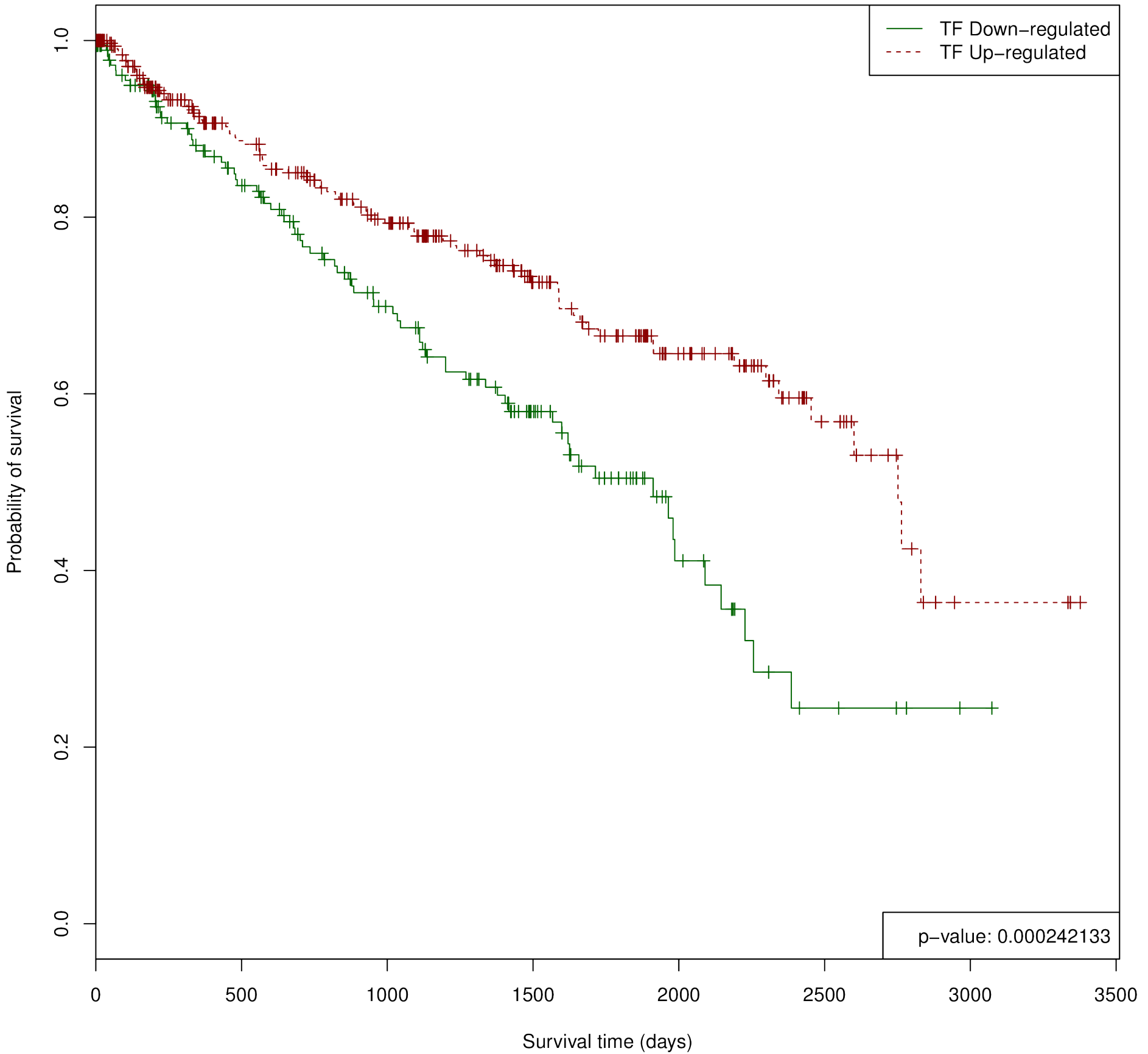
# ELF1 in UCEC



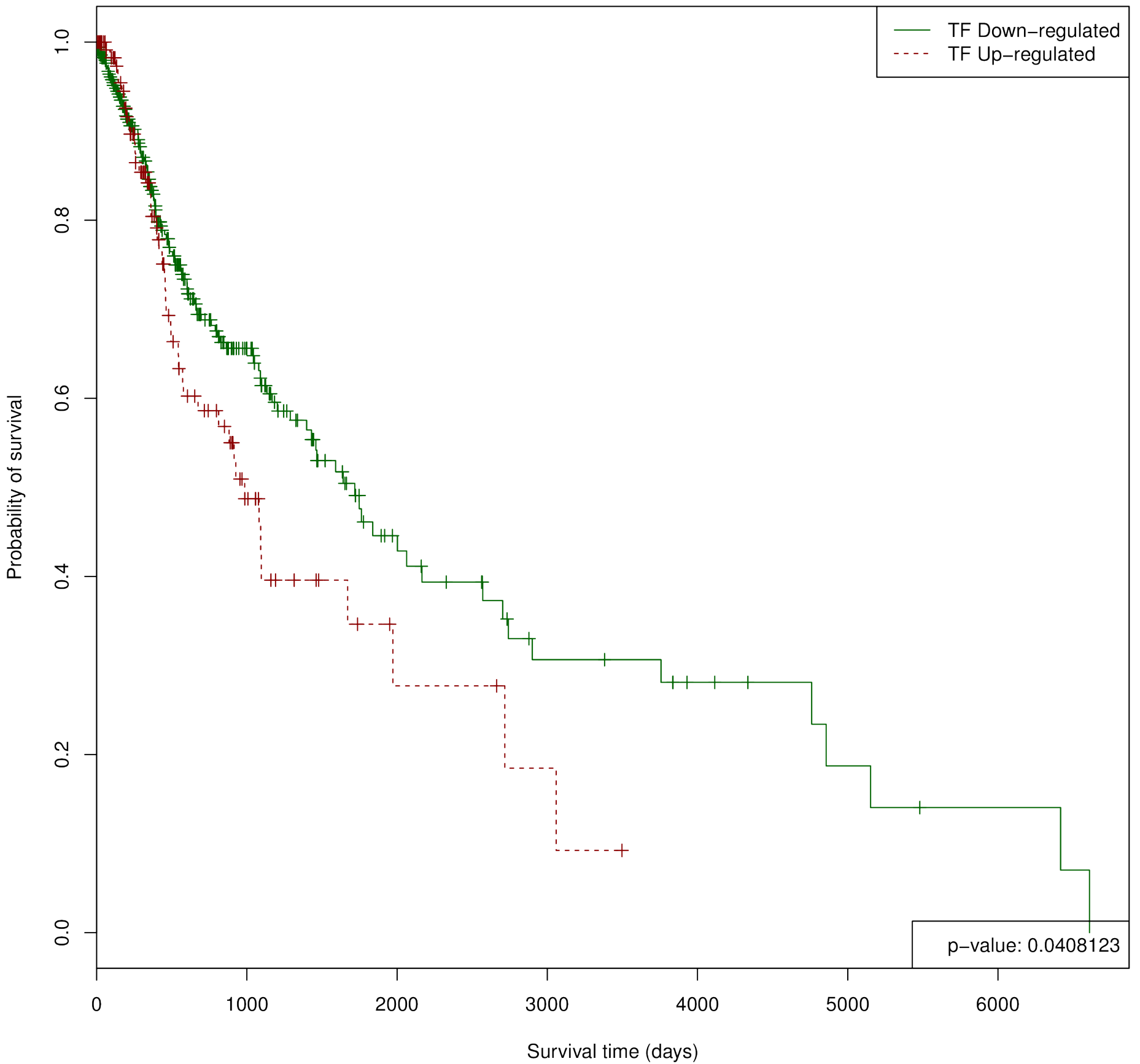
# ETS1 in HNSC



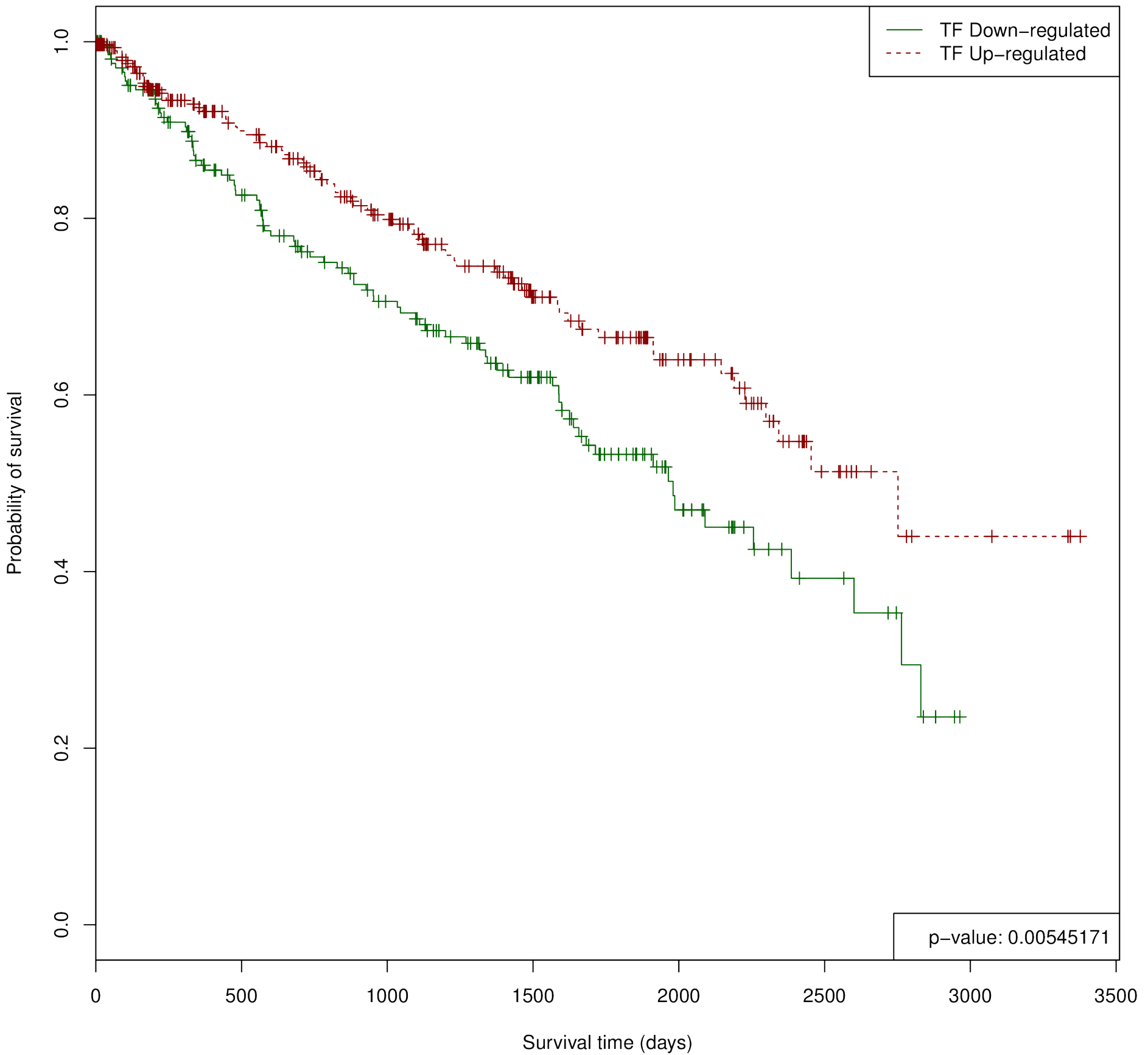
# ETS1 in KIRC



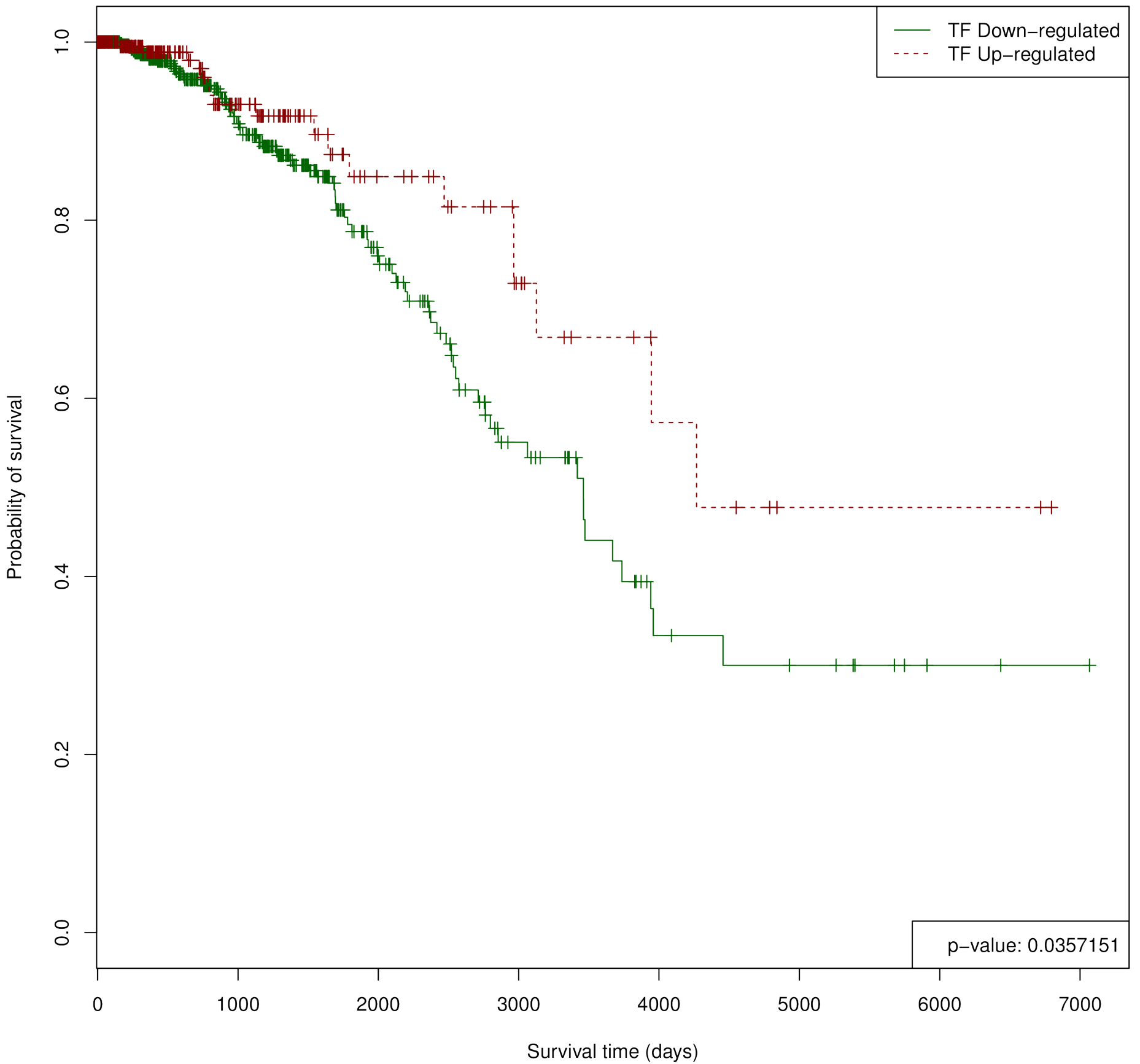
# FOS in HNSC



# FOS in KIRC

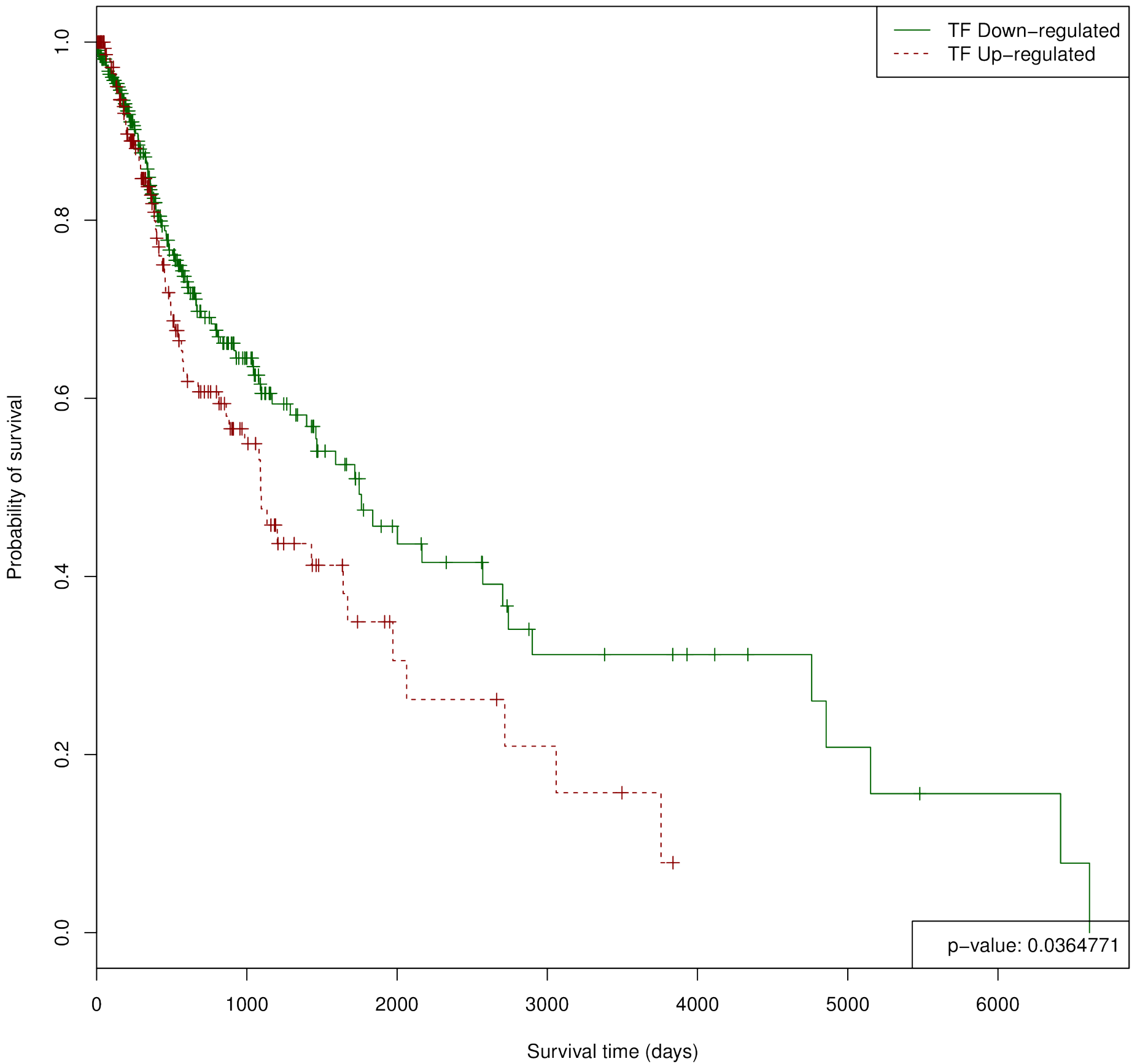


# FOSL1 in BRCA

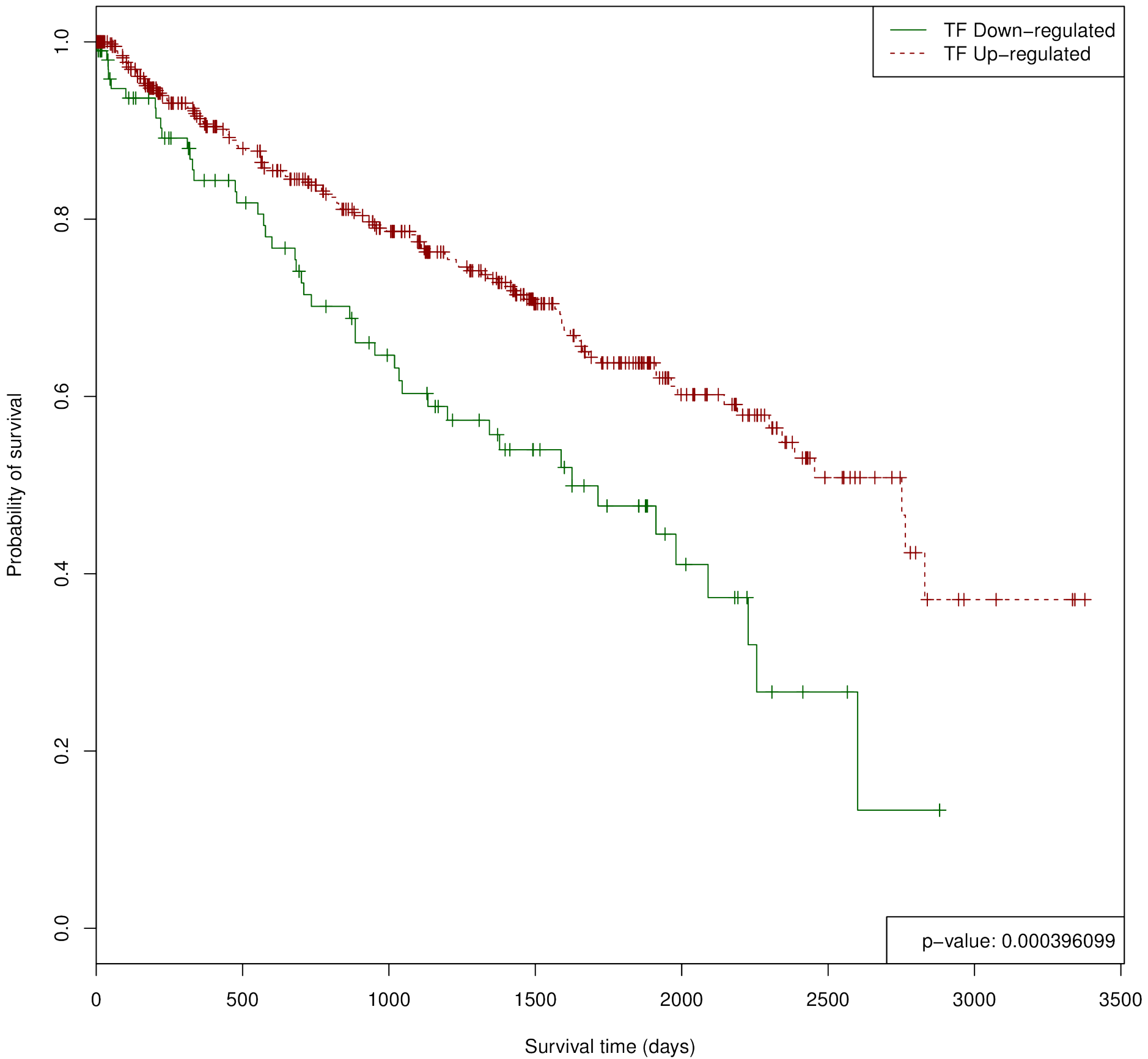




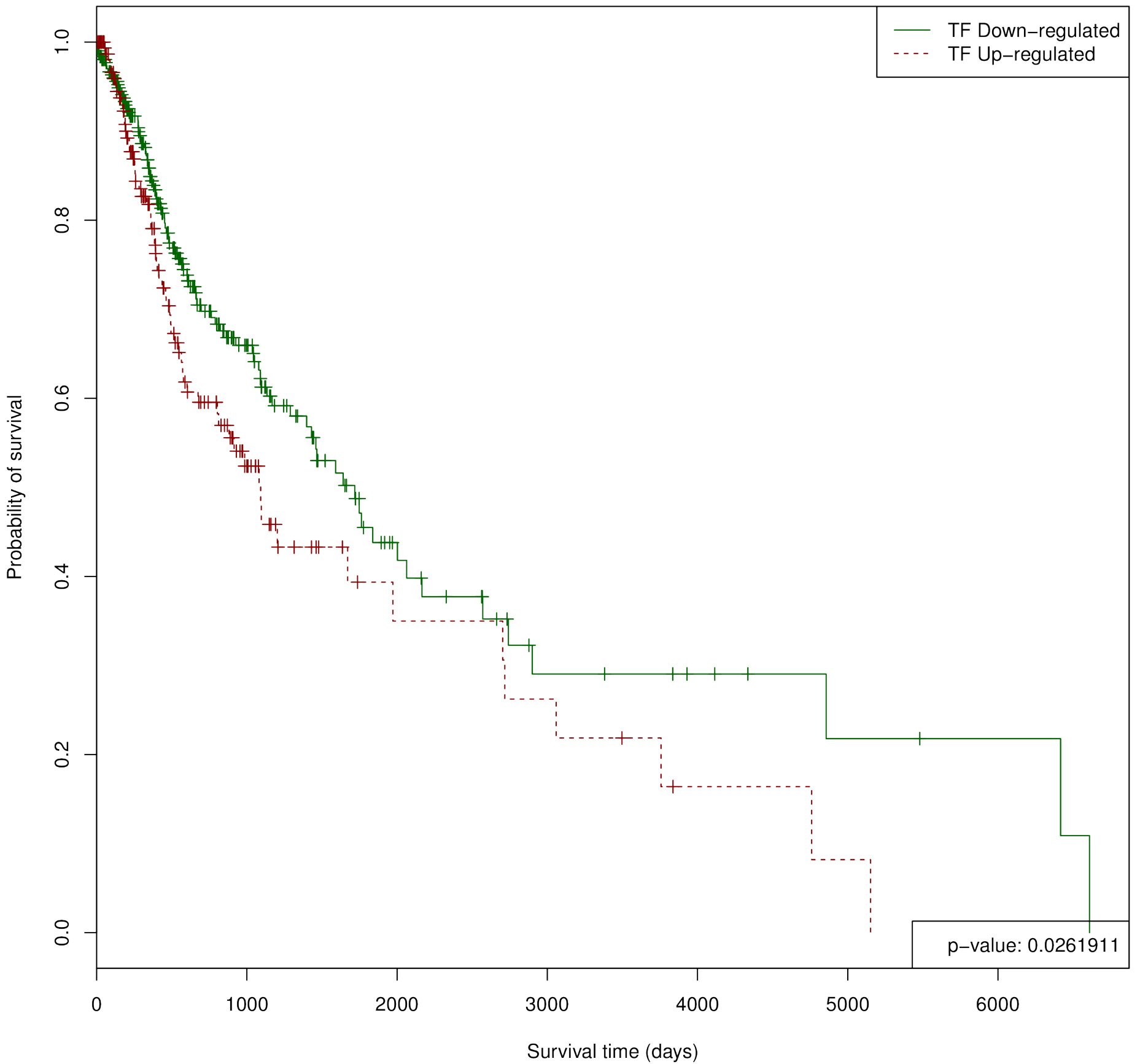
# FOSL1 in HNSC



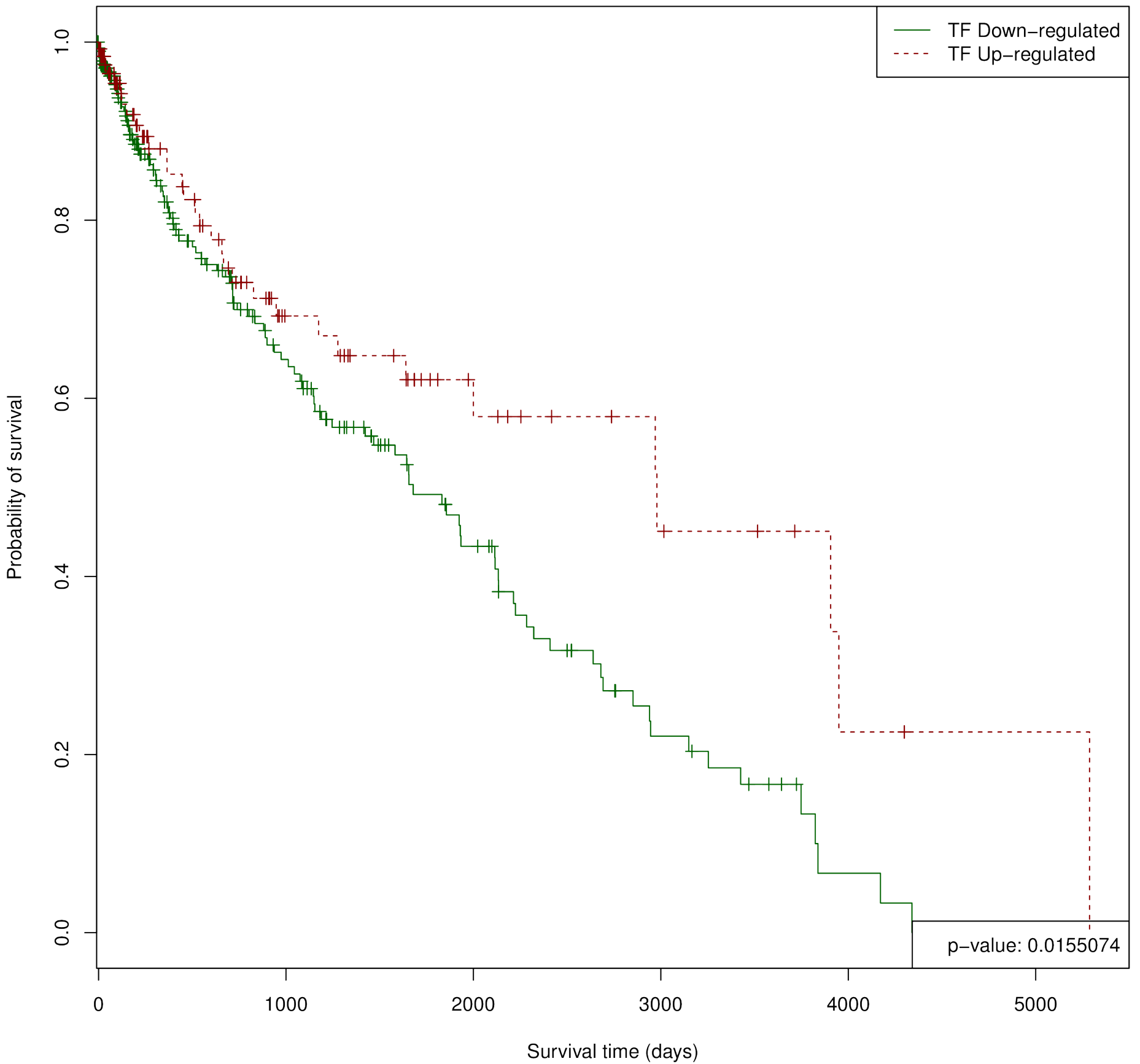
# FOSL1 in KIRC



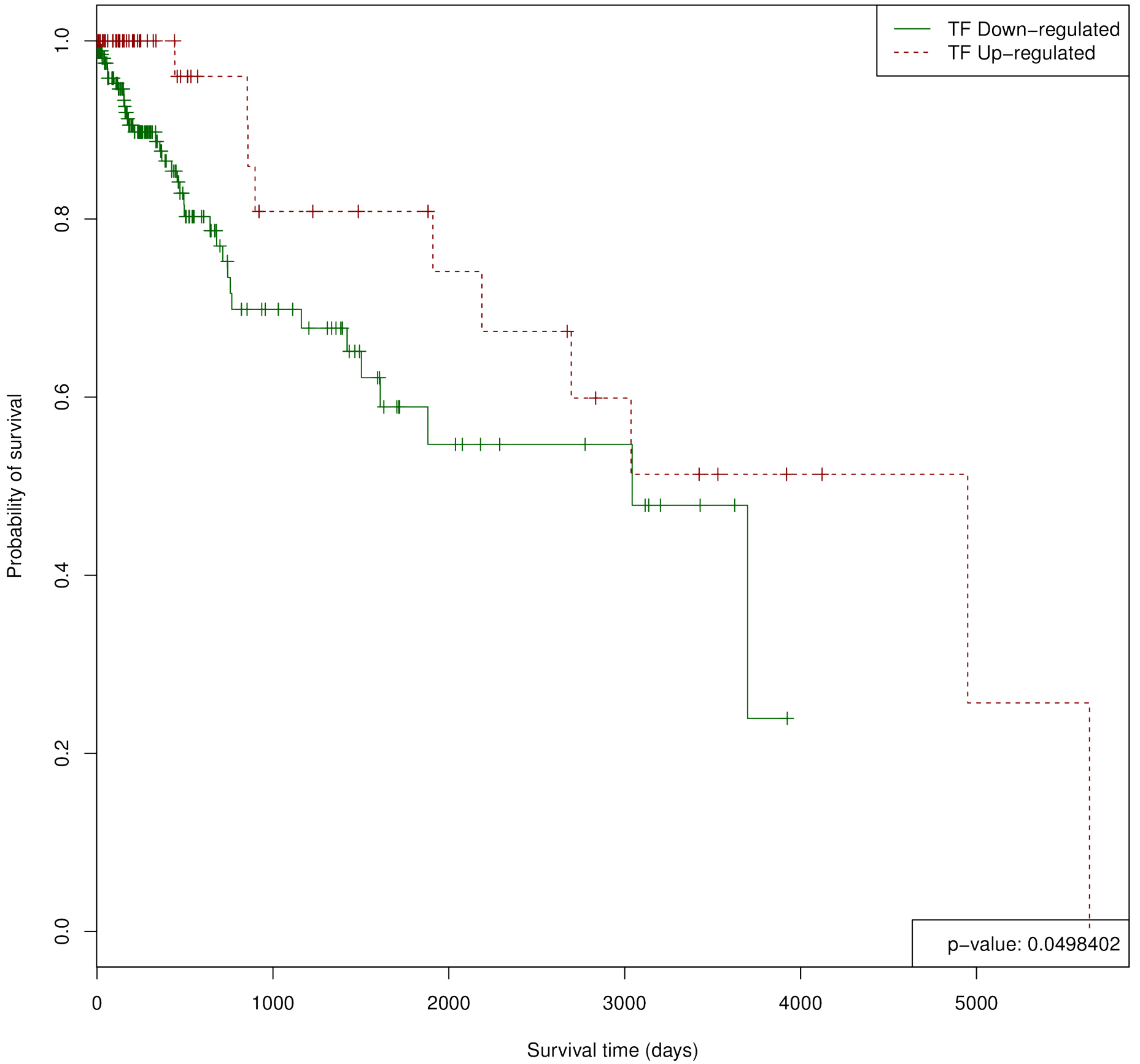
# FOSL2 in HNSC



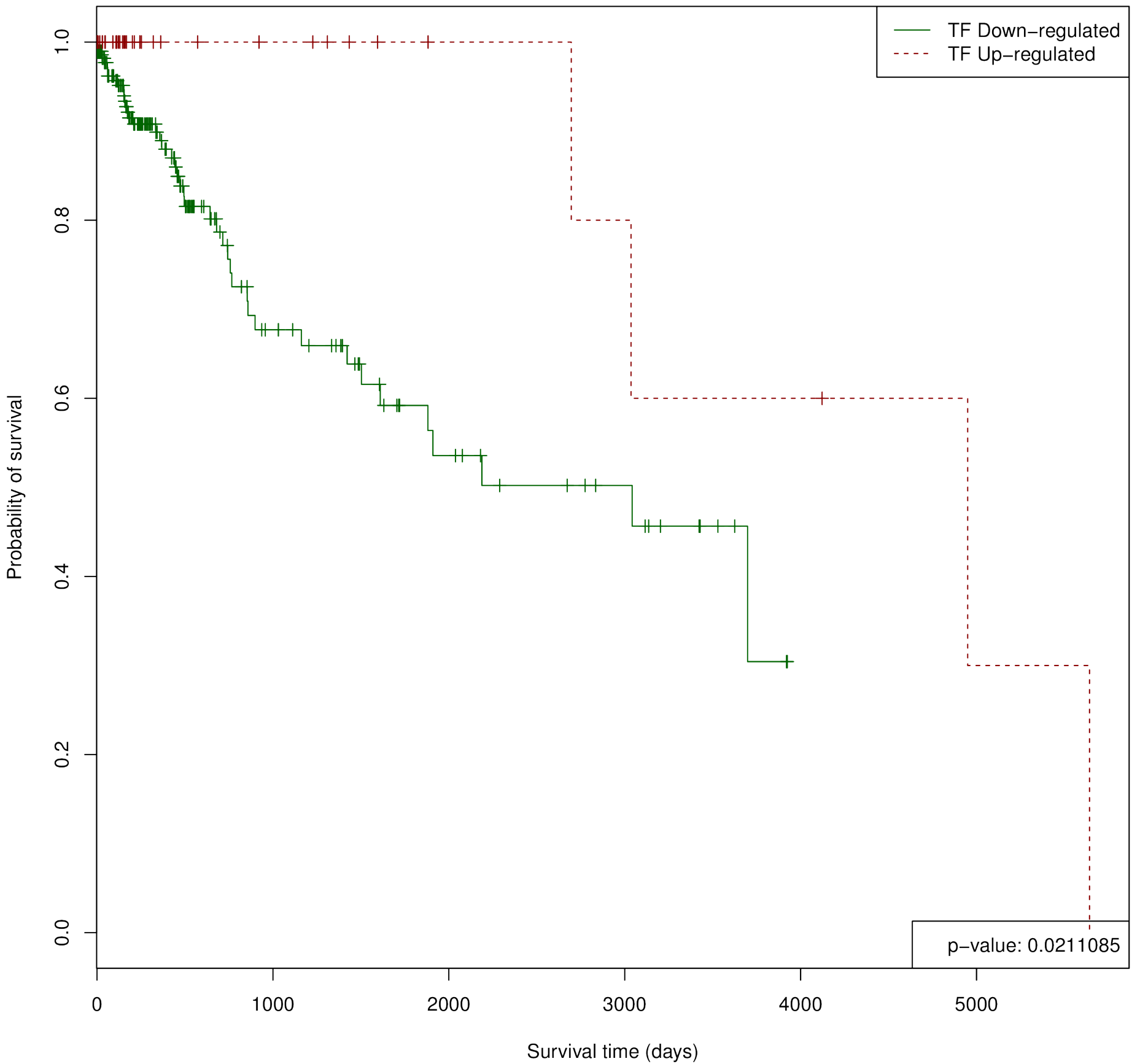
# FOS in LUSC



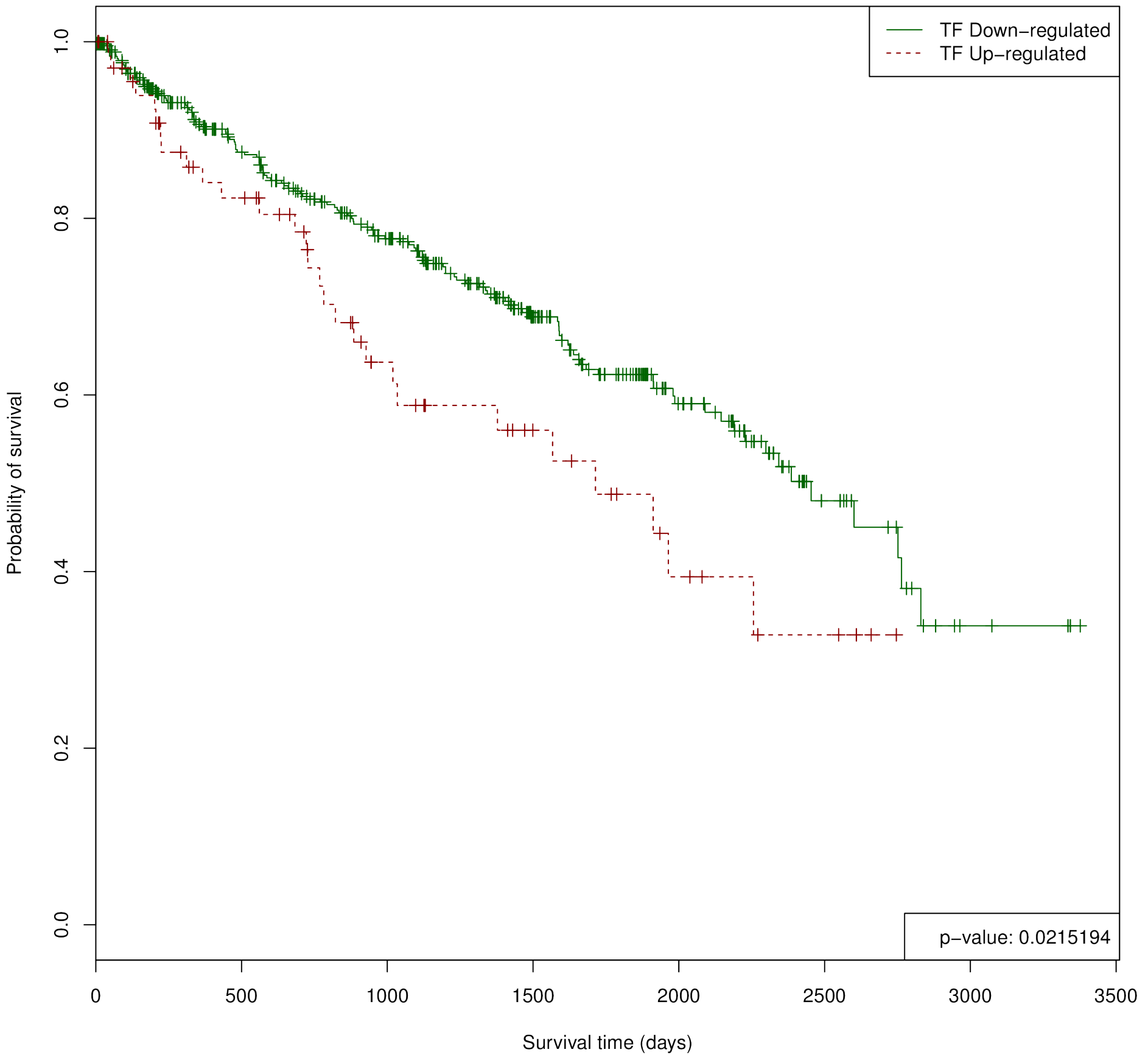
# FOXA1 in COAD



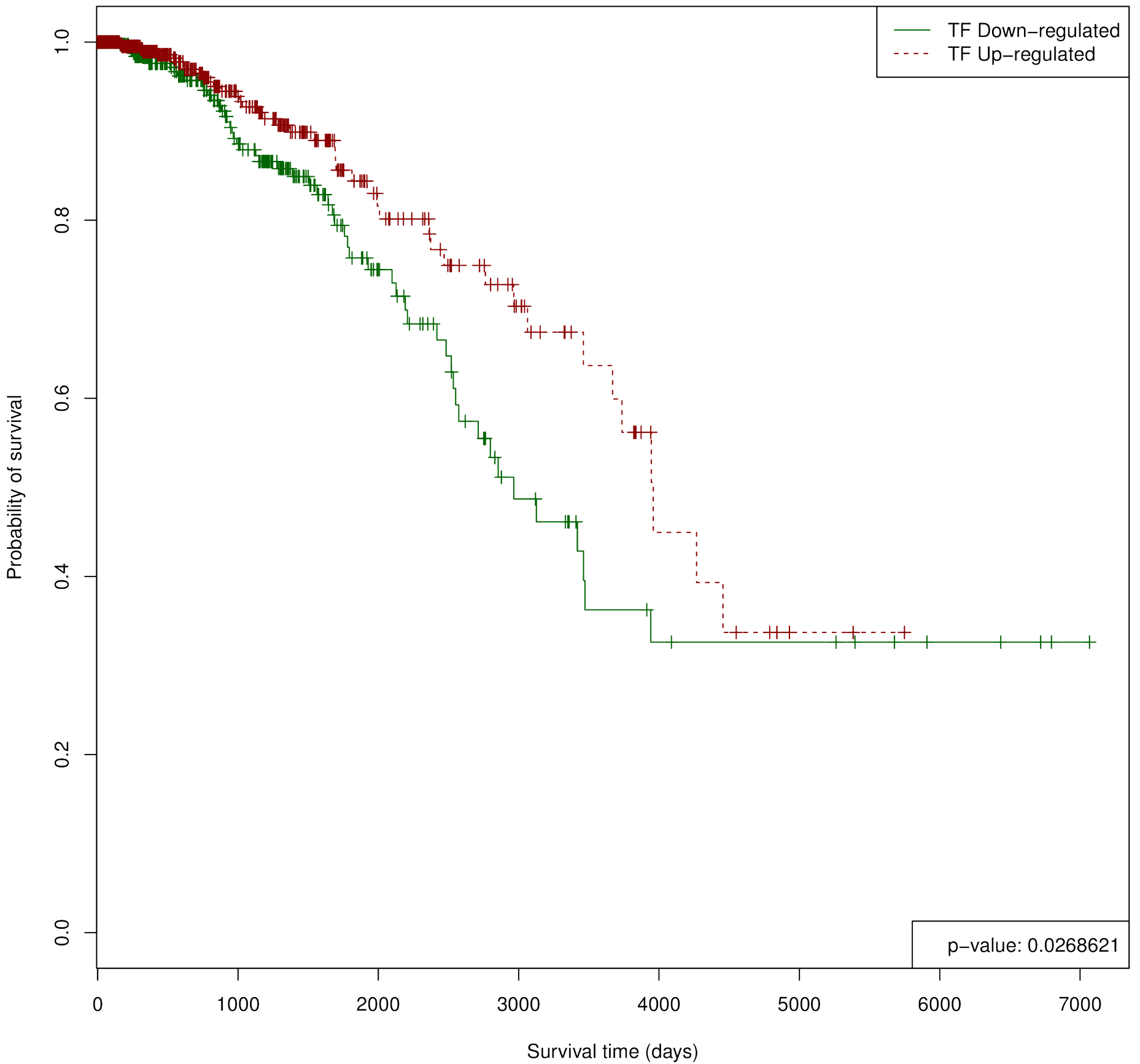
# FOXA2 in COAD



# FOXA2 in KIRC

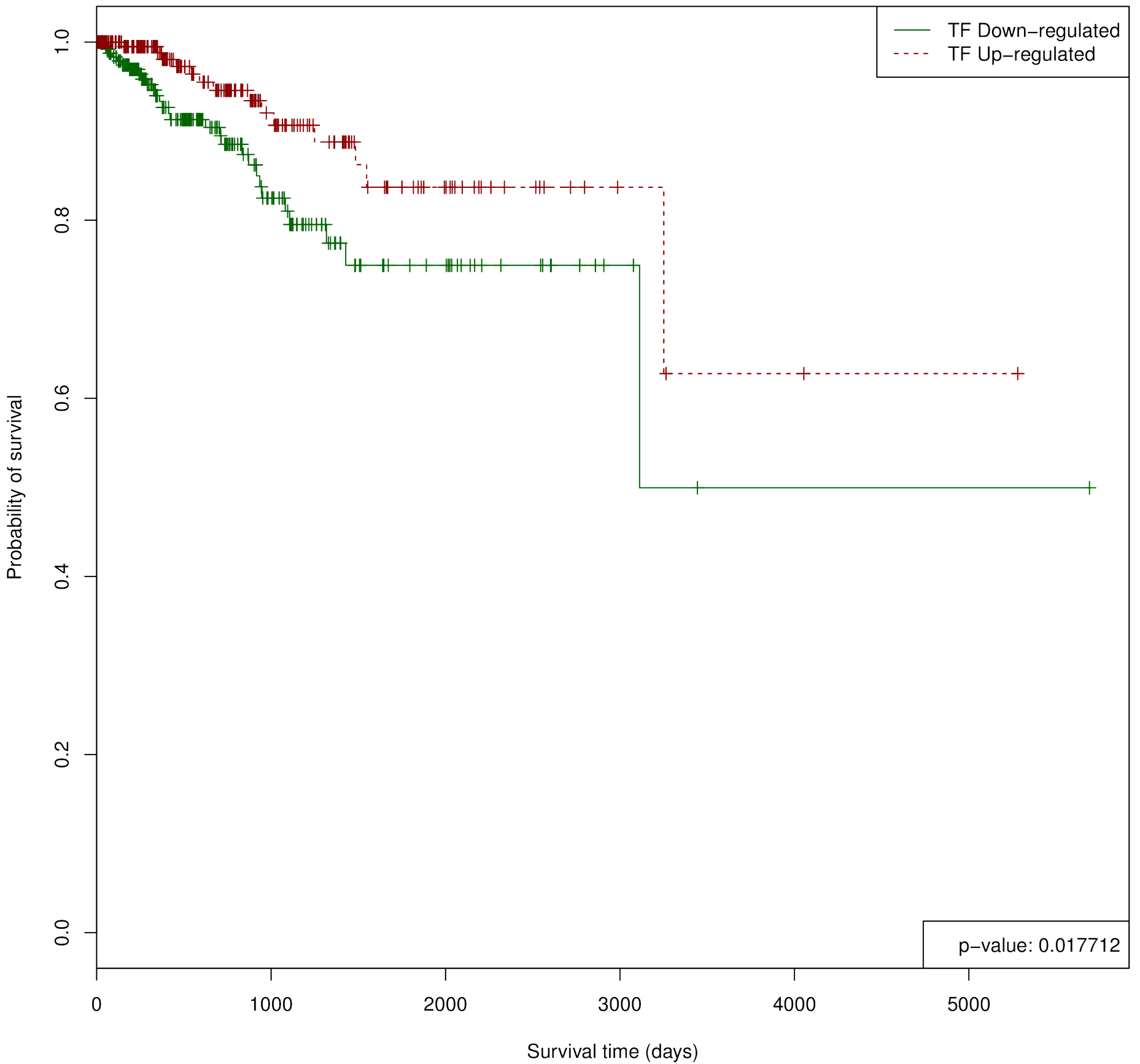


# GATA2 in BRCA

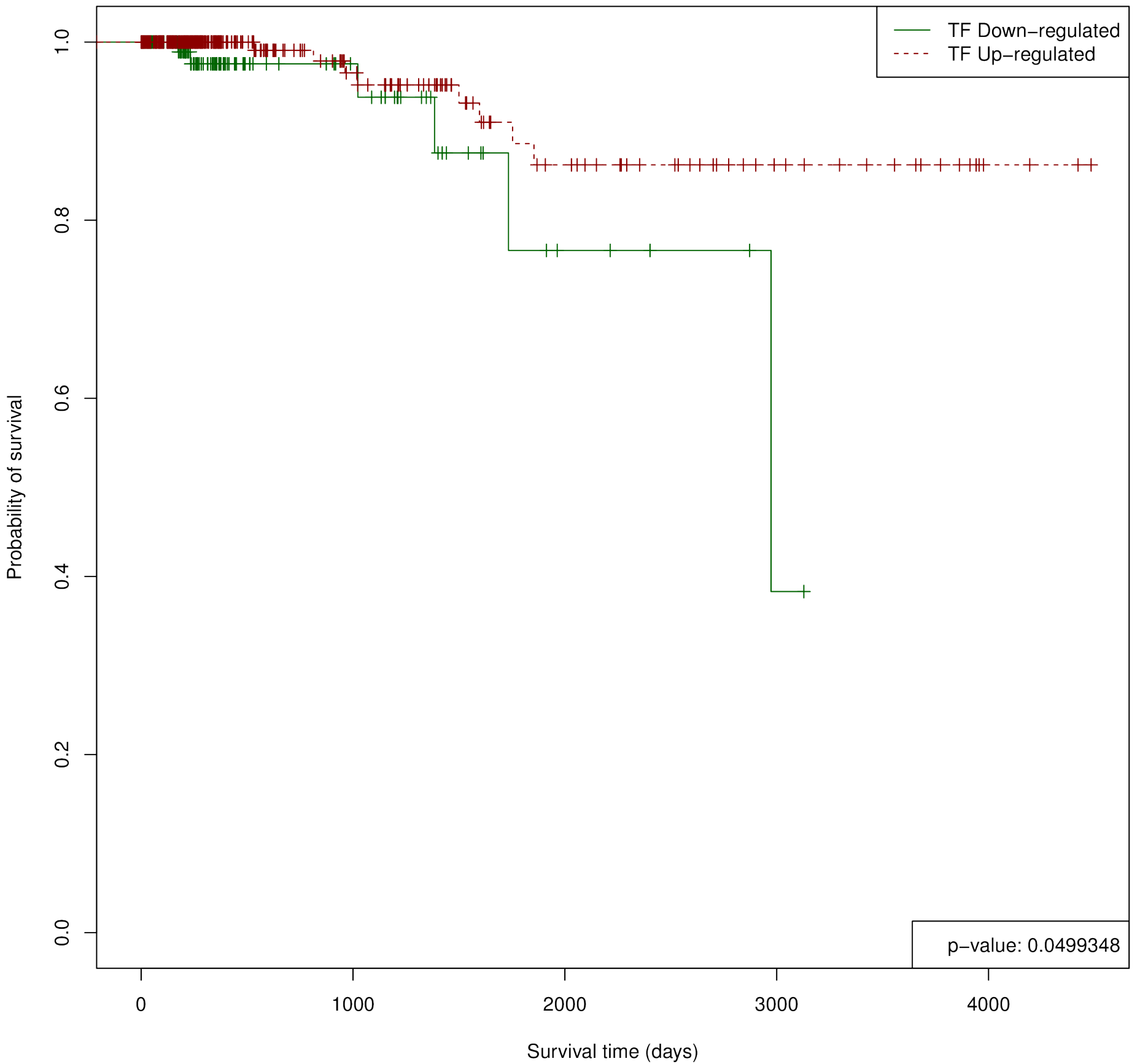




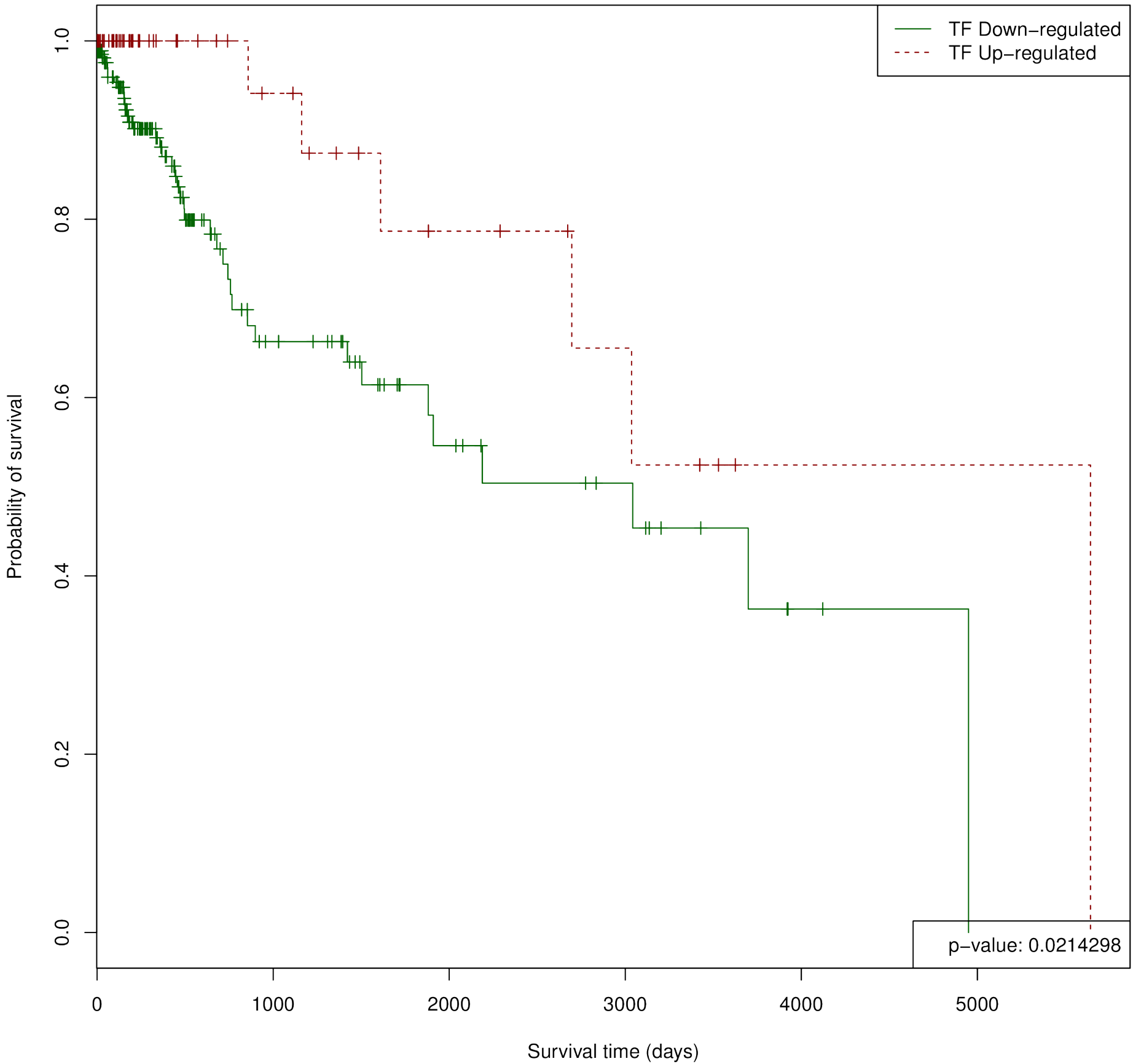
# GATA2 in UCEC



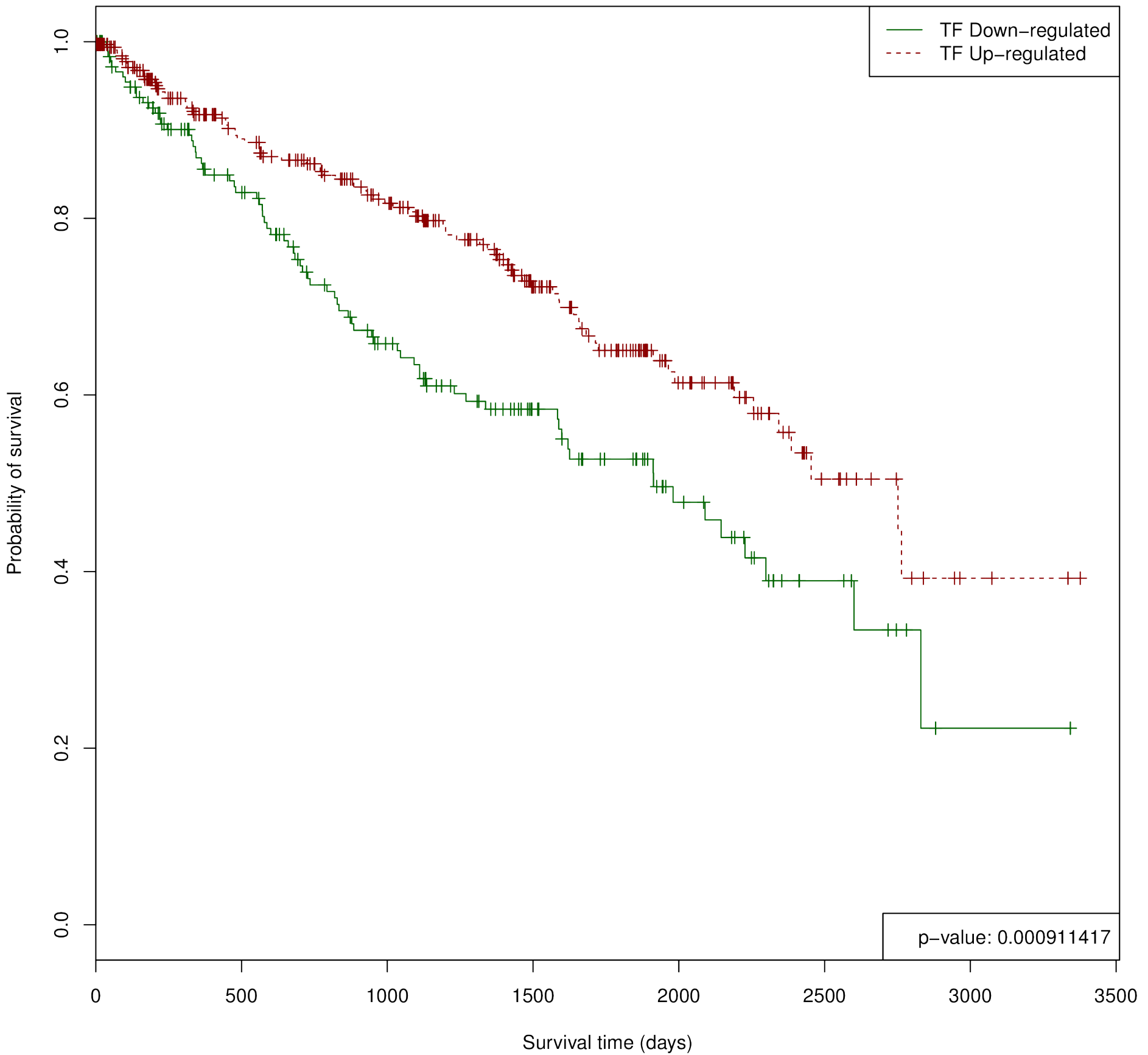
# HNF4A in THCA



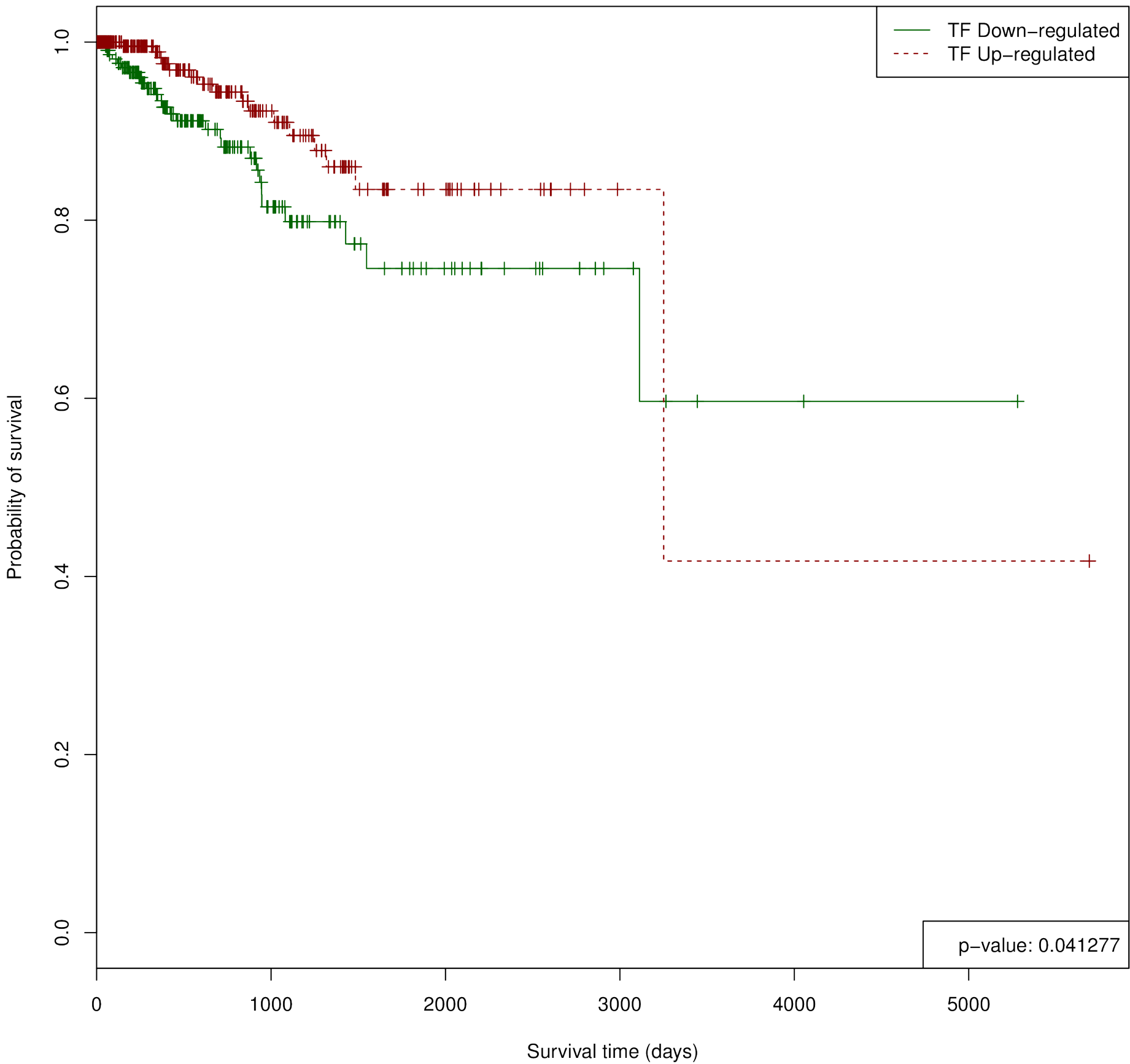
# HNF4G in COAD



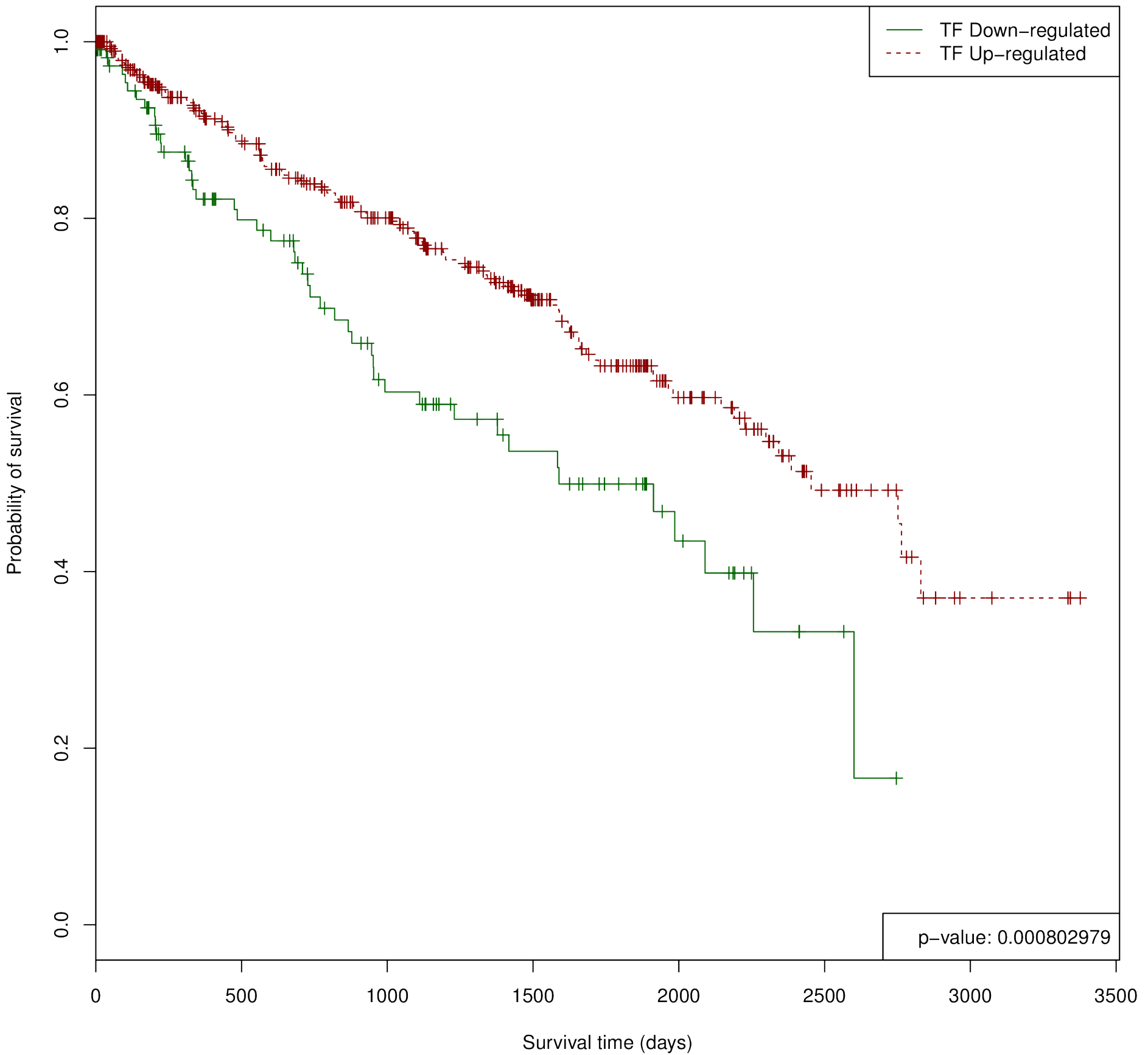
# HNF4G in KIRC



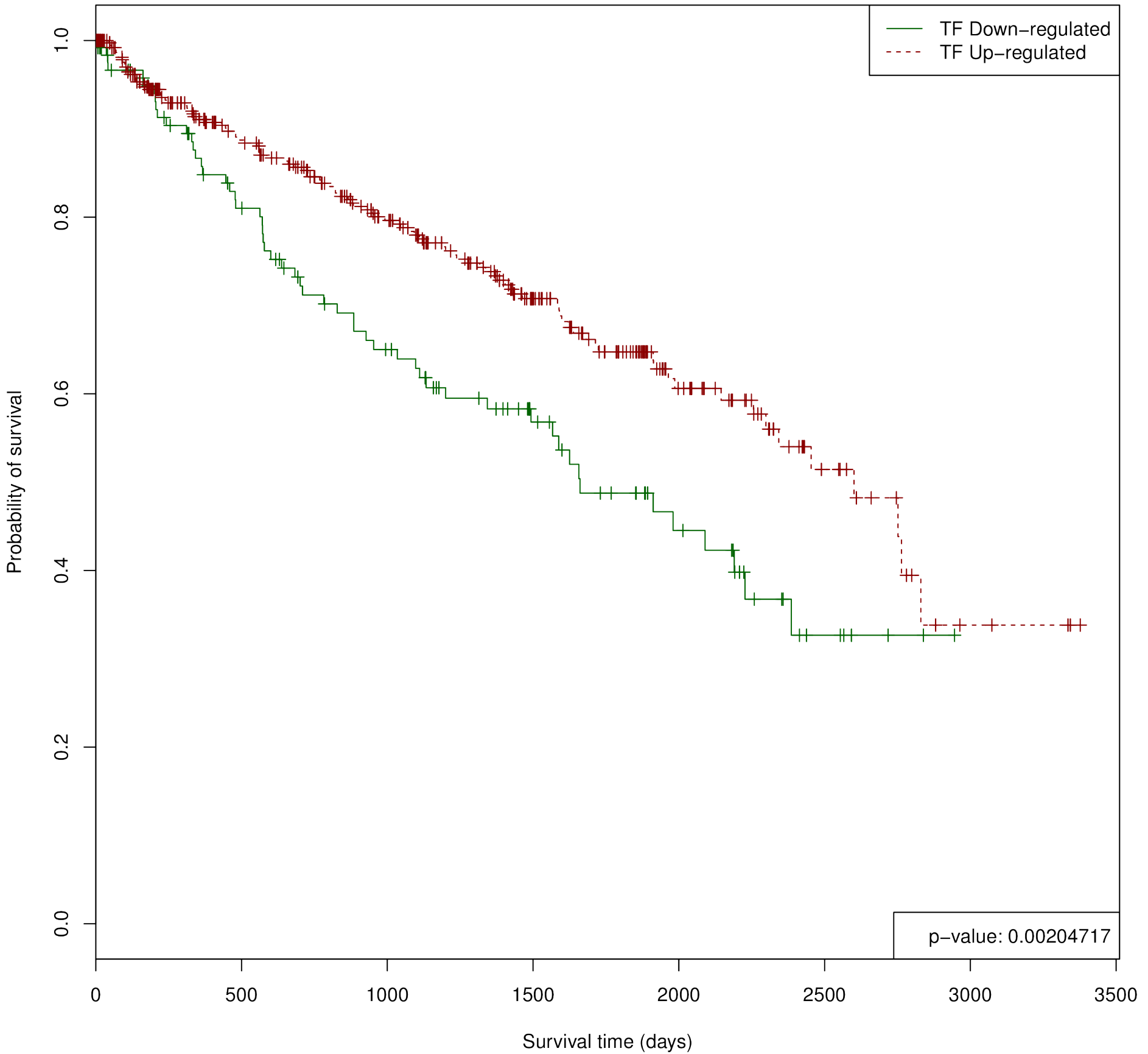
# HNF4G in UCEC



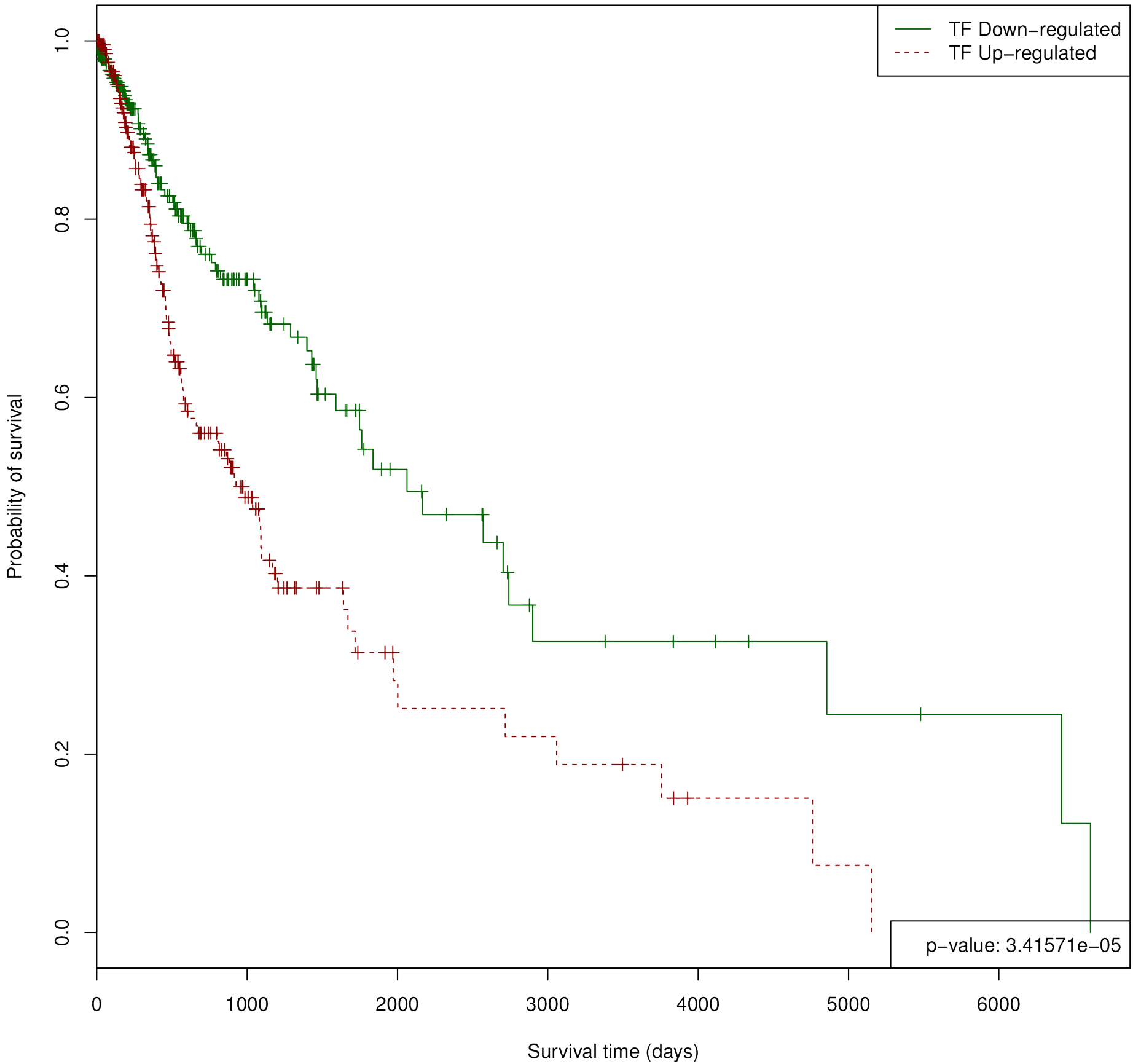
# IRF4 in KIRC



# JUNB in KIRC

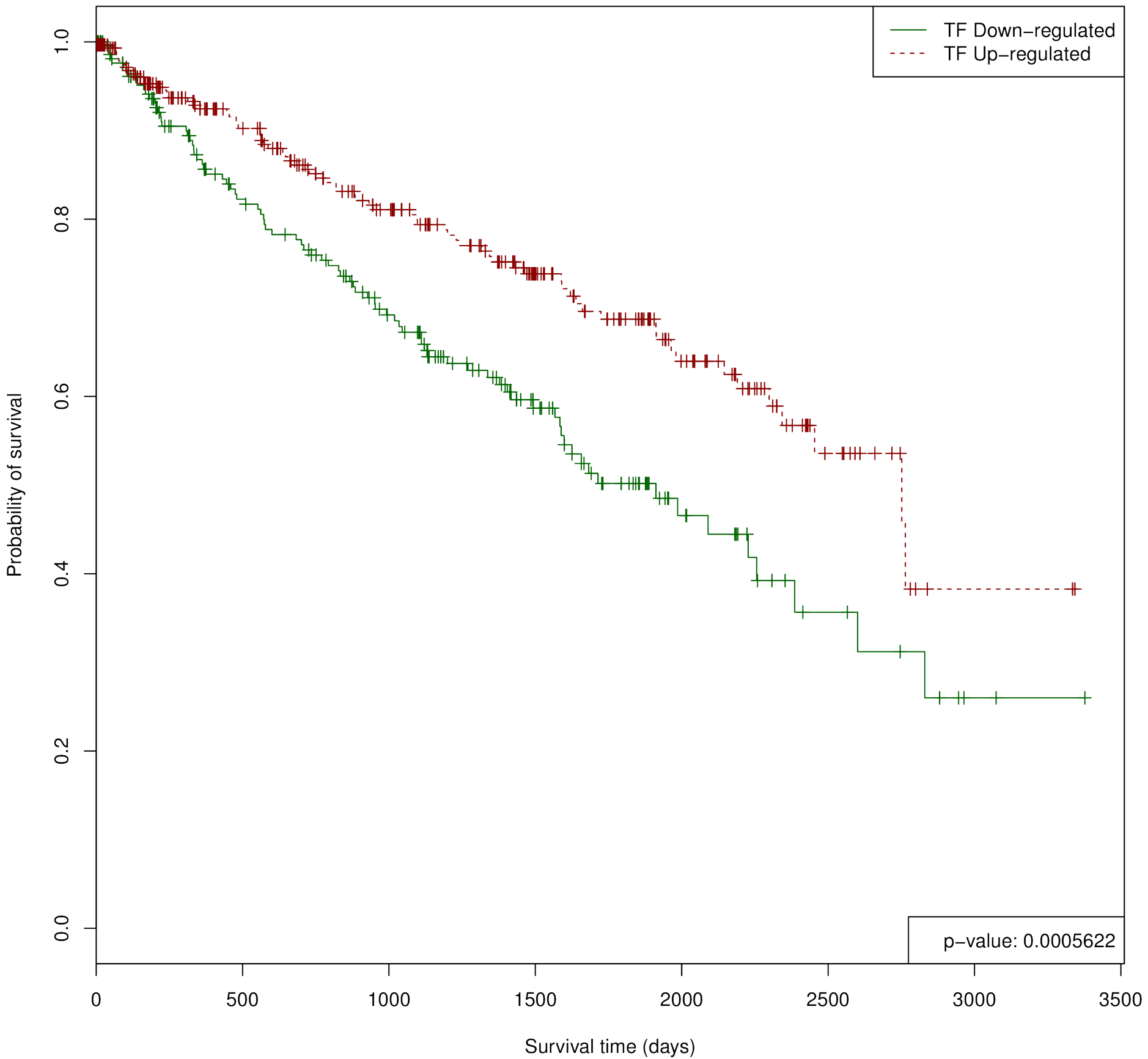


# JUND in HNSC

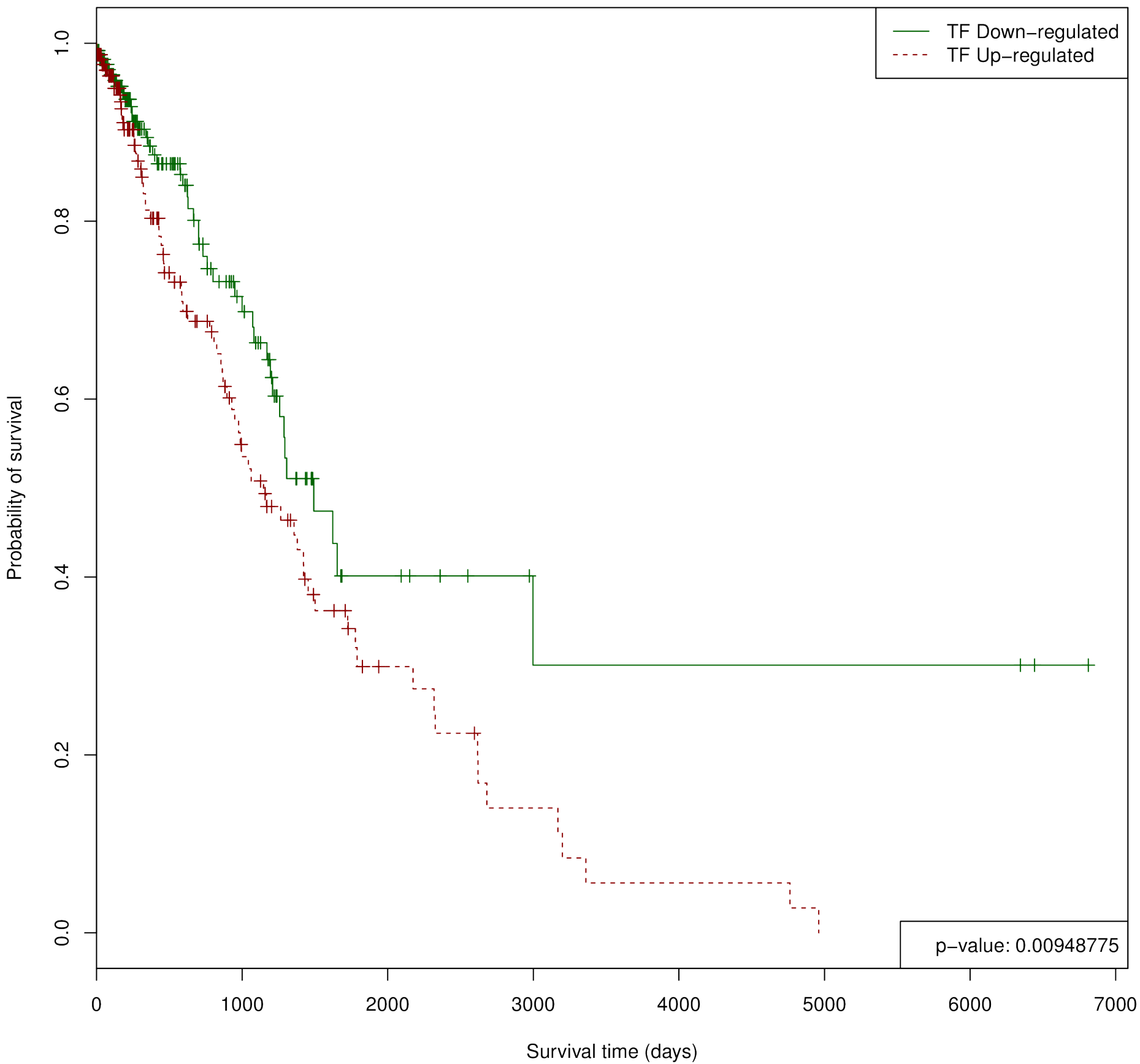




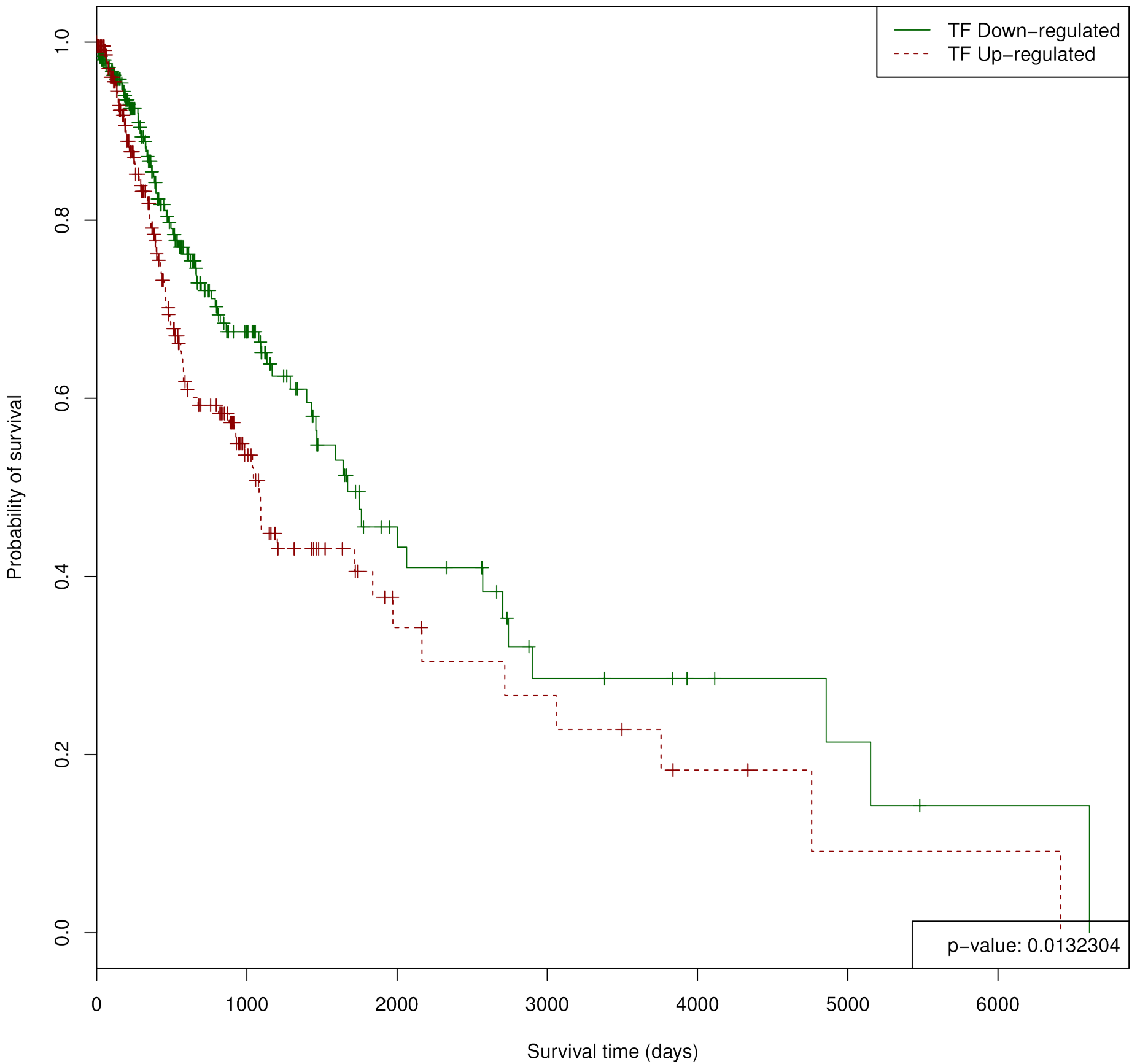
# JUND in KIRC



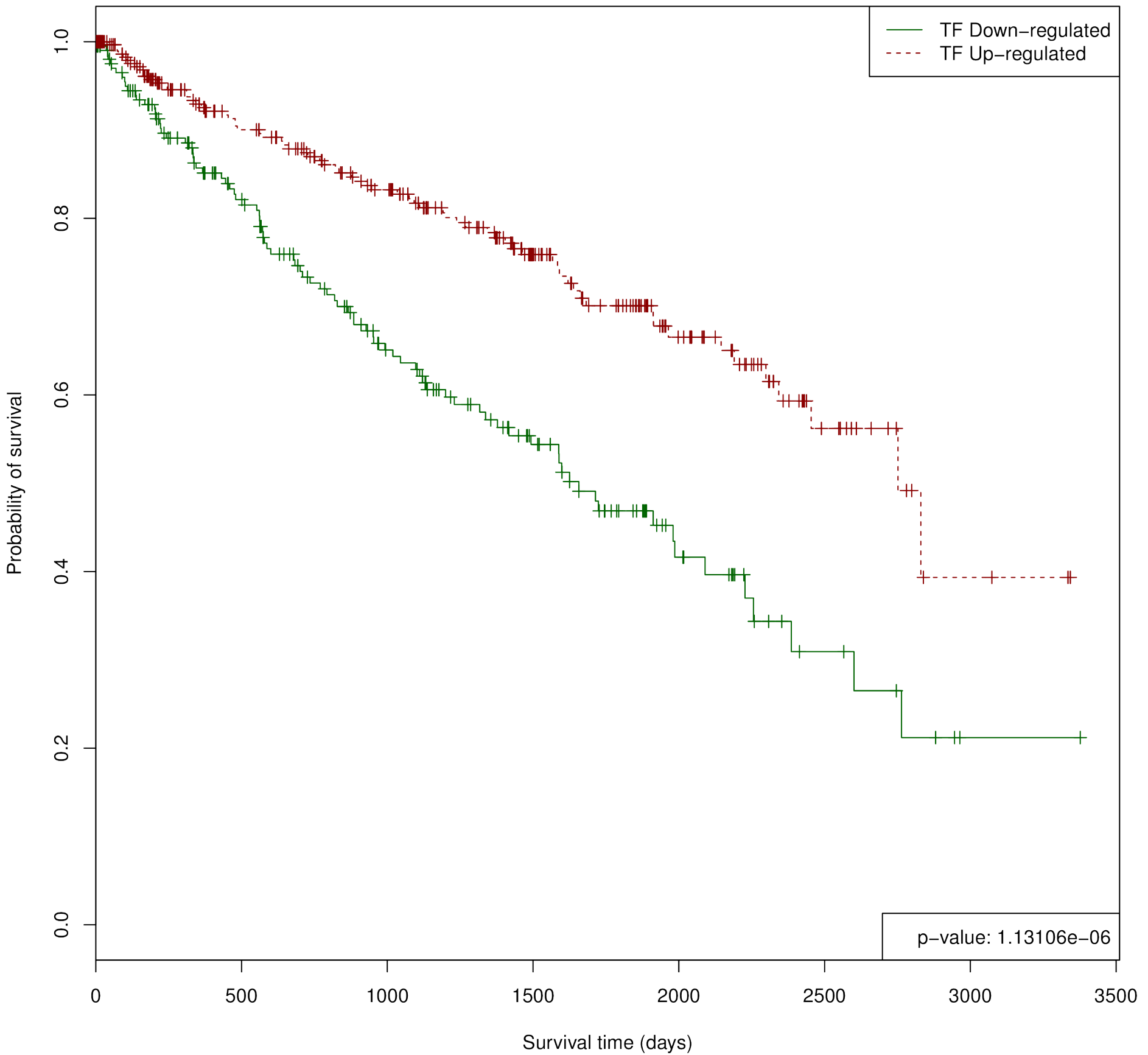
# JUND in LUAD



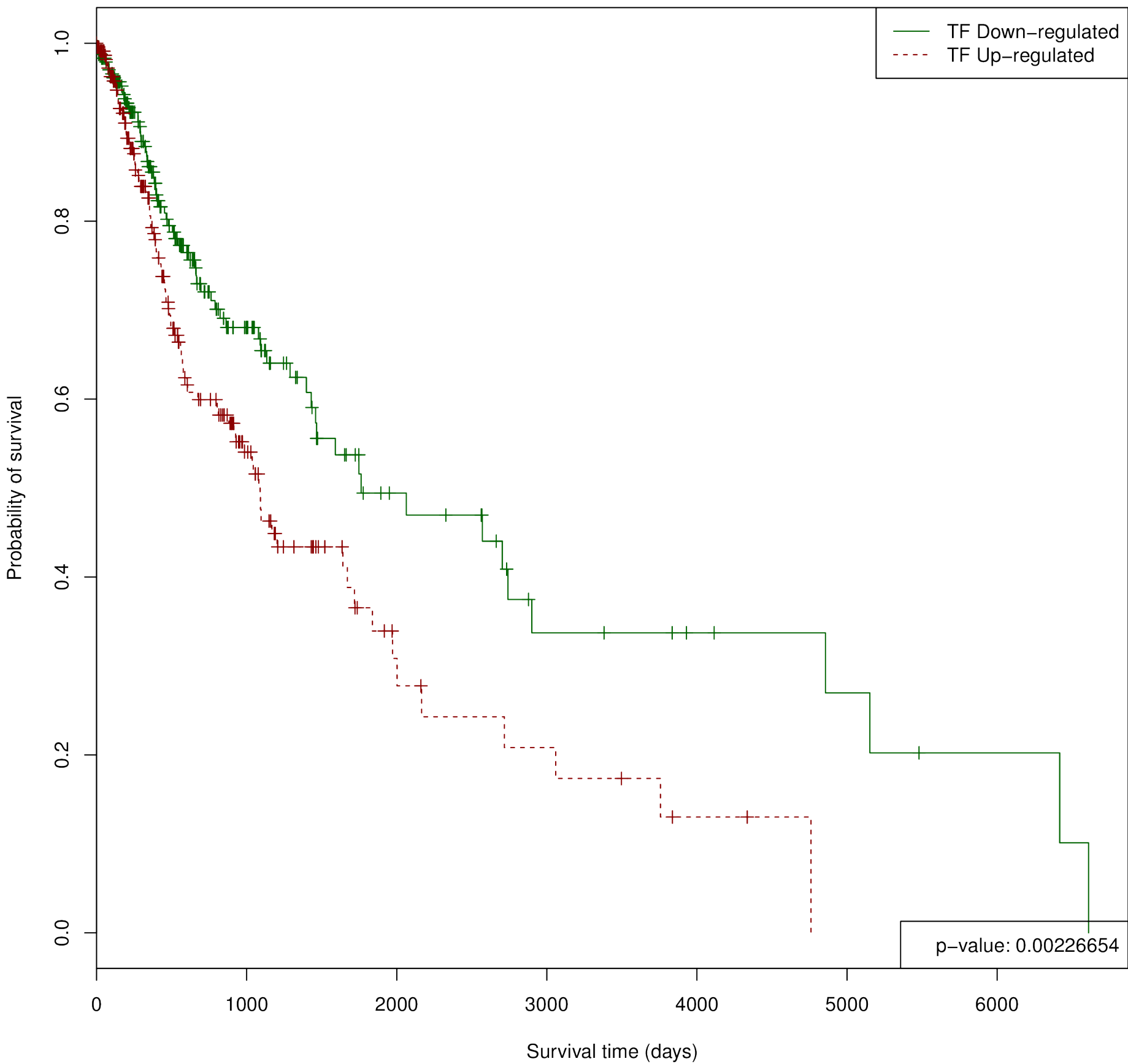
# JUN::FOS in HNSC



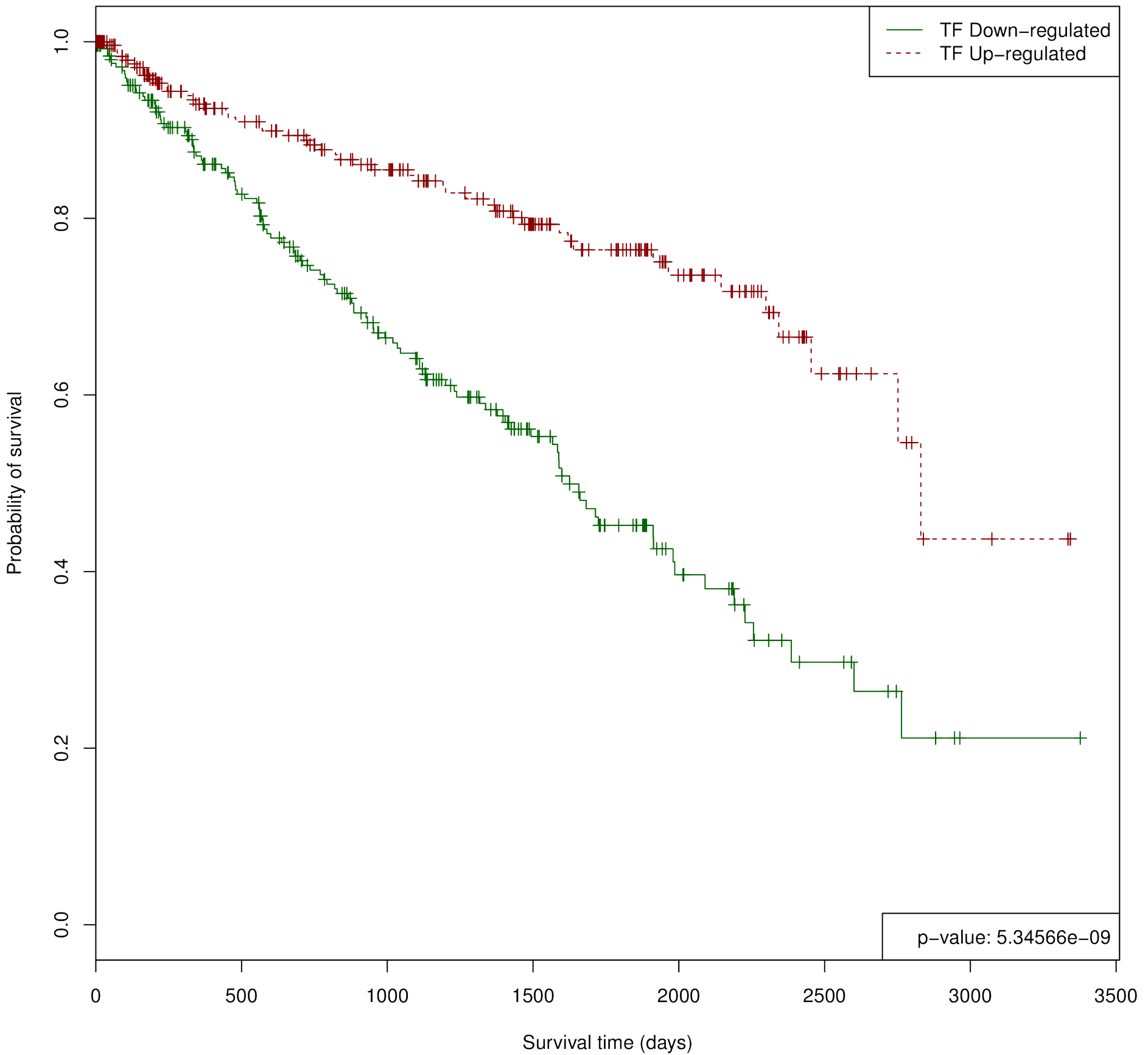
# JUN::FOS in KIRC



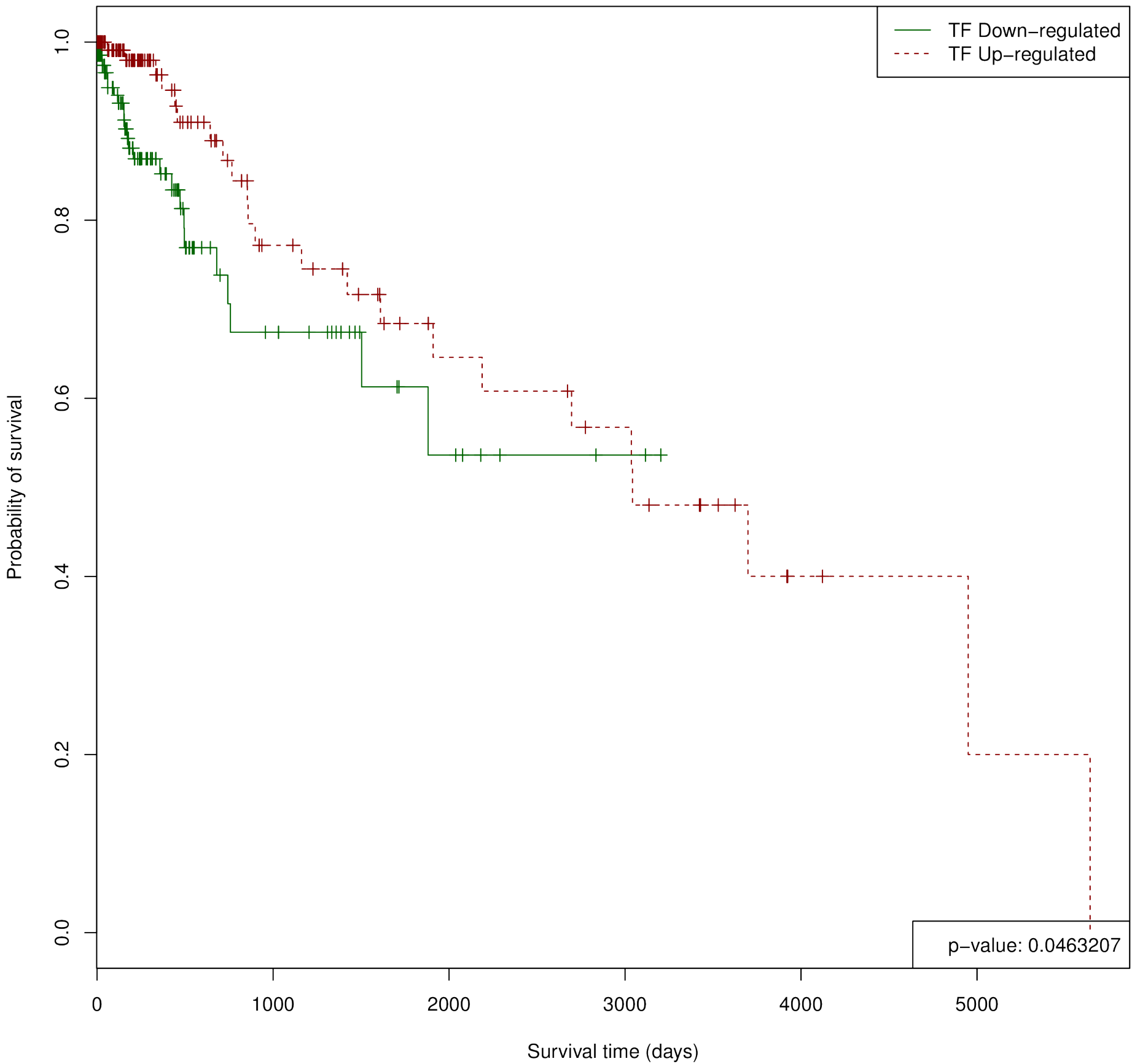
# JUN in HNSC



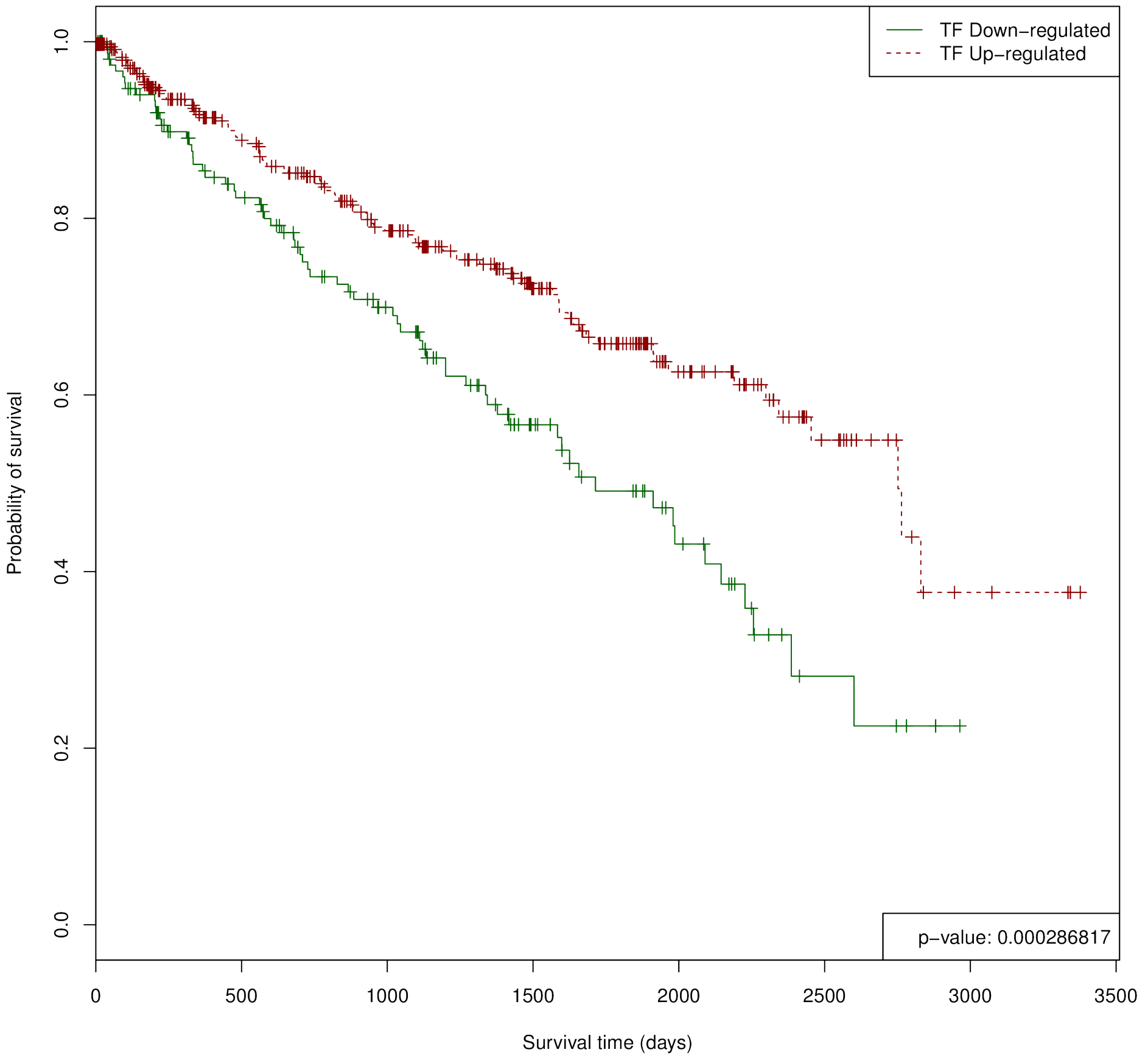
# JUN in KIRC



# MAX in COAD

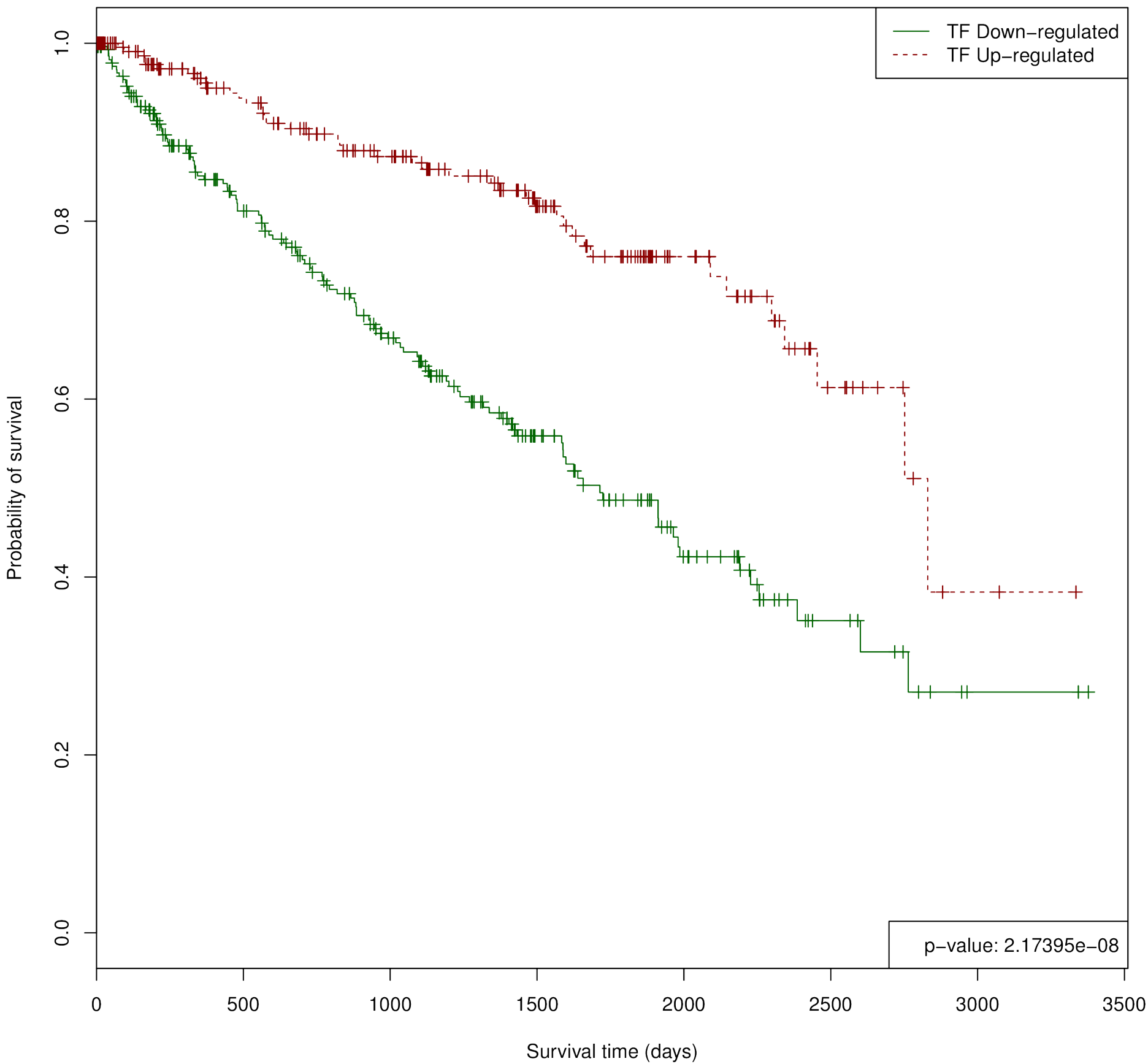


# MAX in KIRC

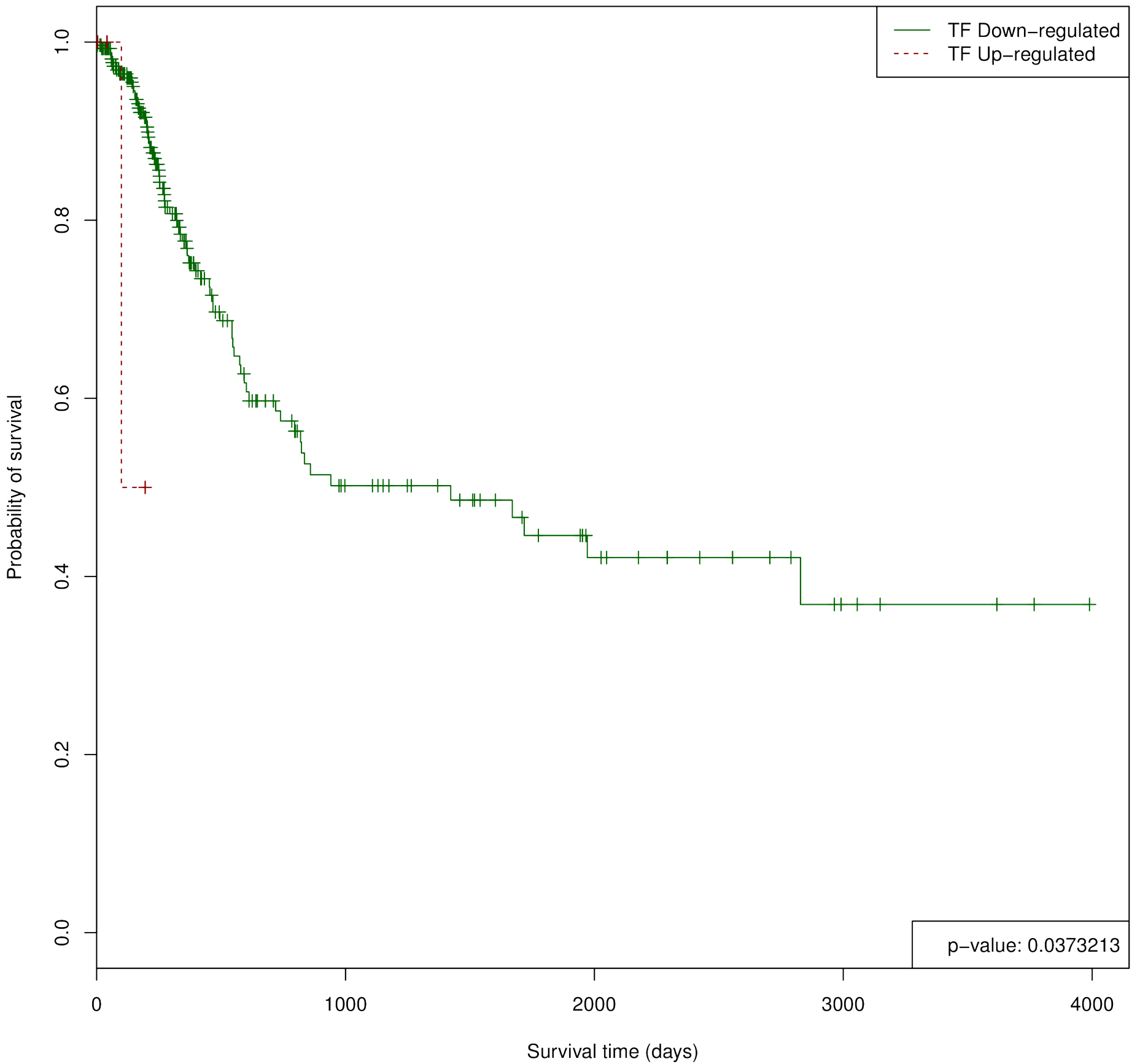




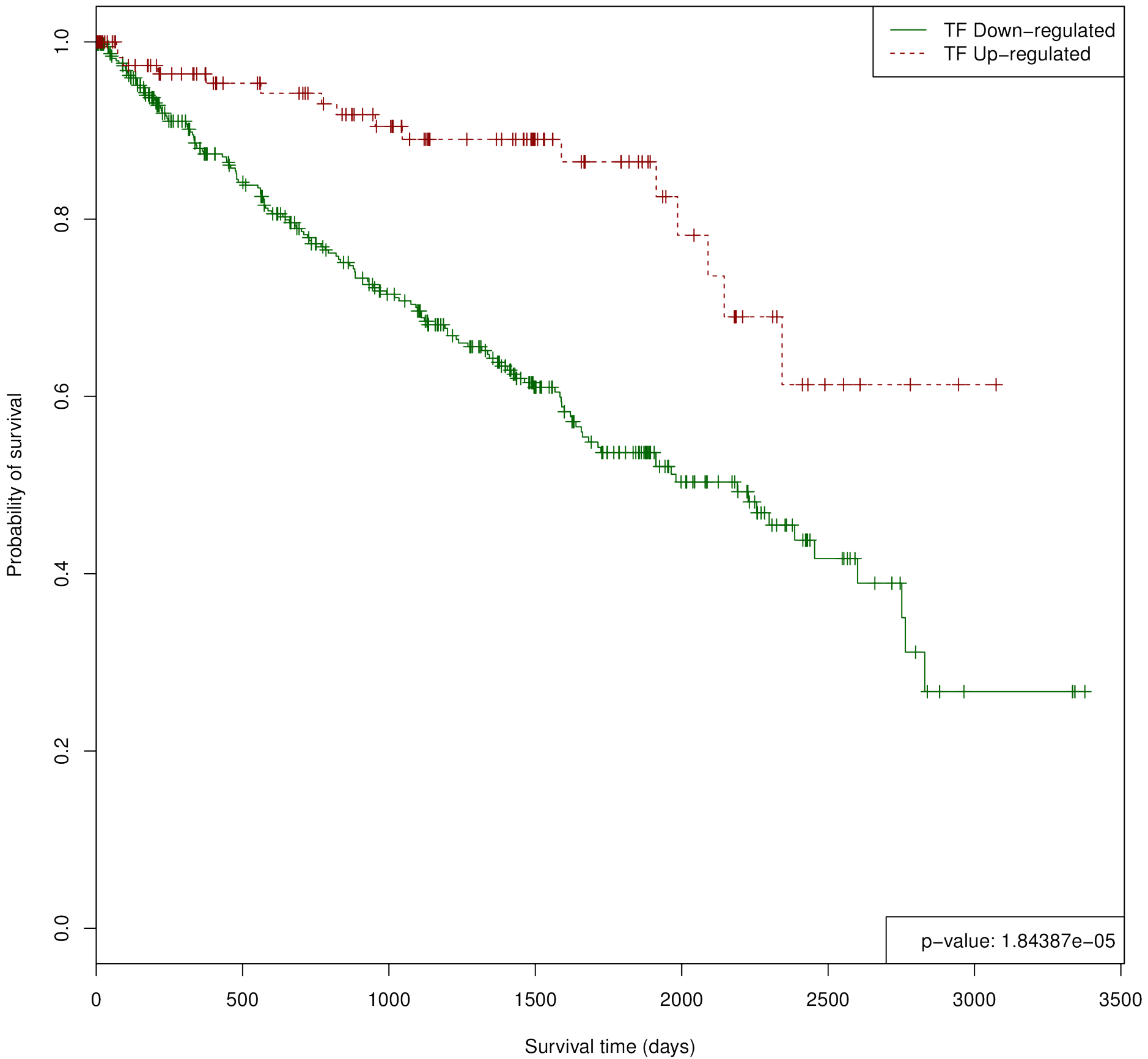
# MEF2A in KIRC



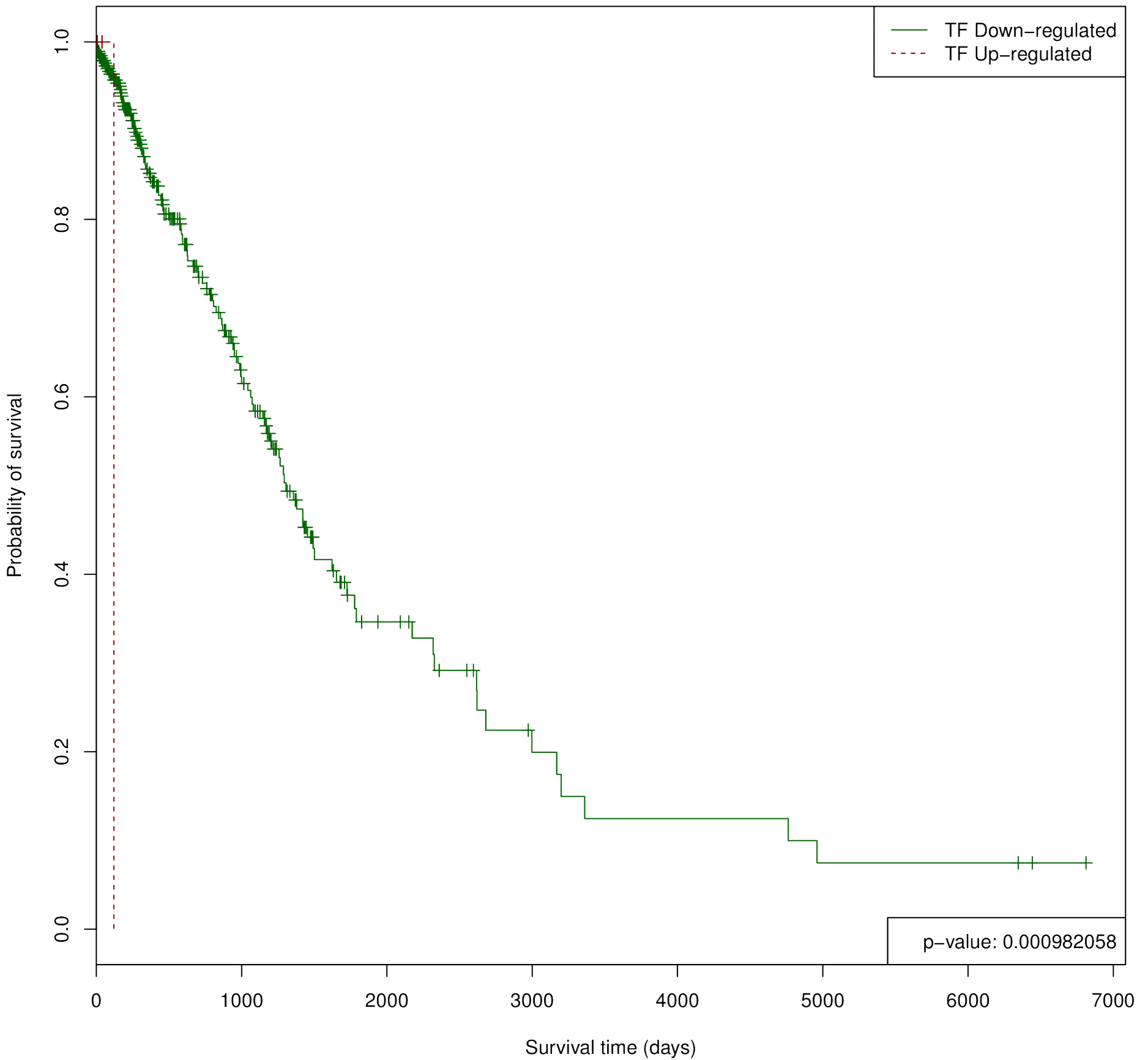
# MEF2C in BLCA



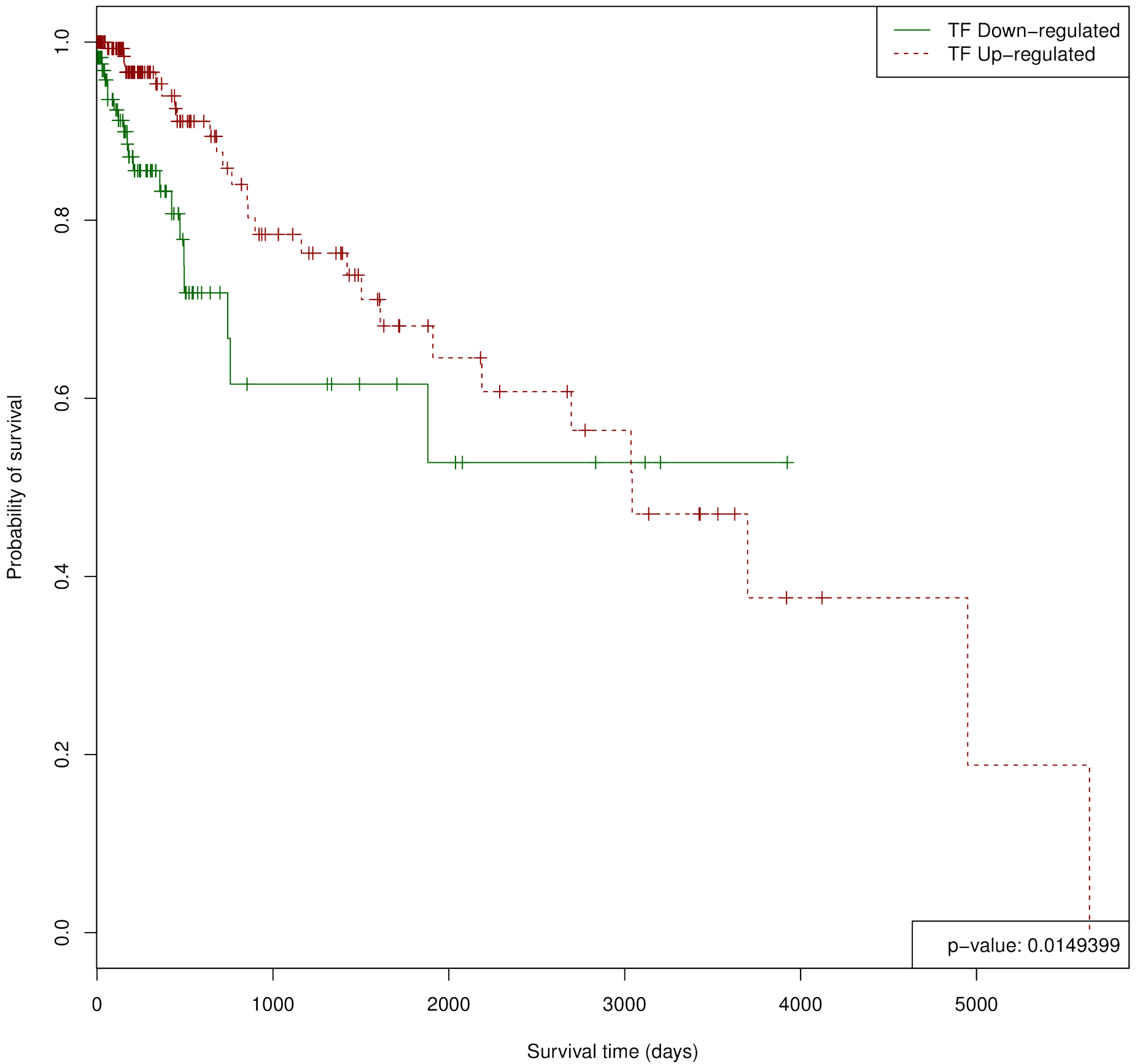
# MEF2C in KIRC



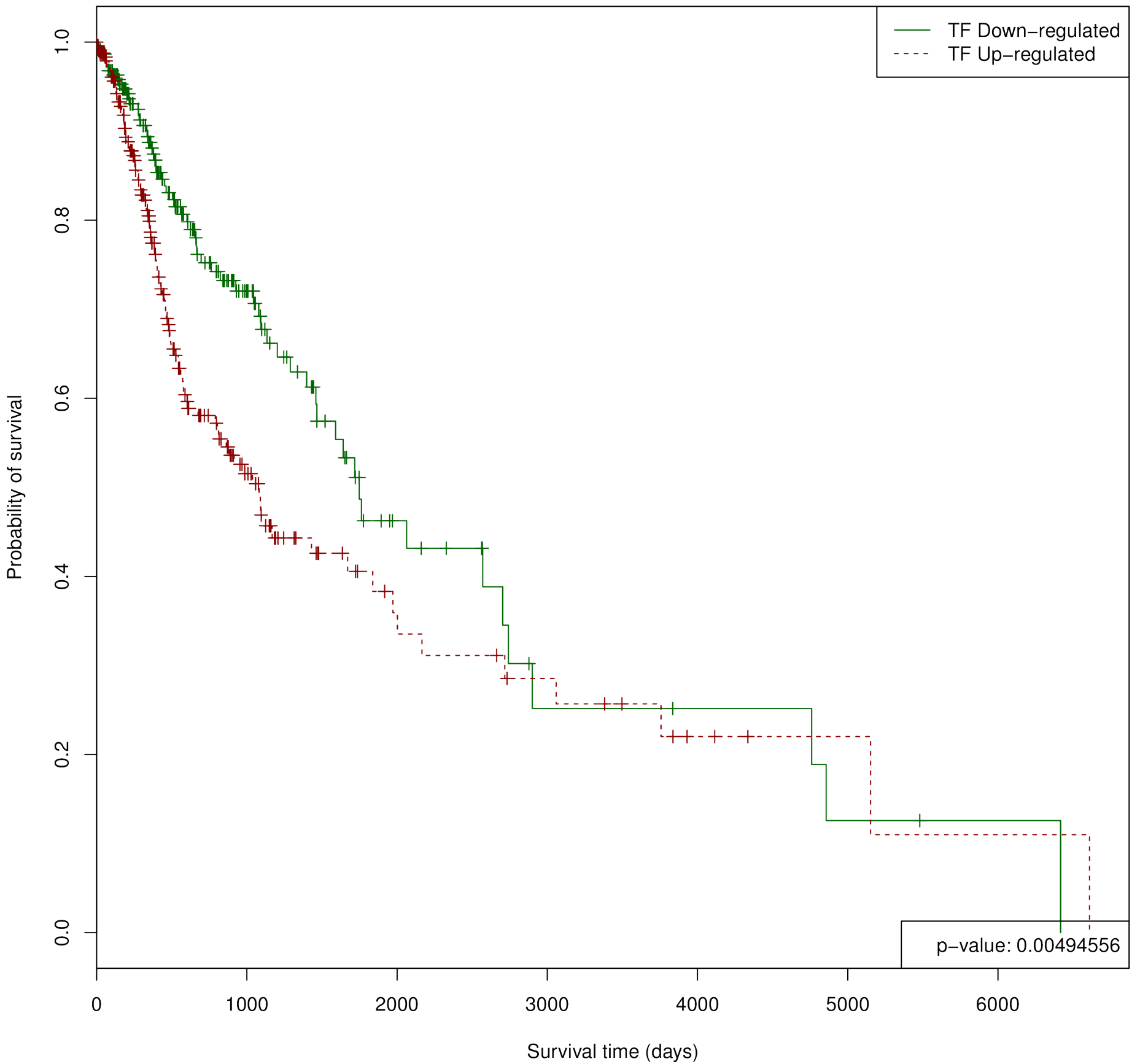
# MEF2C in LUAD



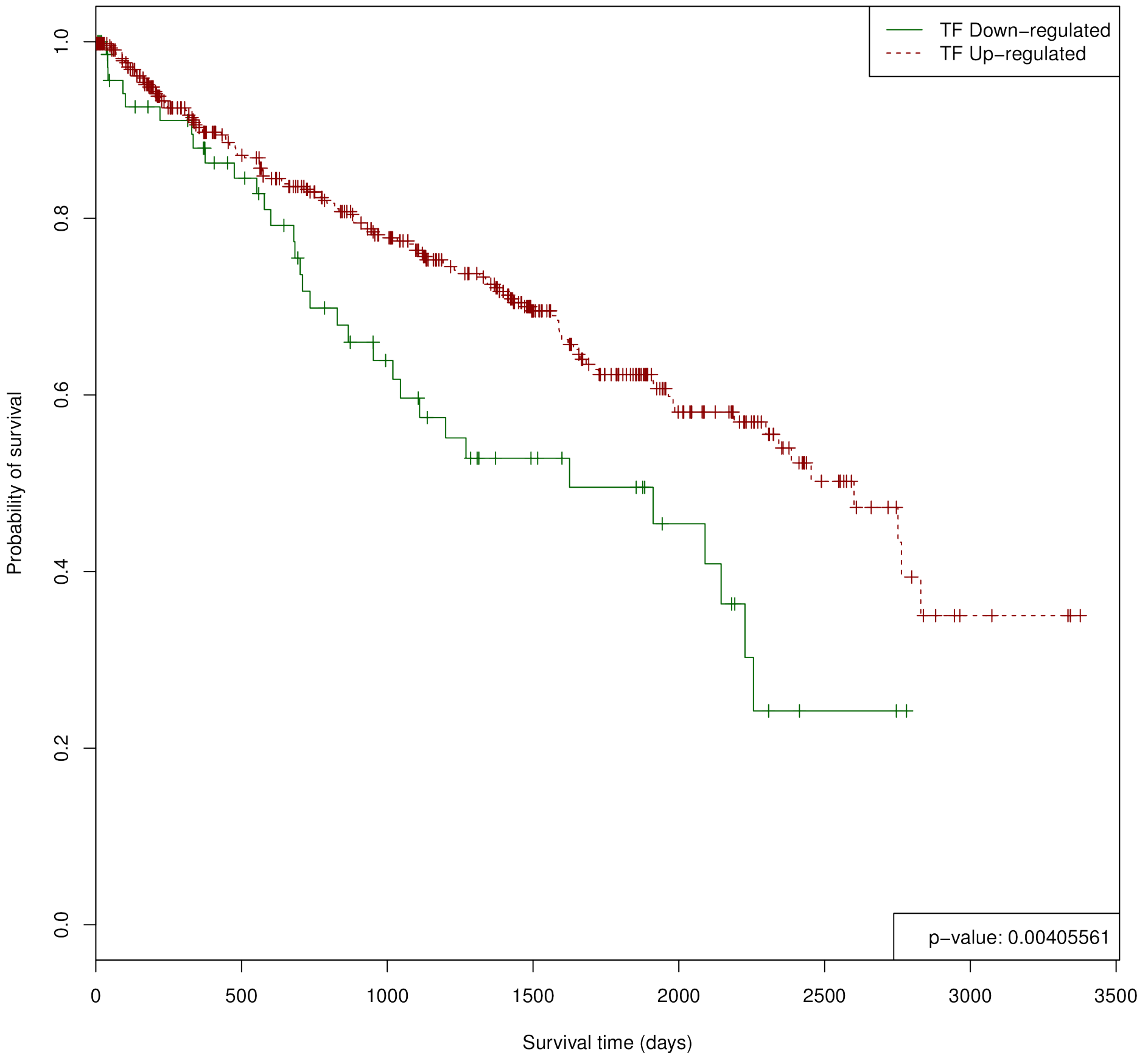
# MYC in COAD



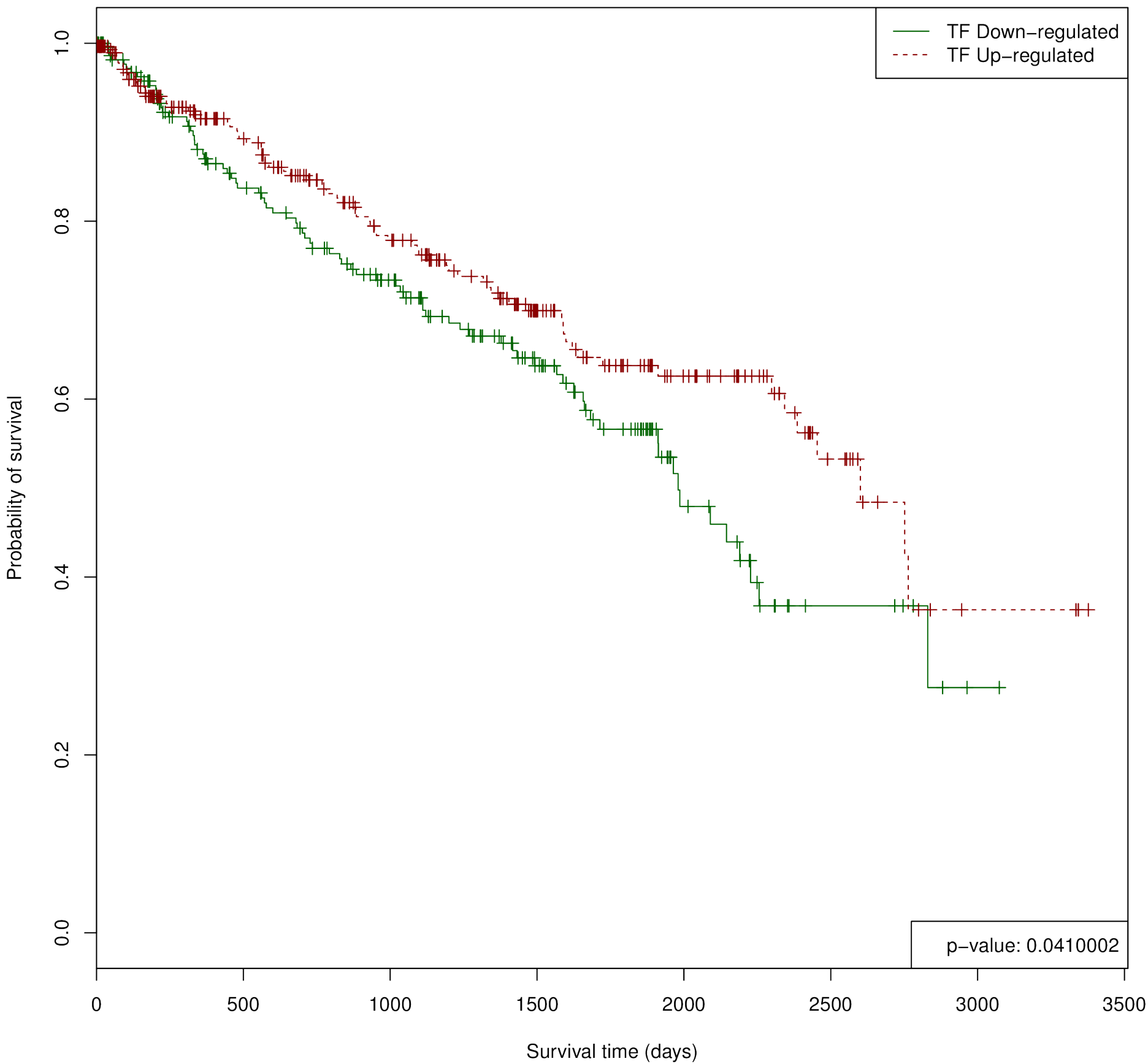
# MYC in HNSC



# MYC in KIRC

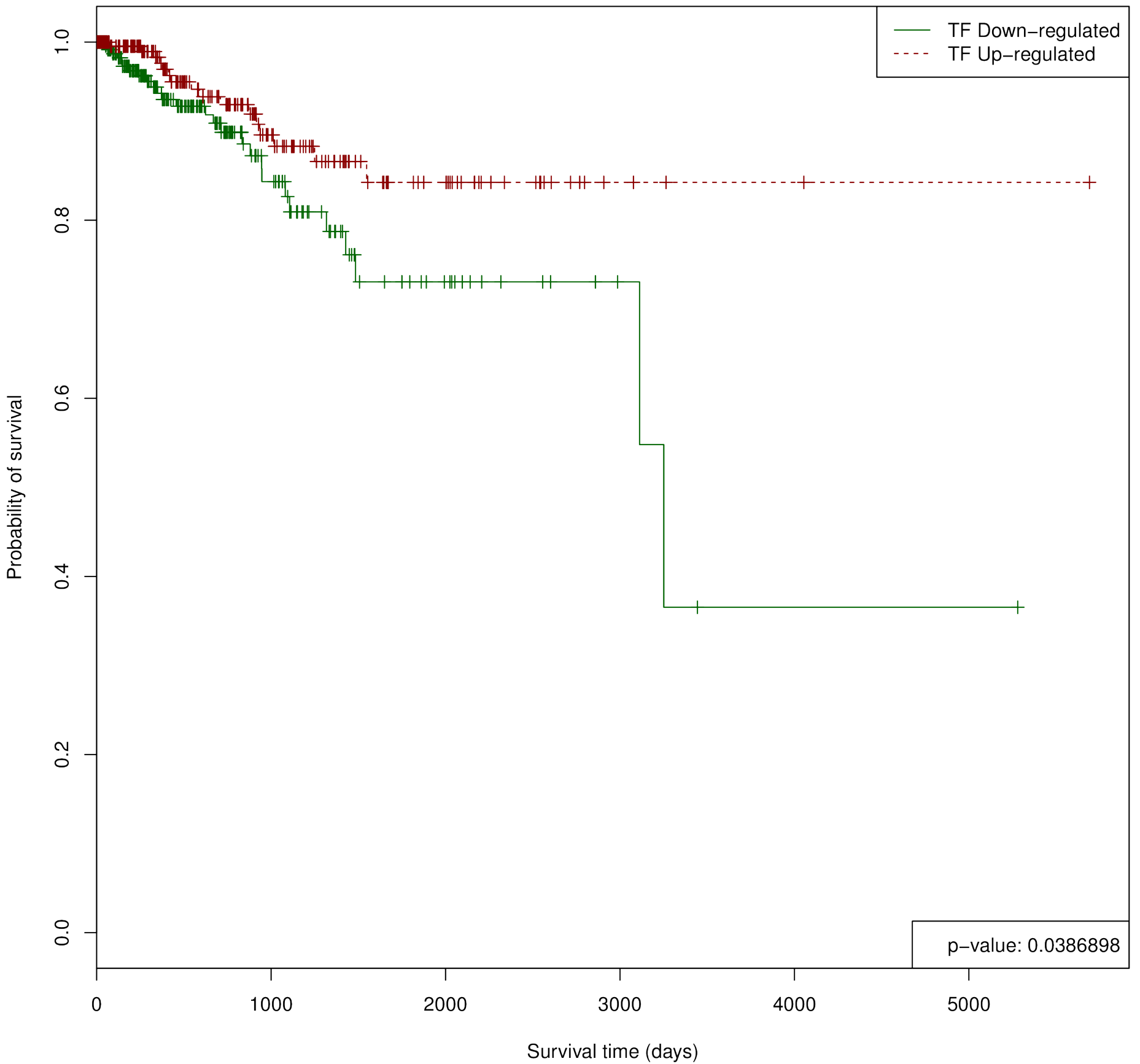


# MYC::MAX in KIRC

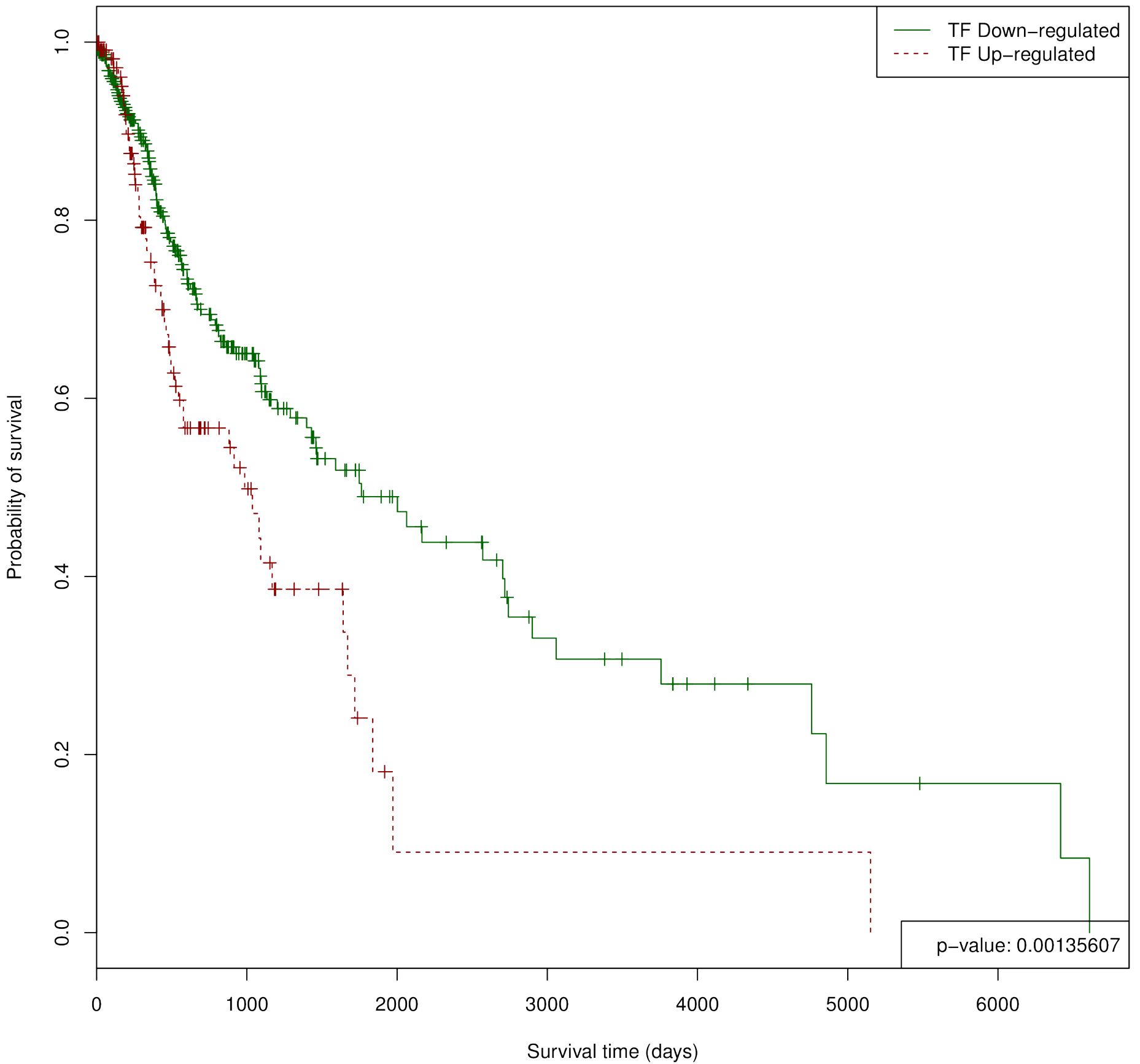




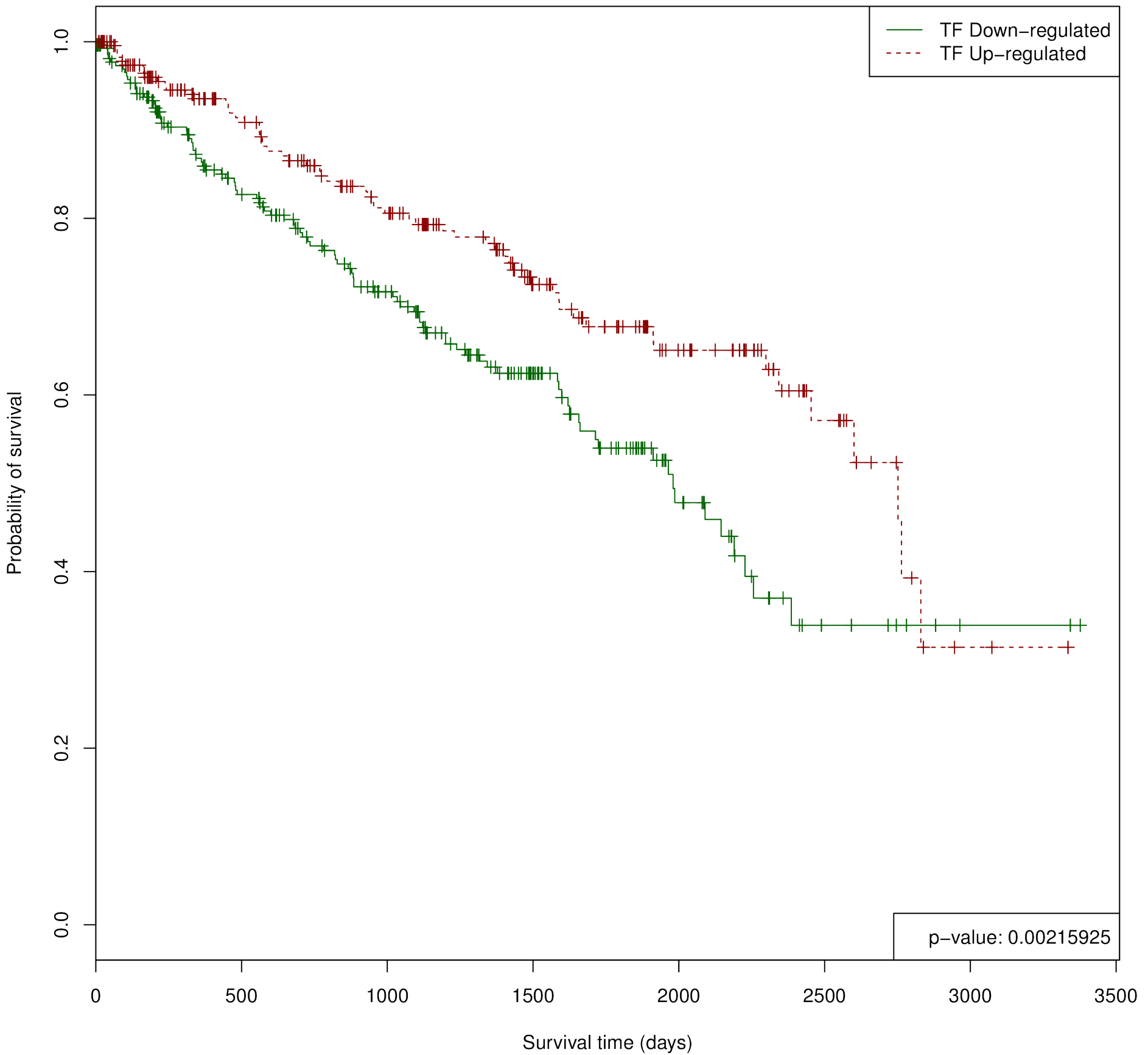
# NR1H3::RXRA in UCEC



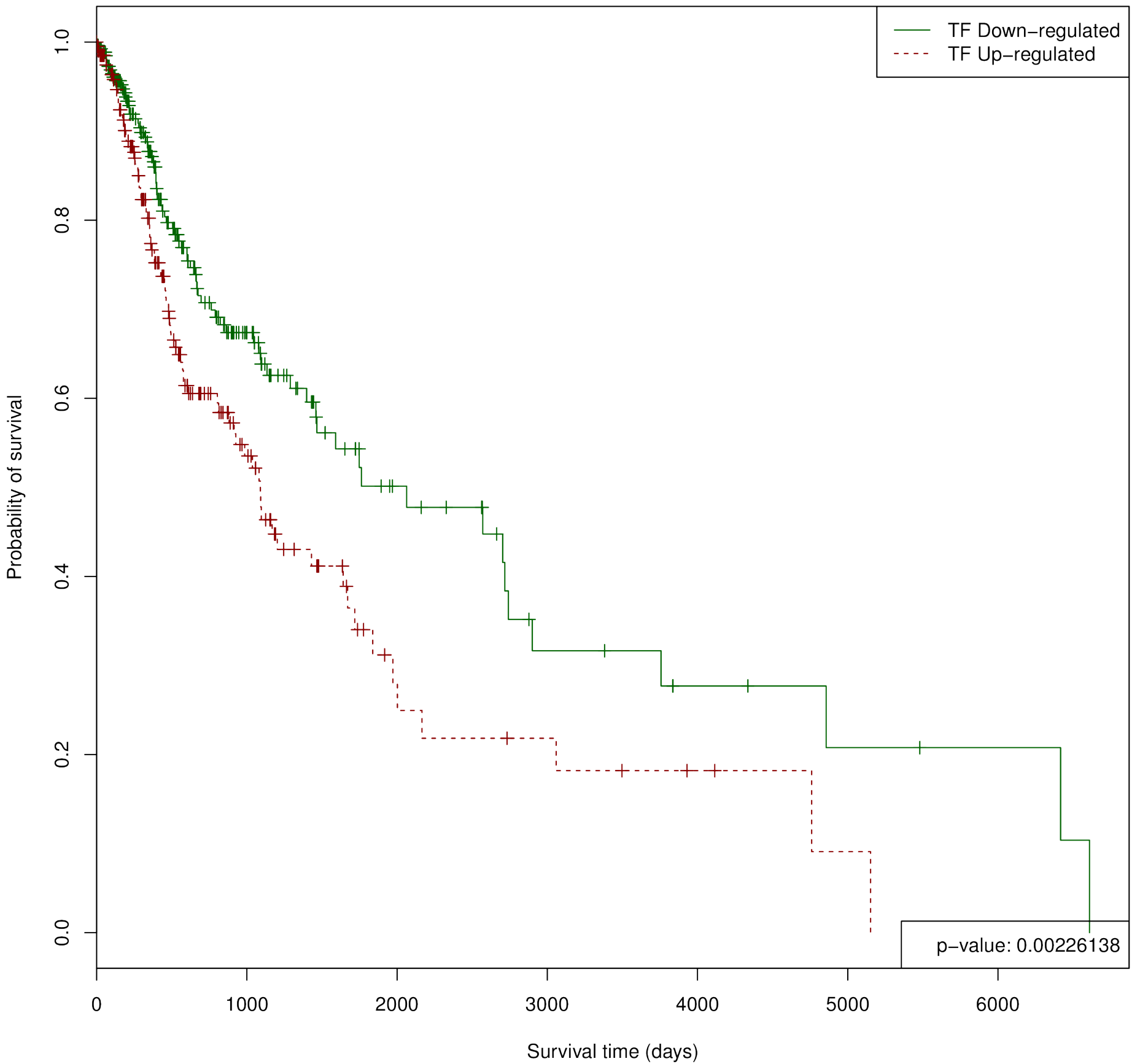
# NR2C2 in HNSC



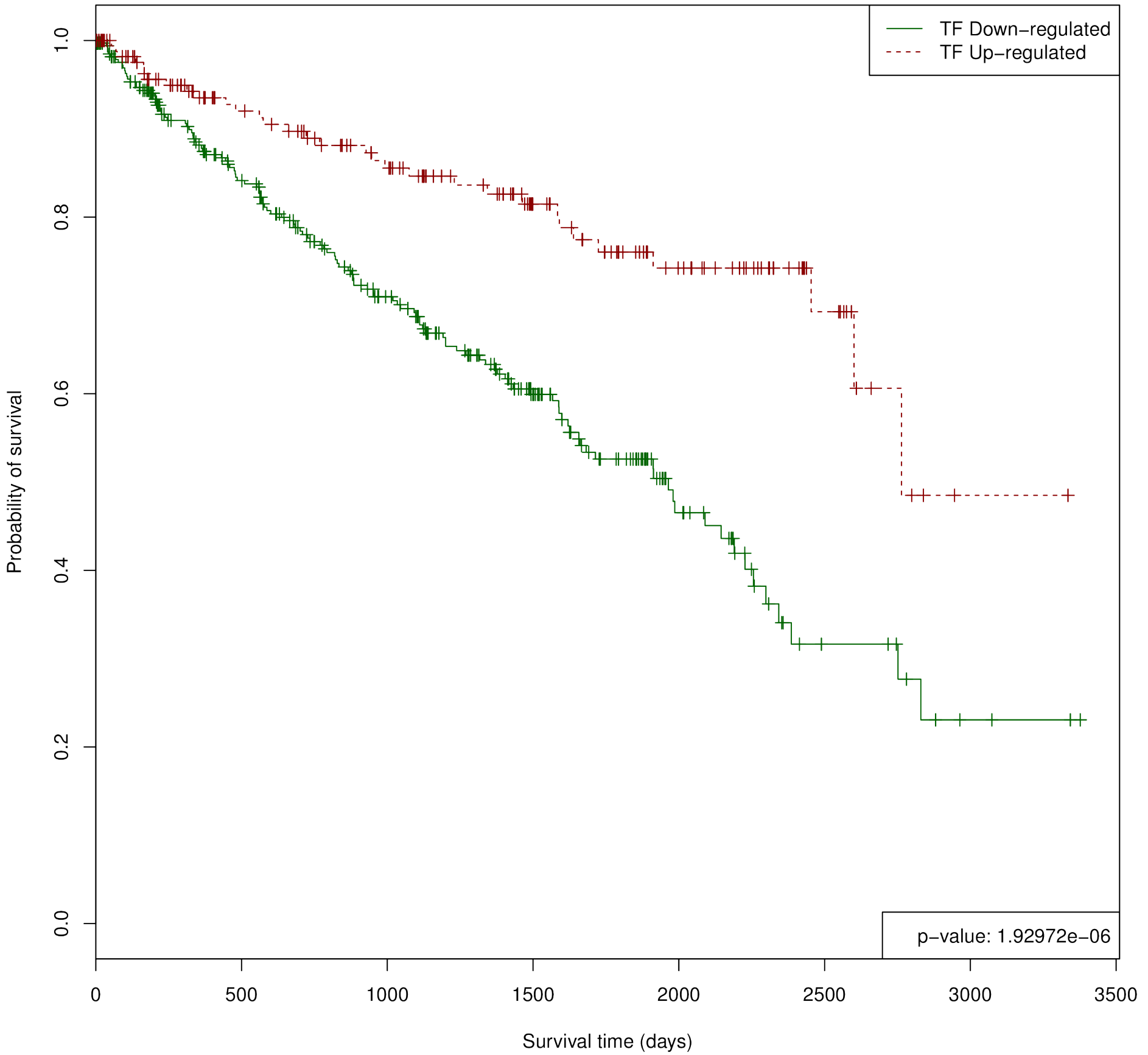
# NR2C2 in KIRC



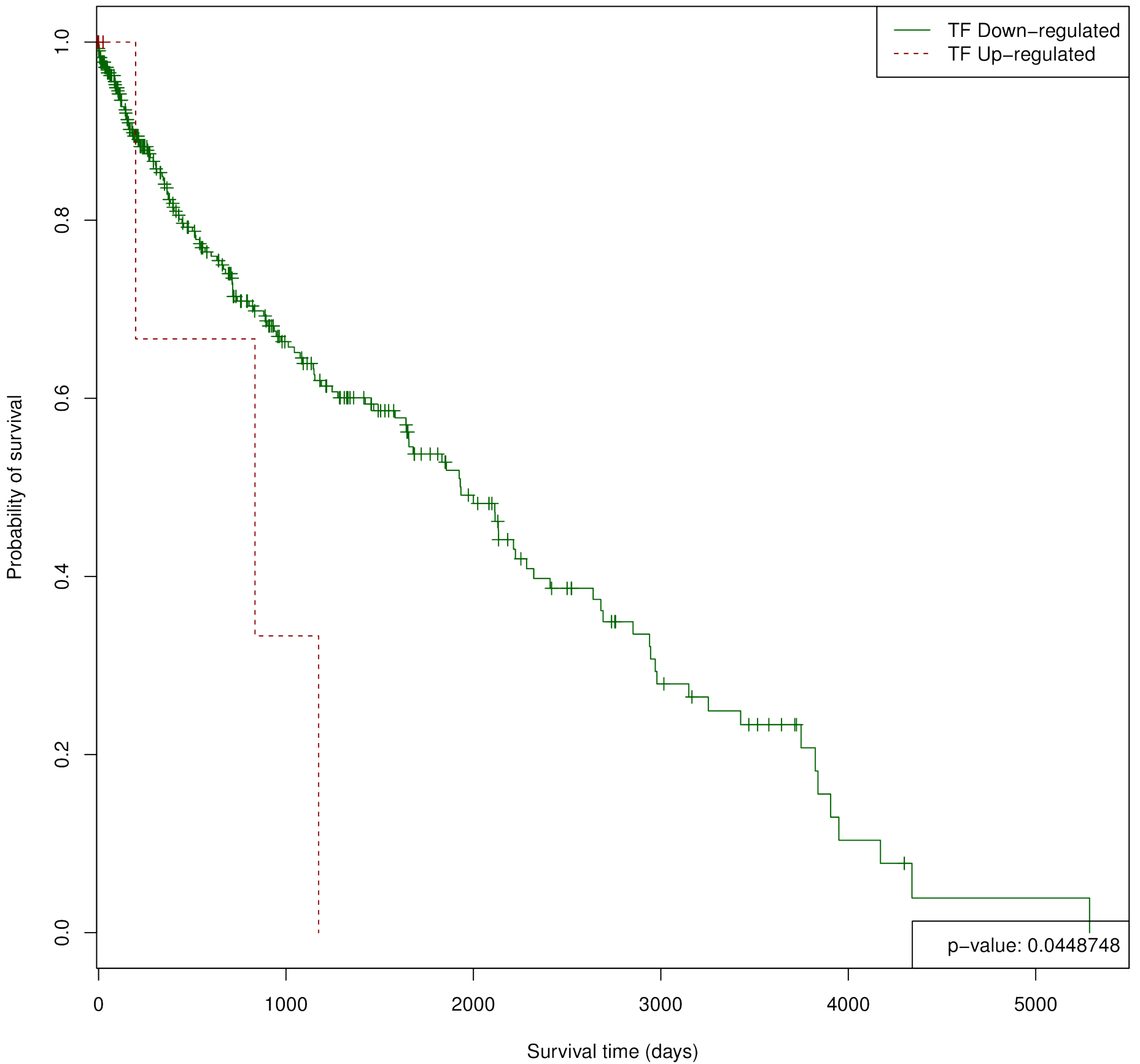
# NRF1 in HNSC



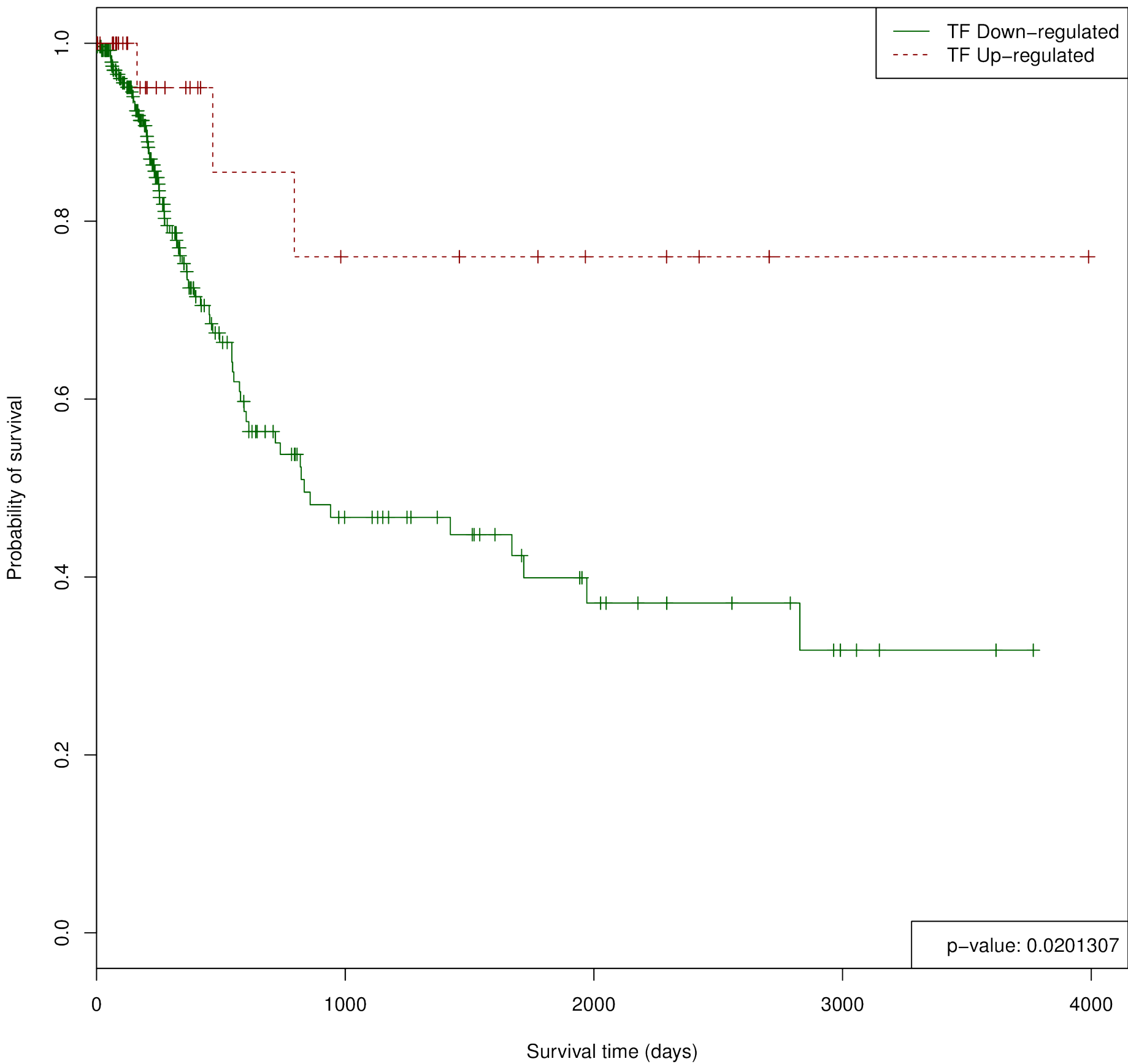
# NRF1 in KIRC



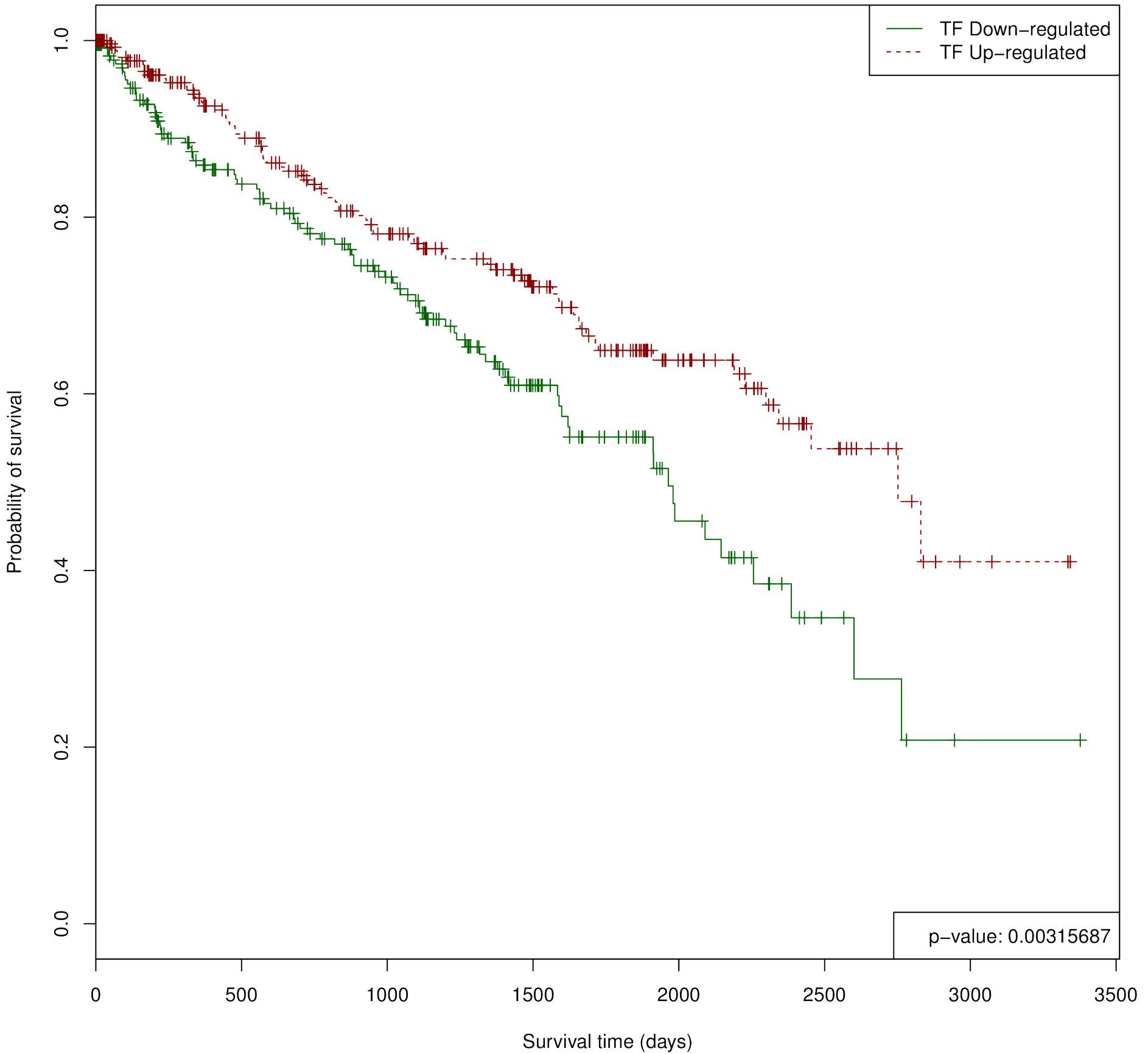
# NRF1 in LUSC



# PAX5 in BLCA

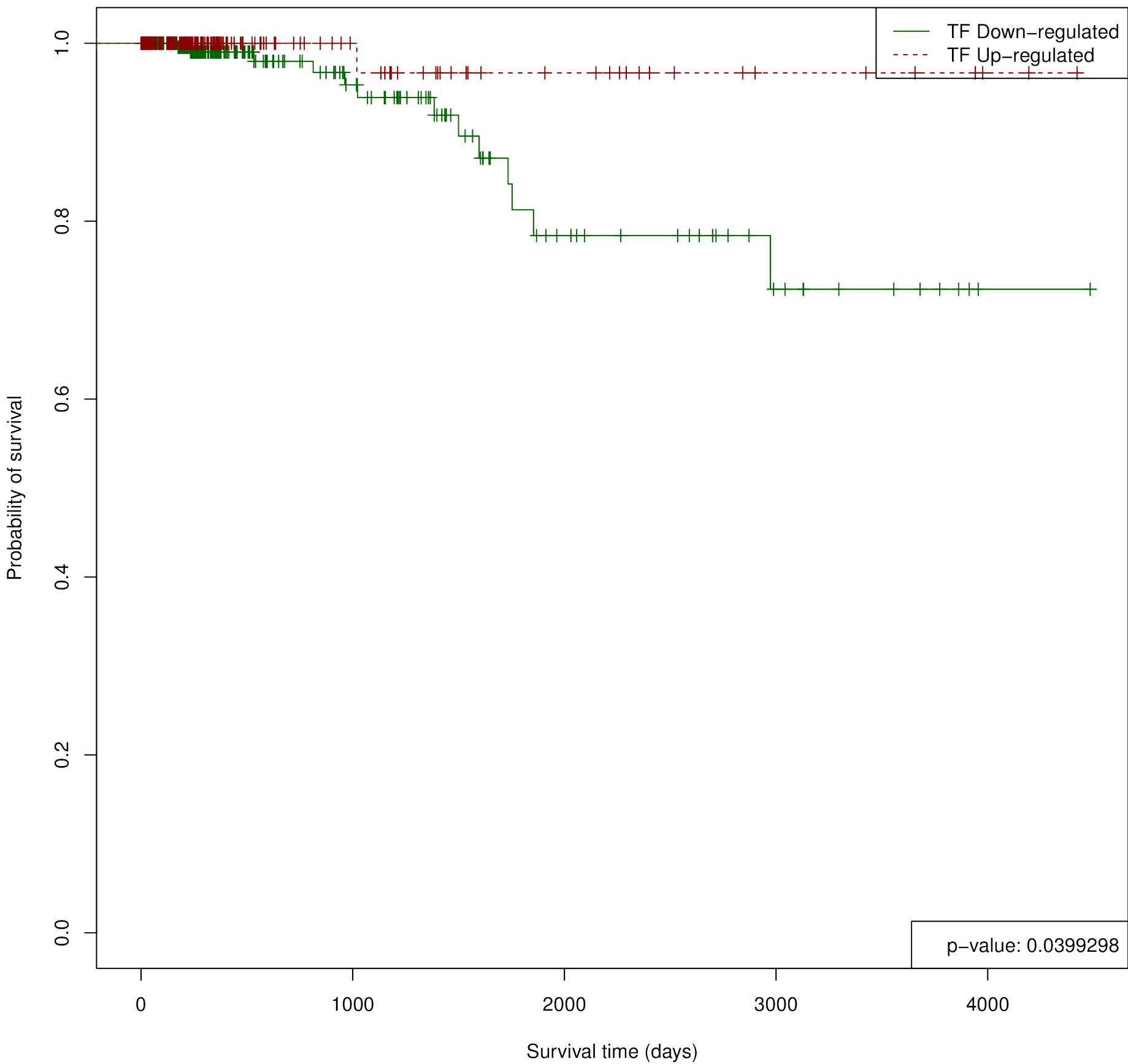


# PAX5 in KIRC

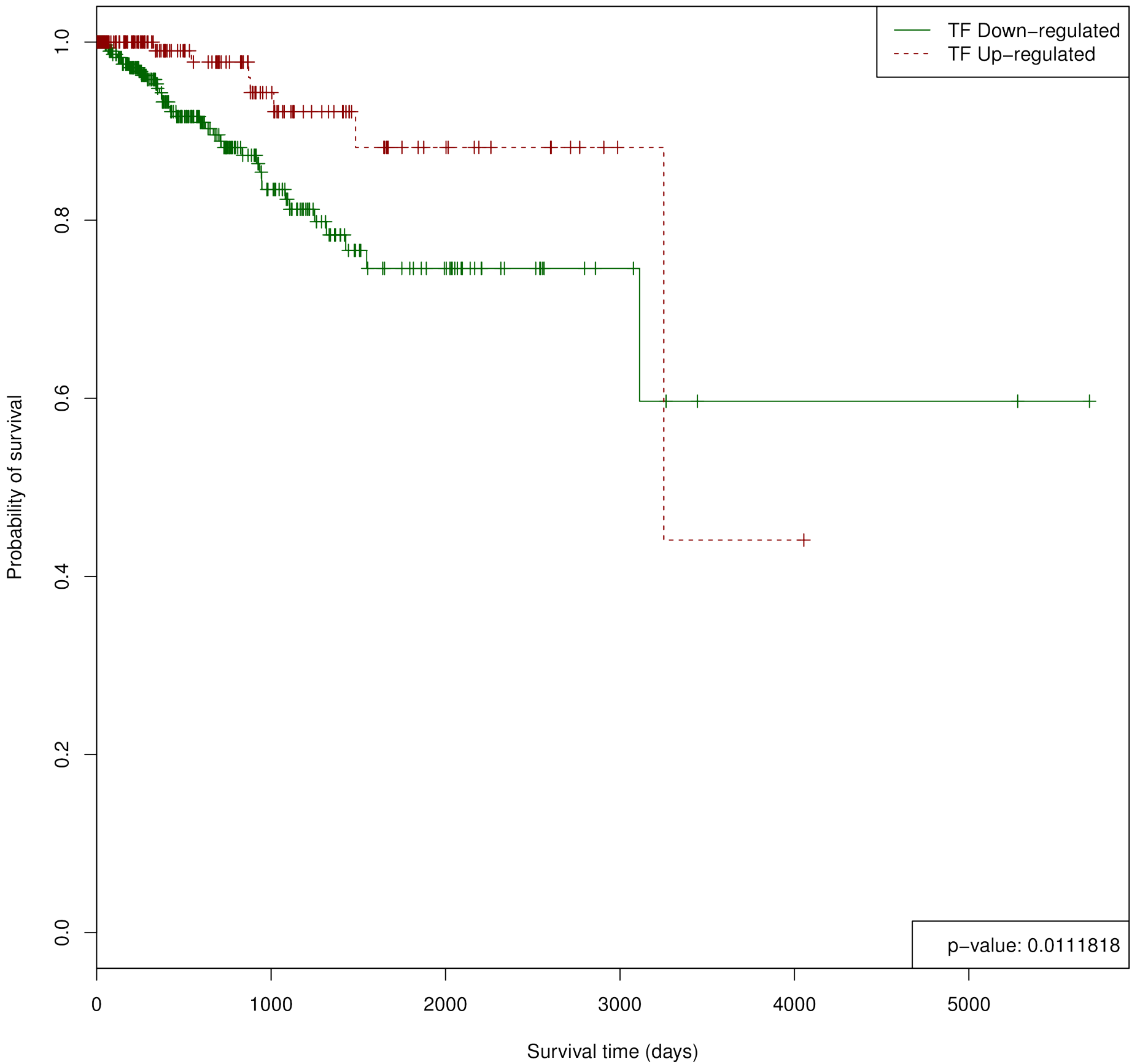




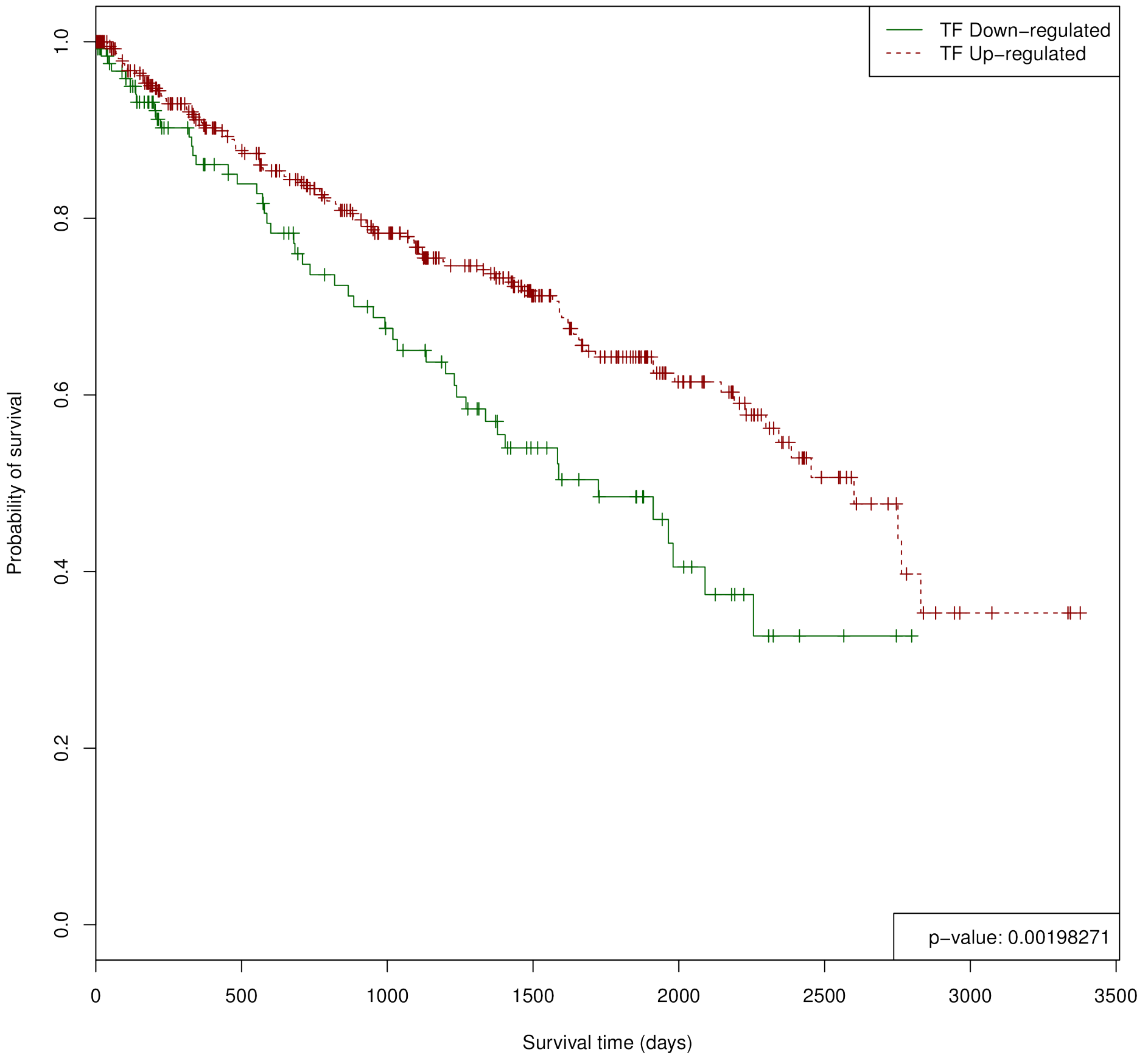
# PAX5 in THCA



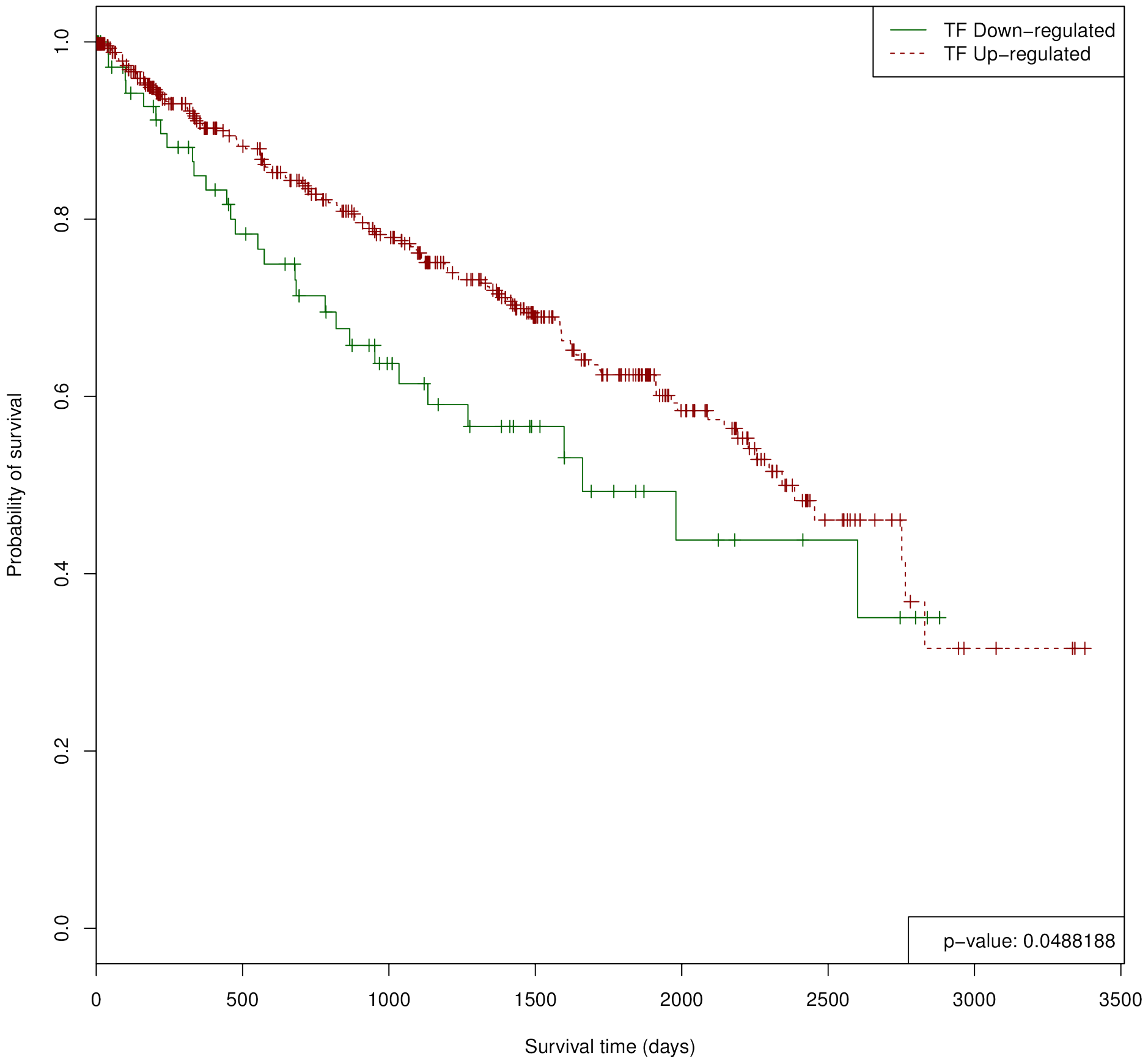
# PAX5 in UCEC



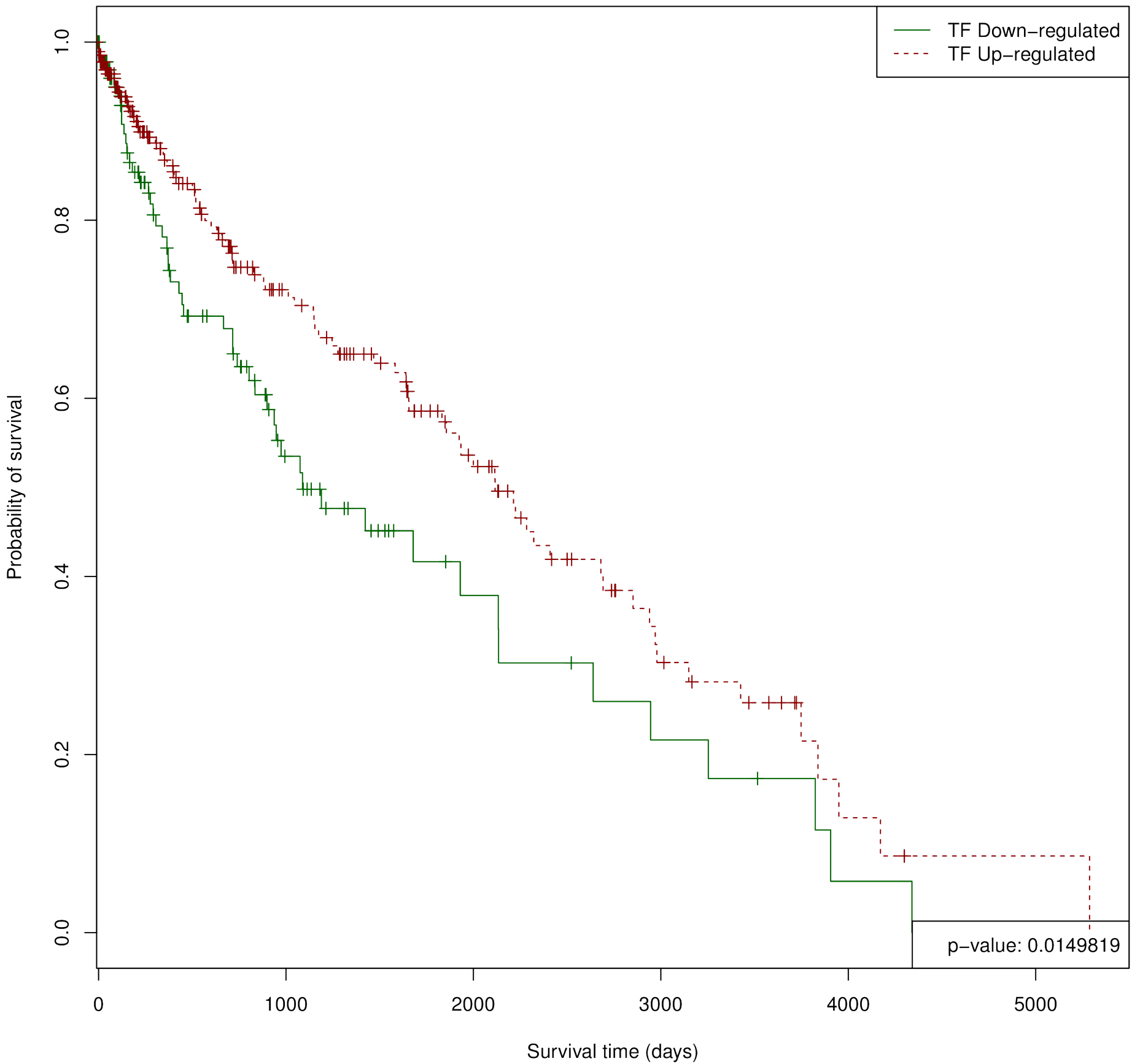
# PBX3 in KIRC



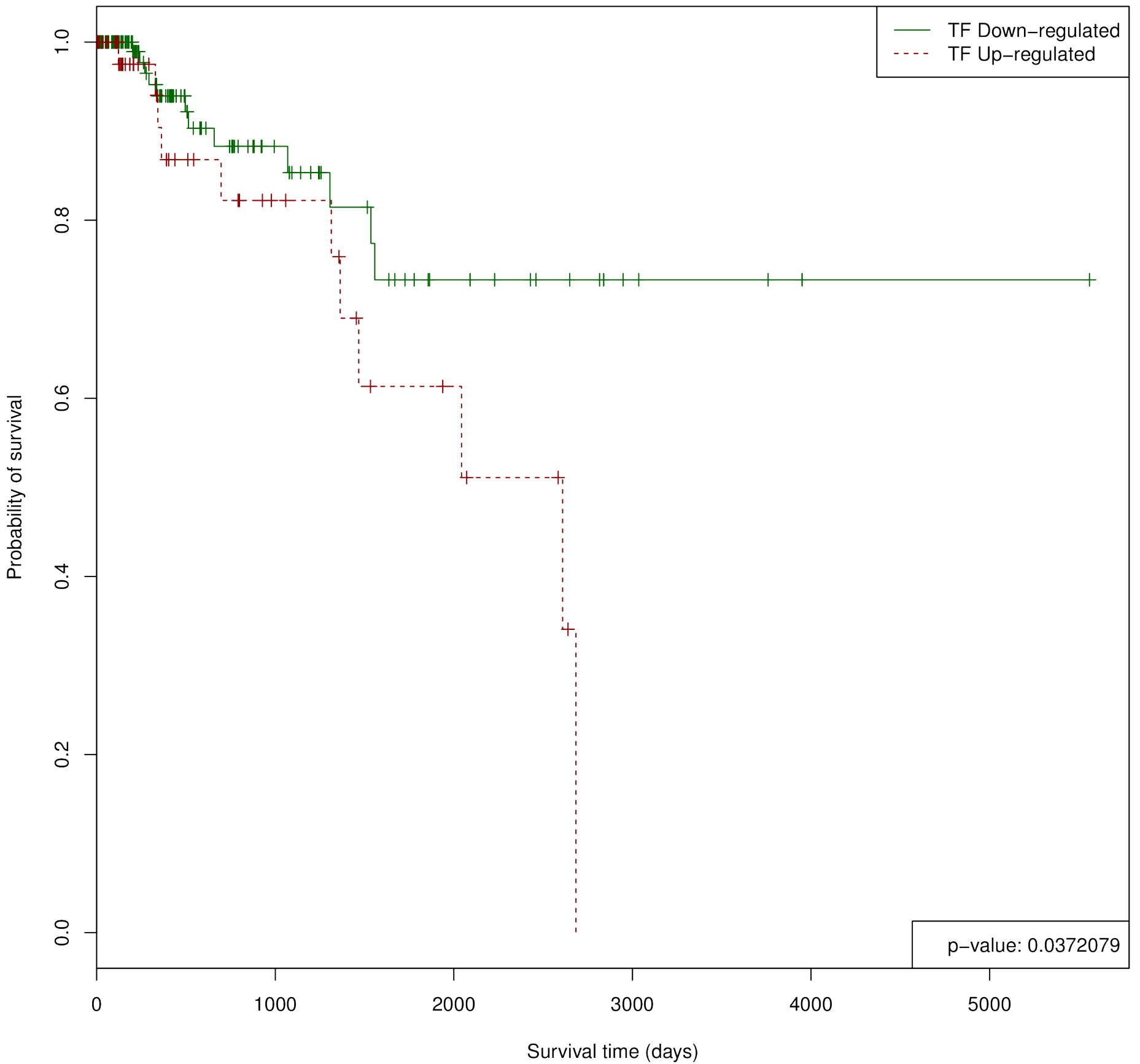
# REST in KIRC



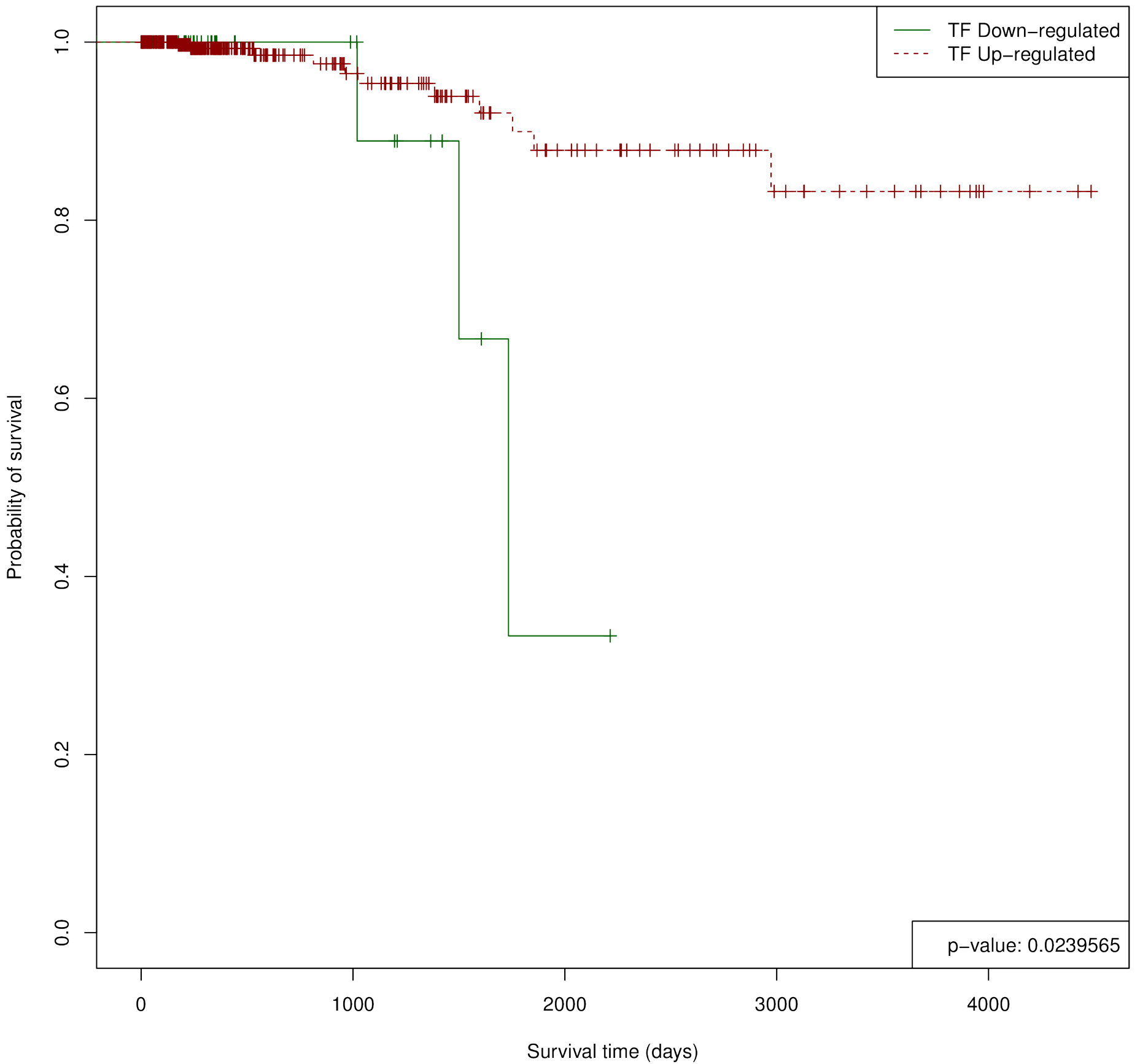
# REST in LUSC



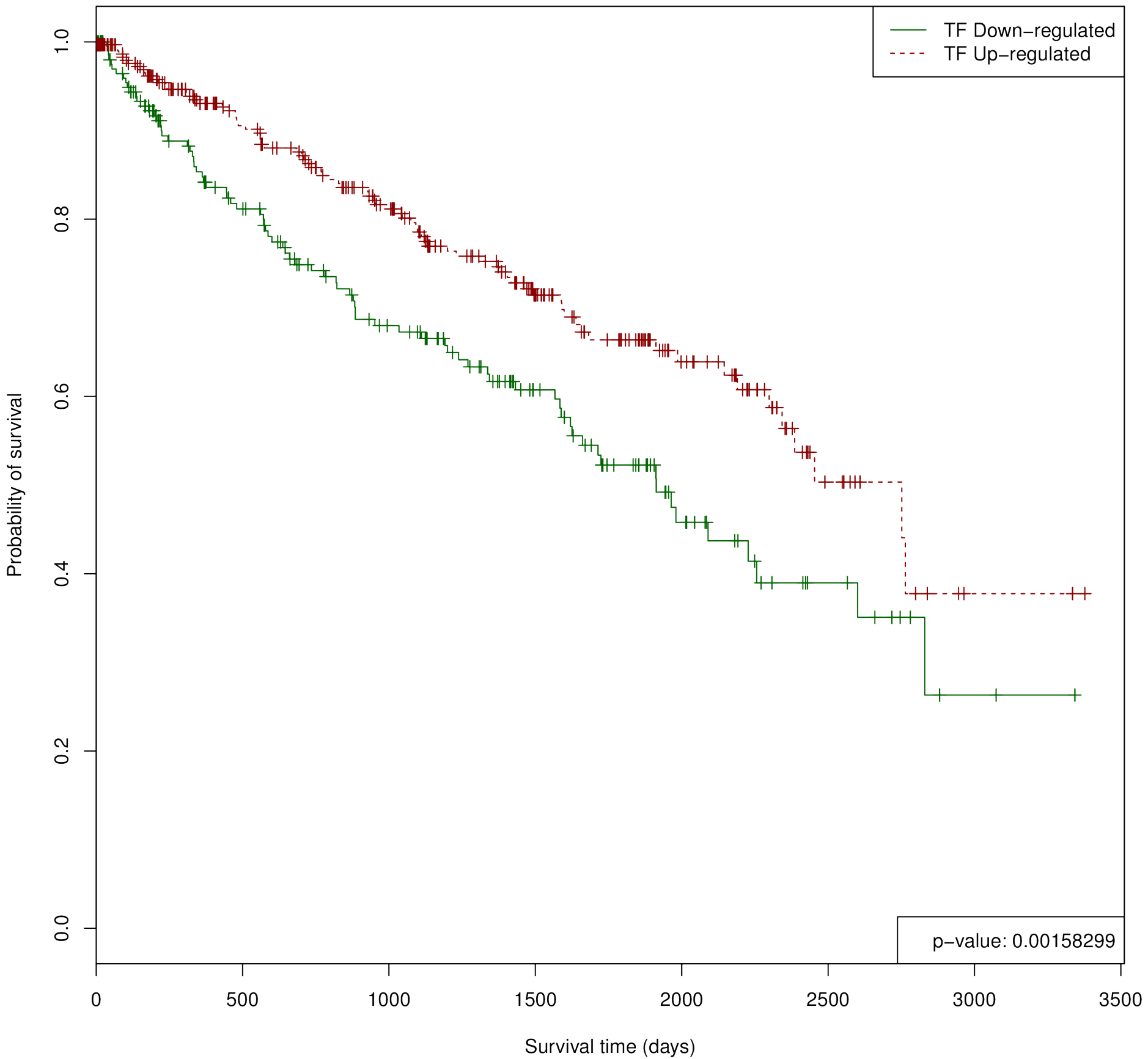
# RXRA in KIRP



# RXRA in THCA

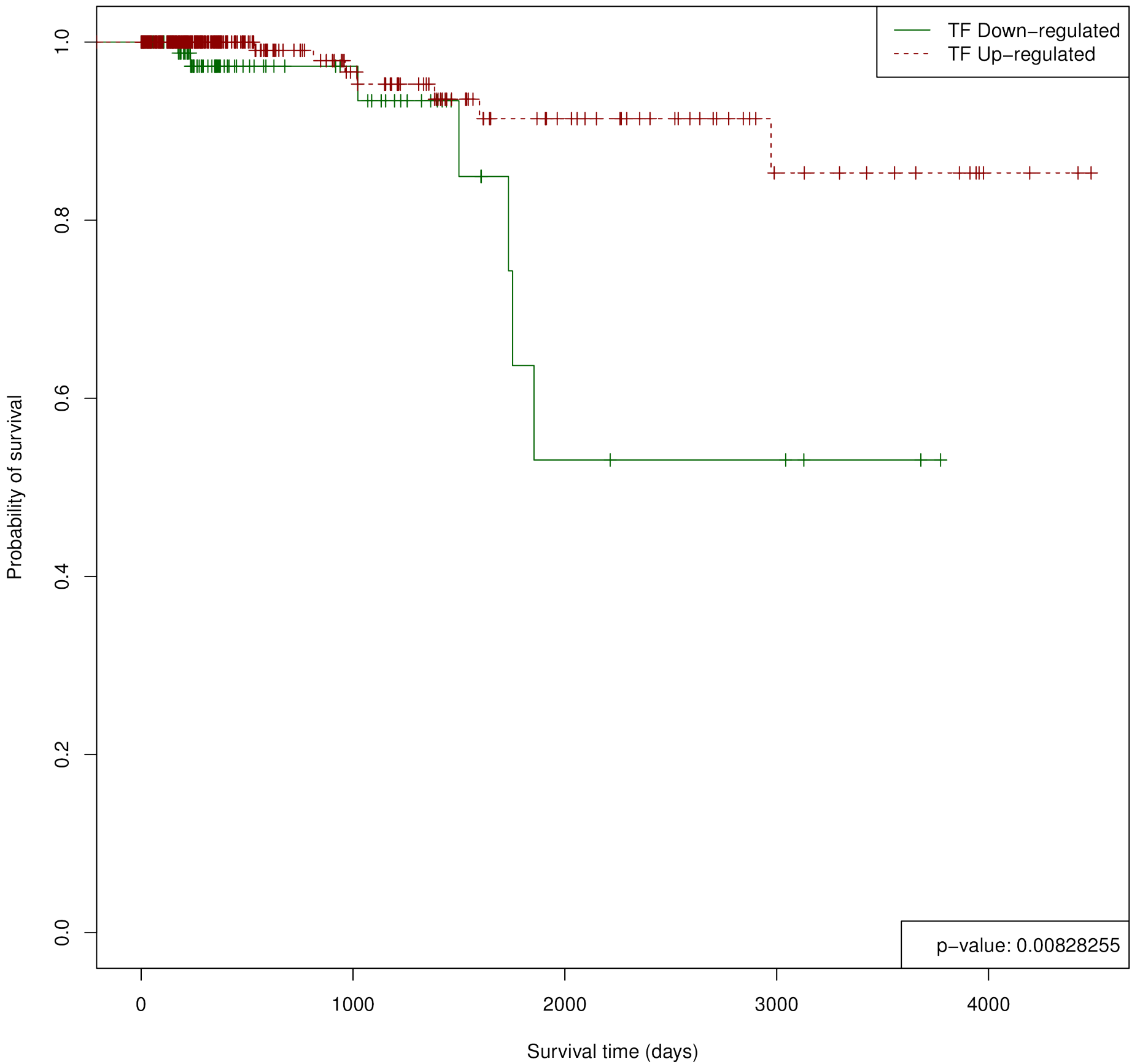


# RXRA::VDR in KIRC

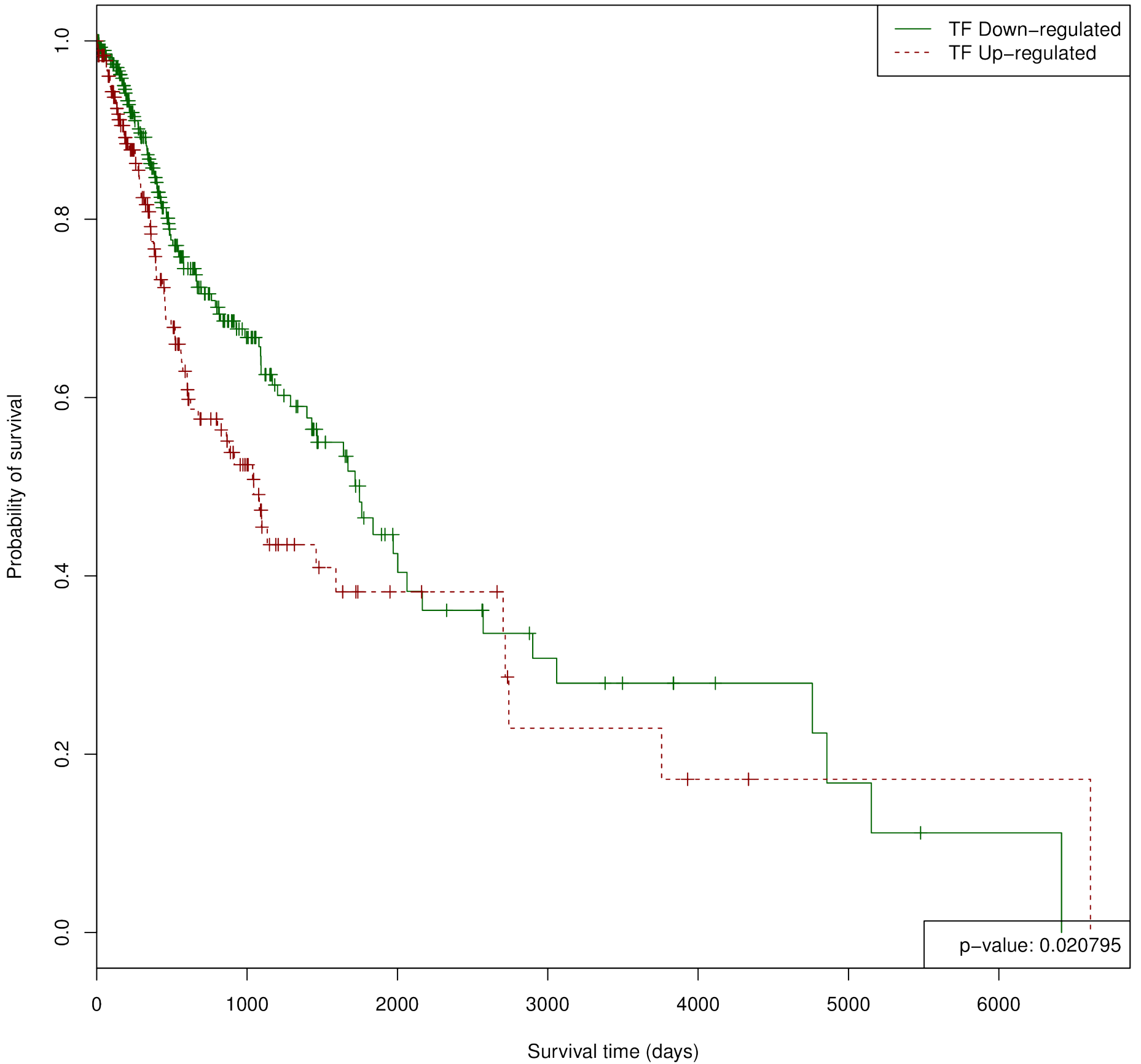




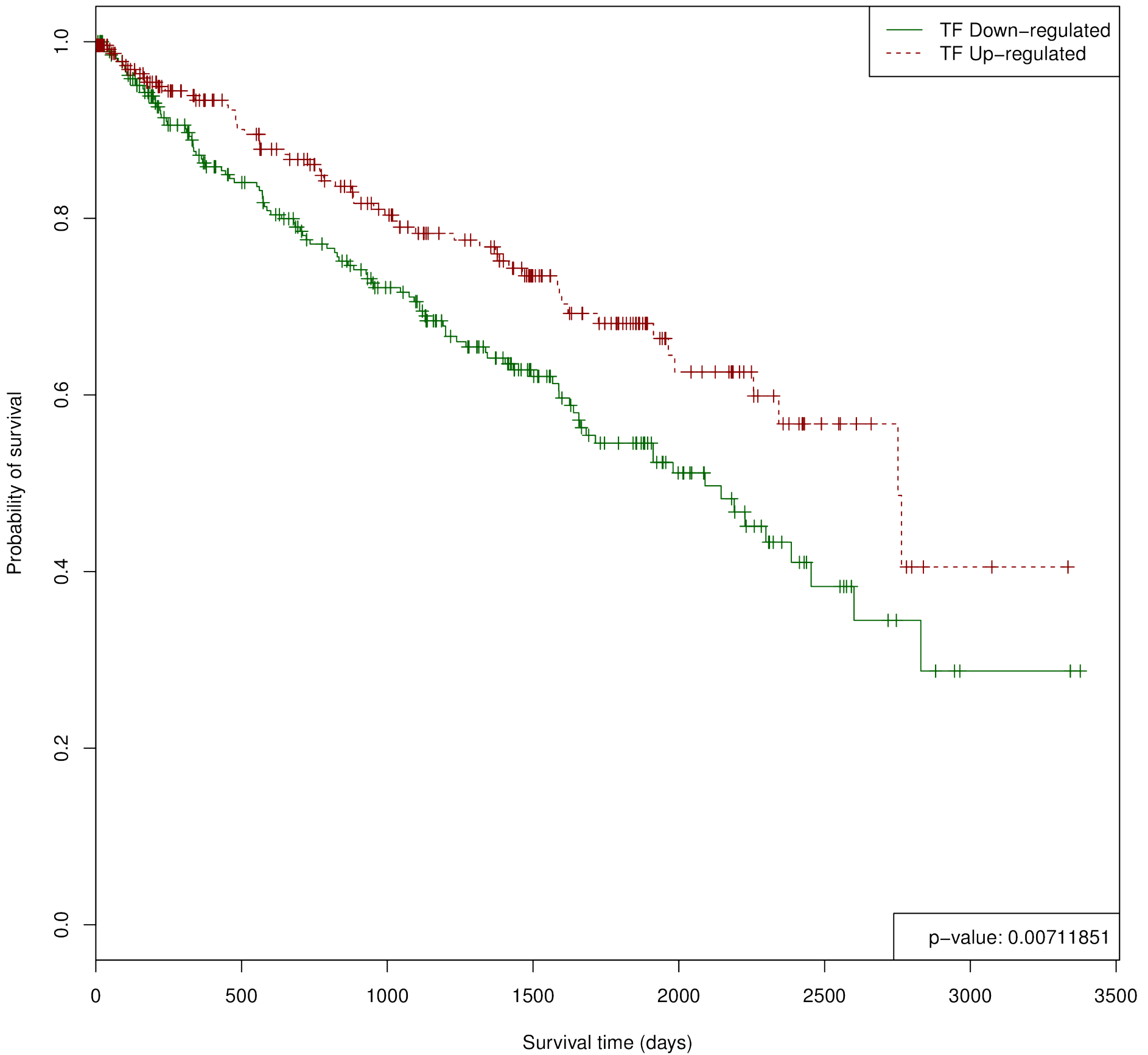
# RXRA::VDR in THCA



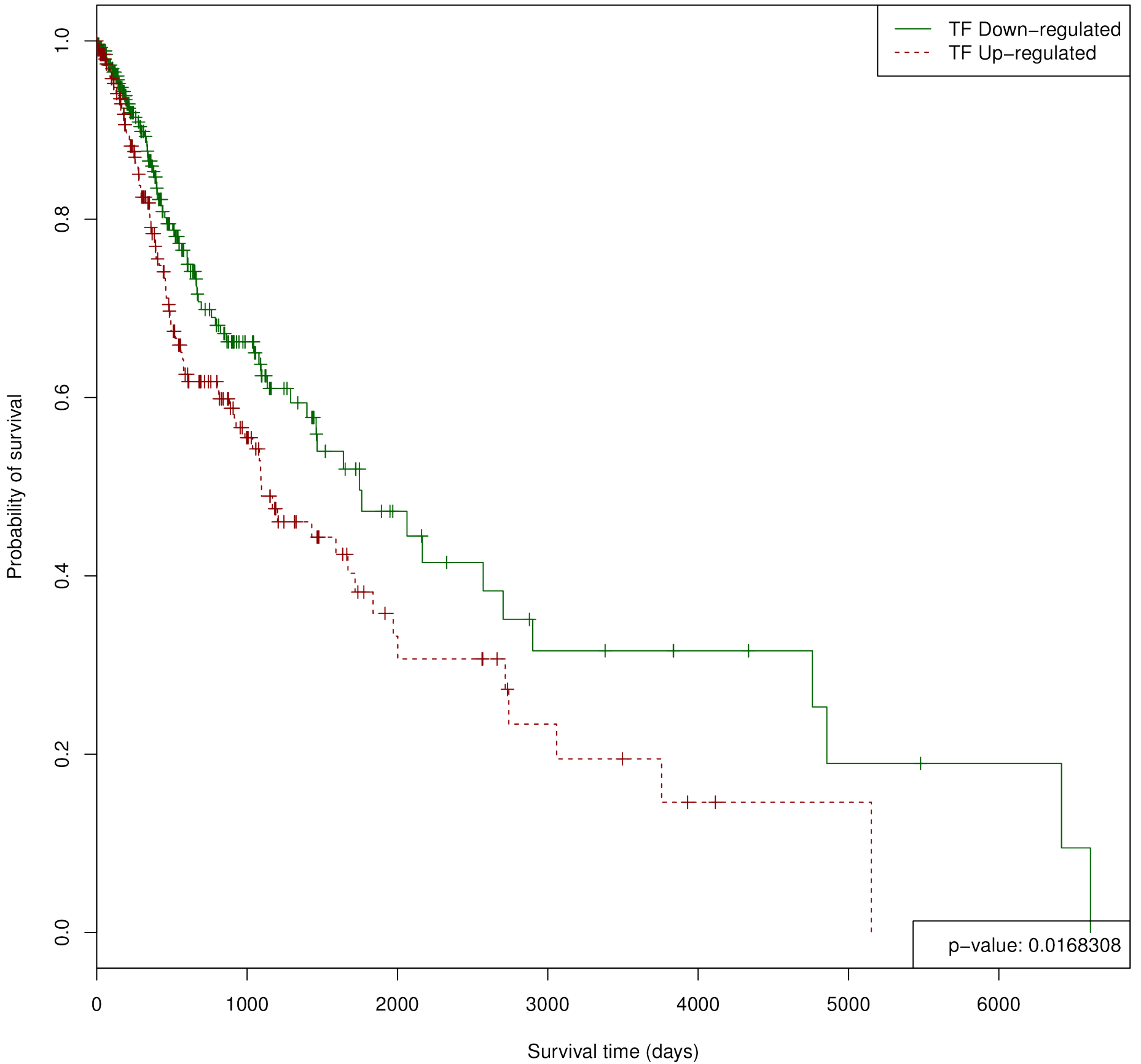
# RXR::RAR\_DR5 in HNSC



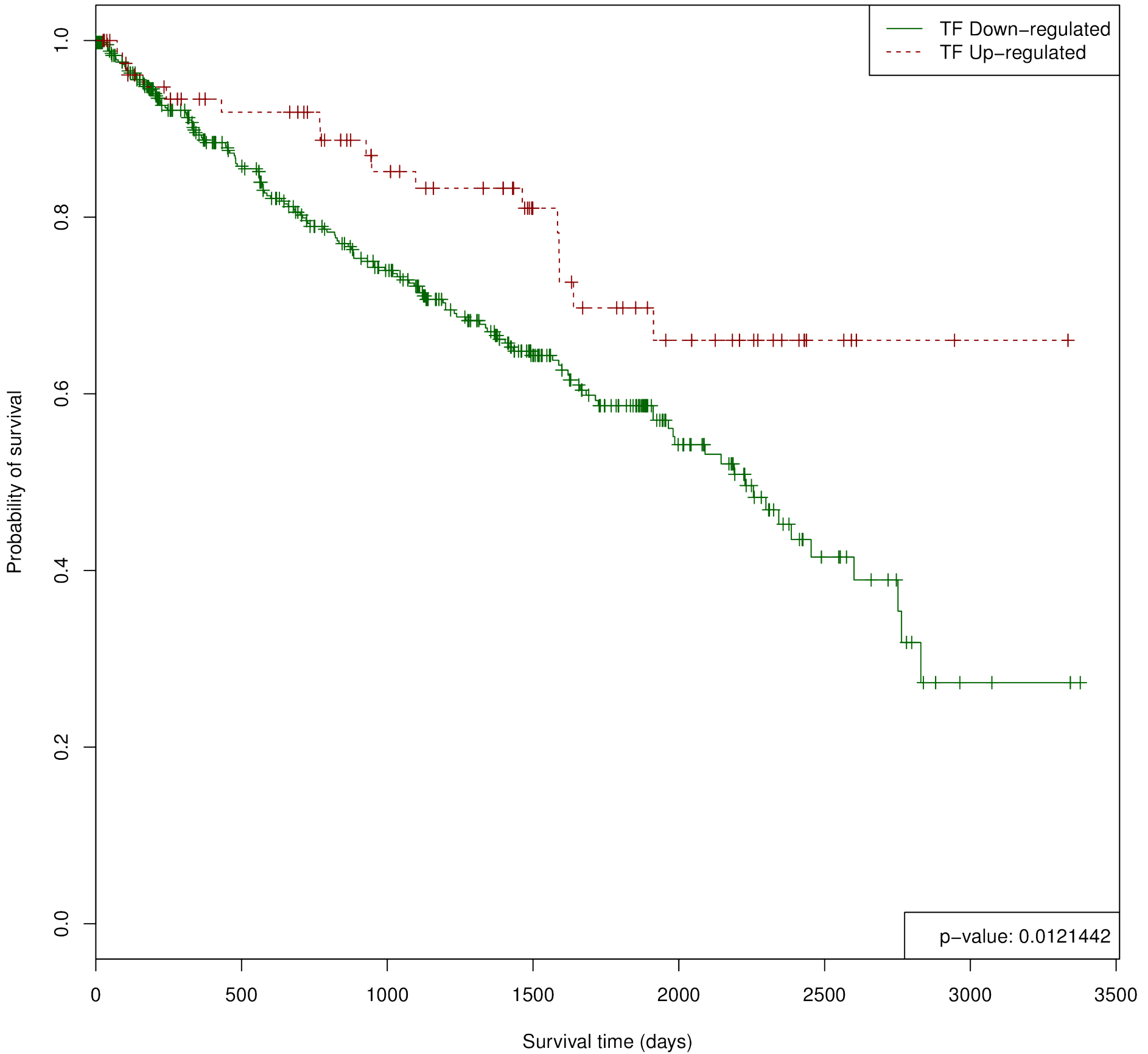
# RXR::RAR\_DR5 in KIRC



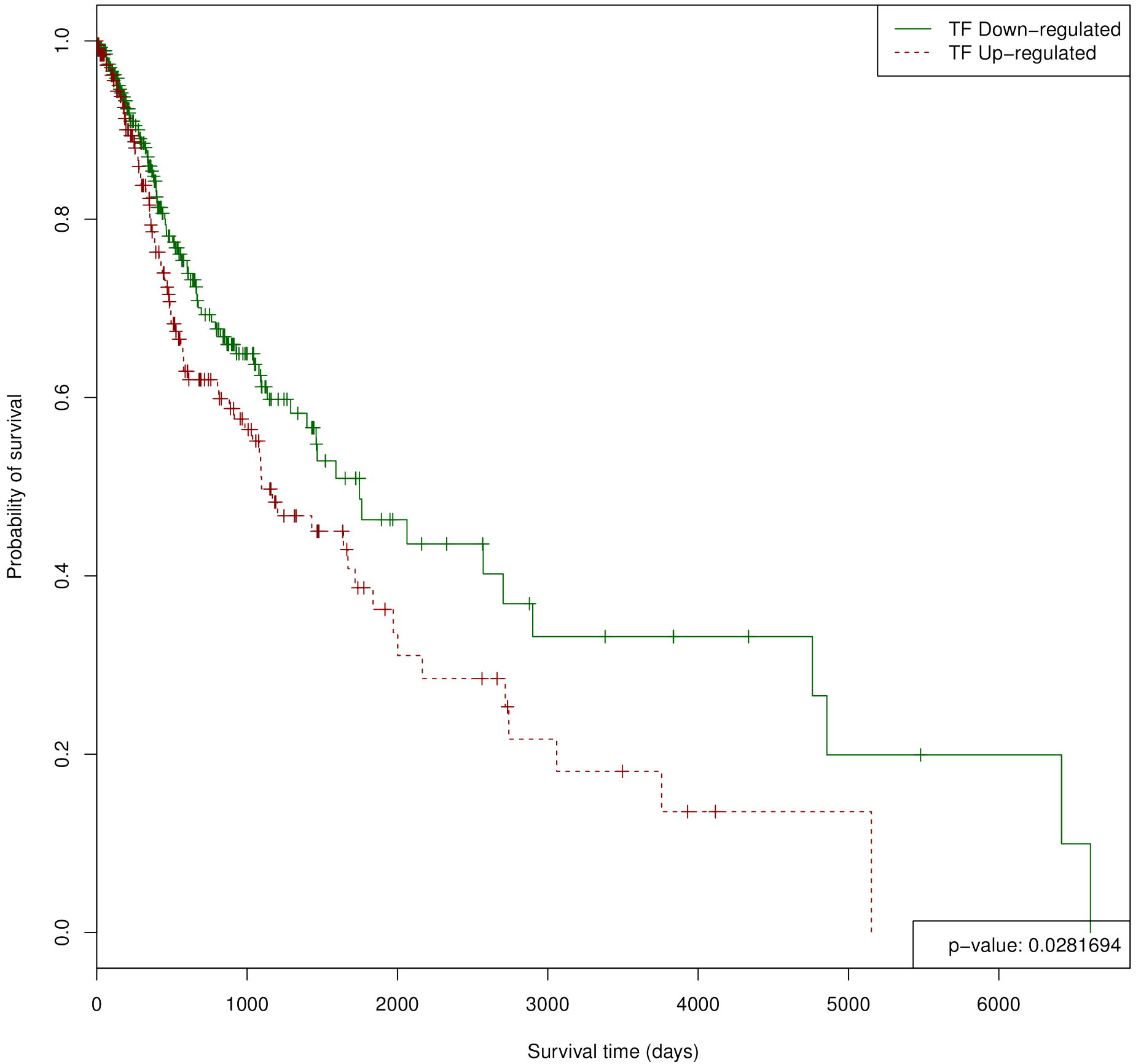
# SP1 in HNSC



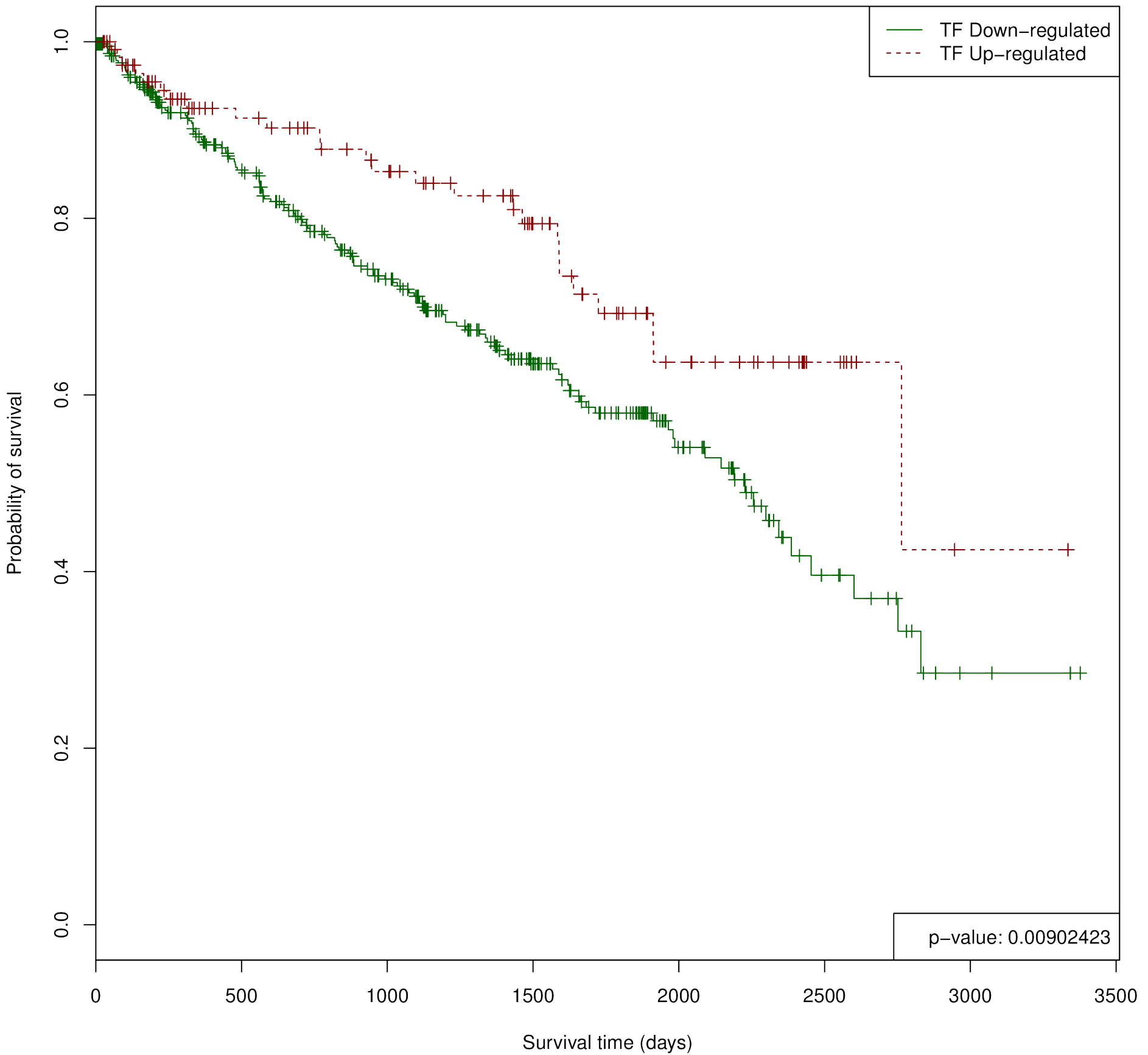
# SP1 in KIRC



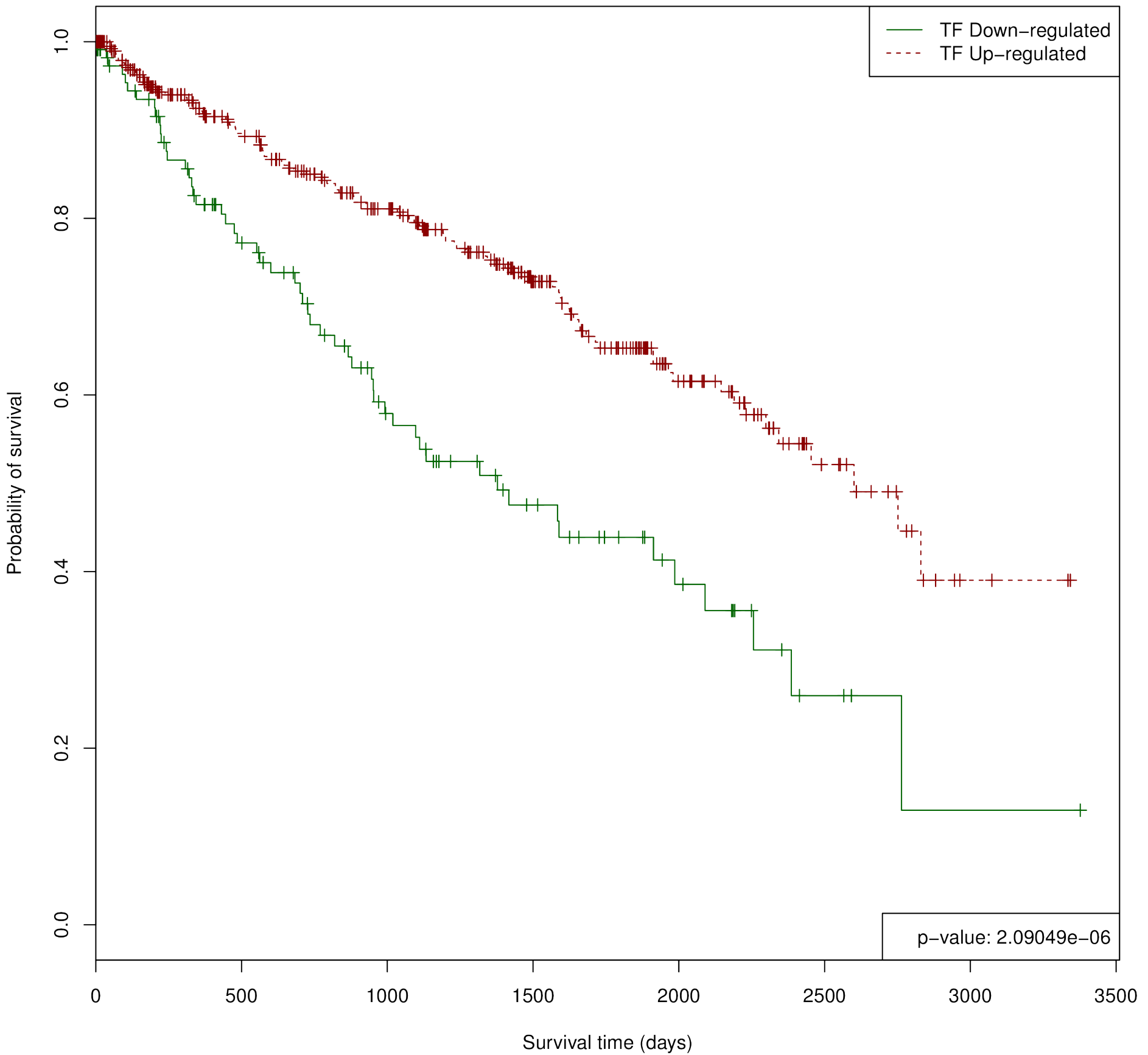
# SP2 in HNSC



# SP2 in KIRC

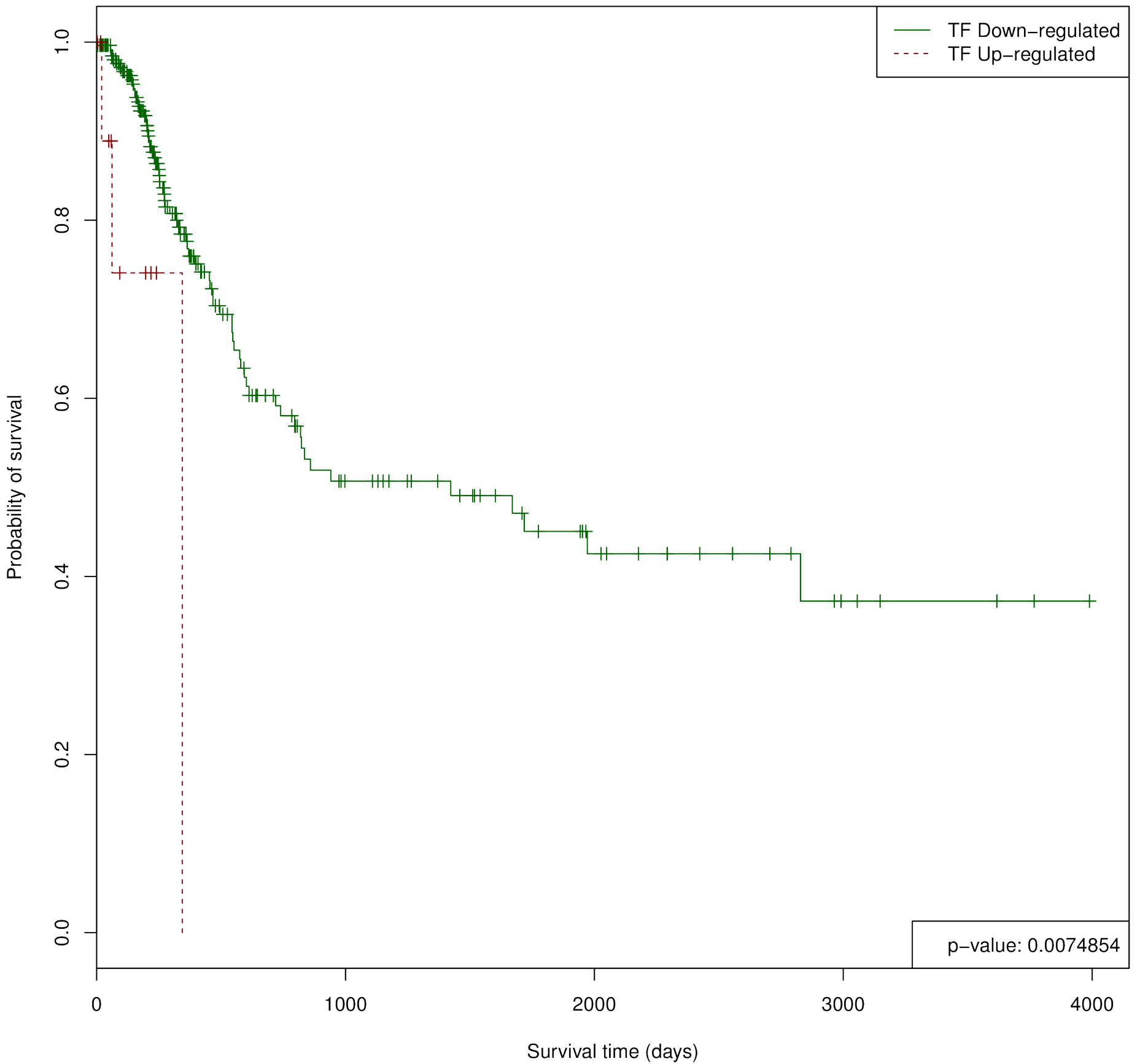


# SPI1 in KIRC

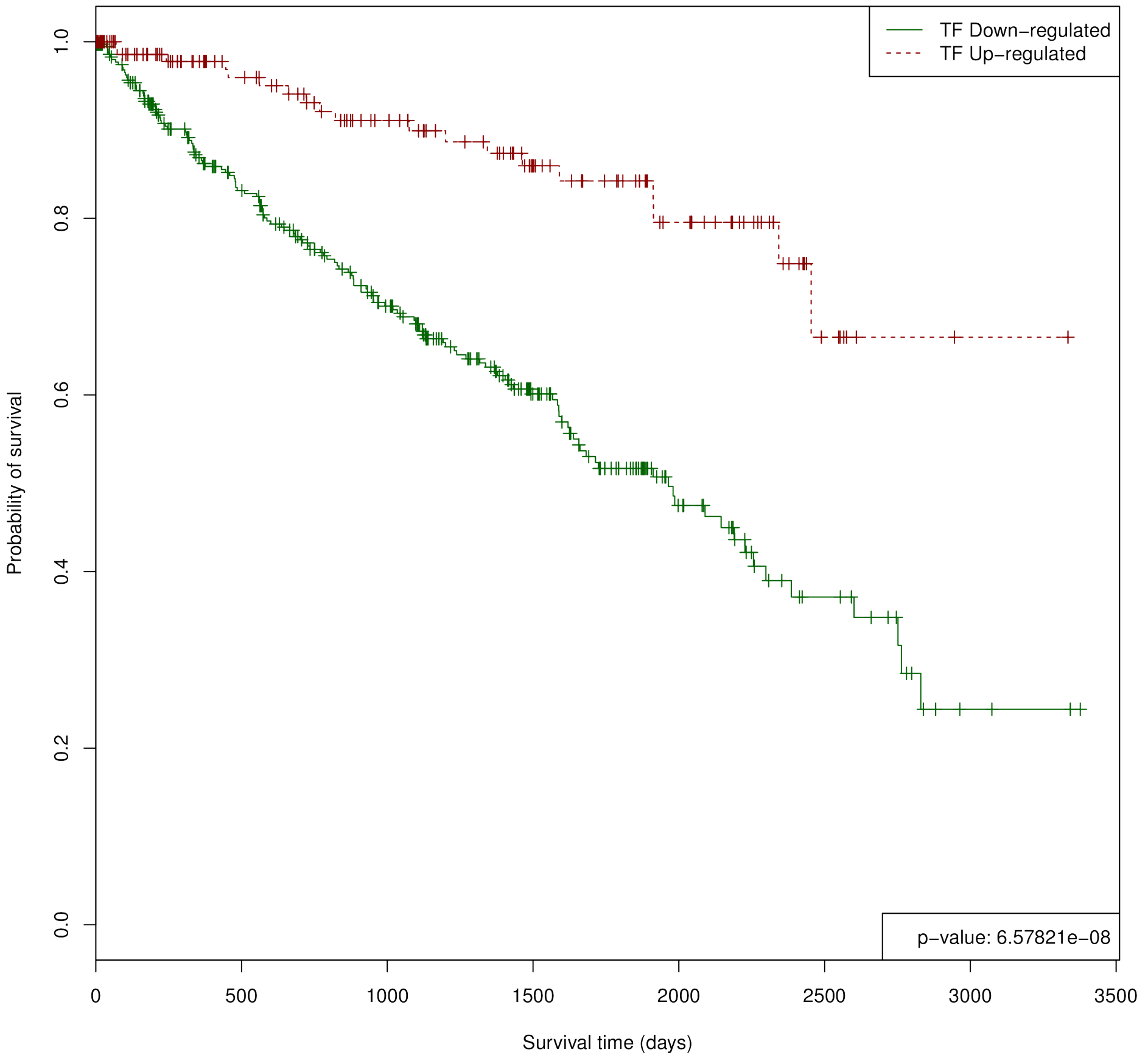




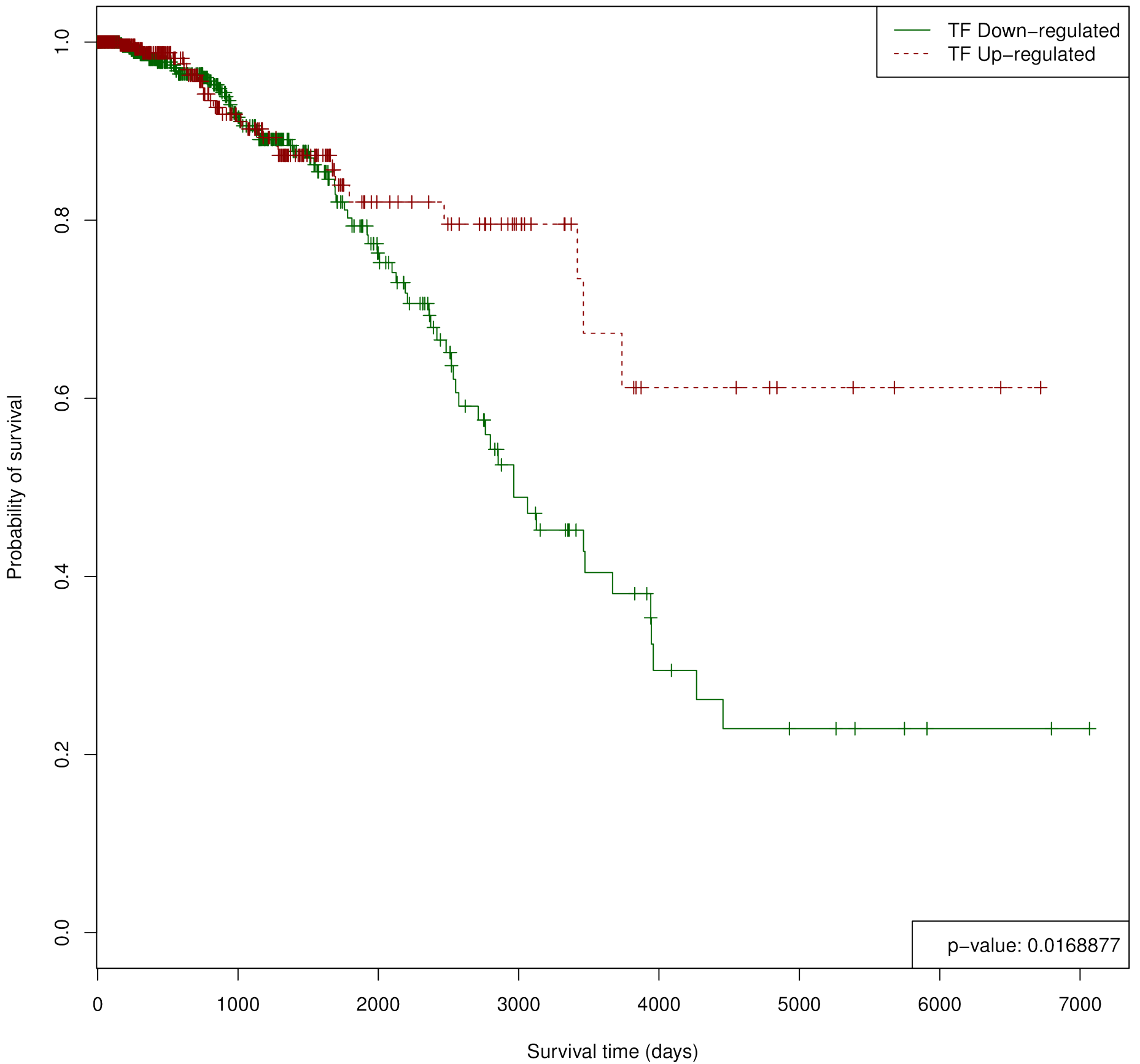
# SRF in BLCA



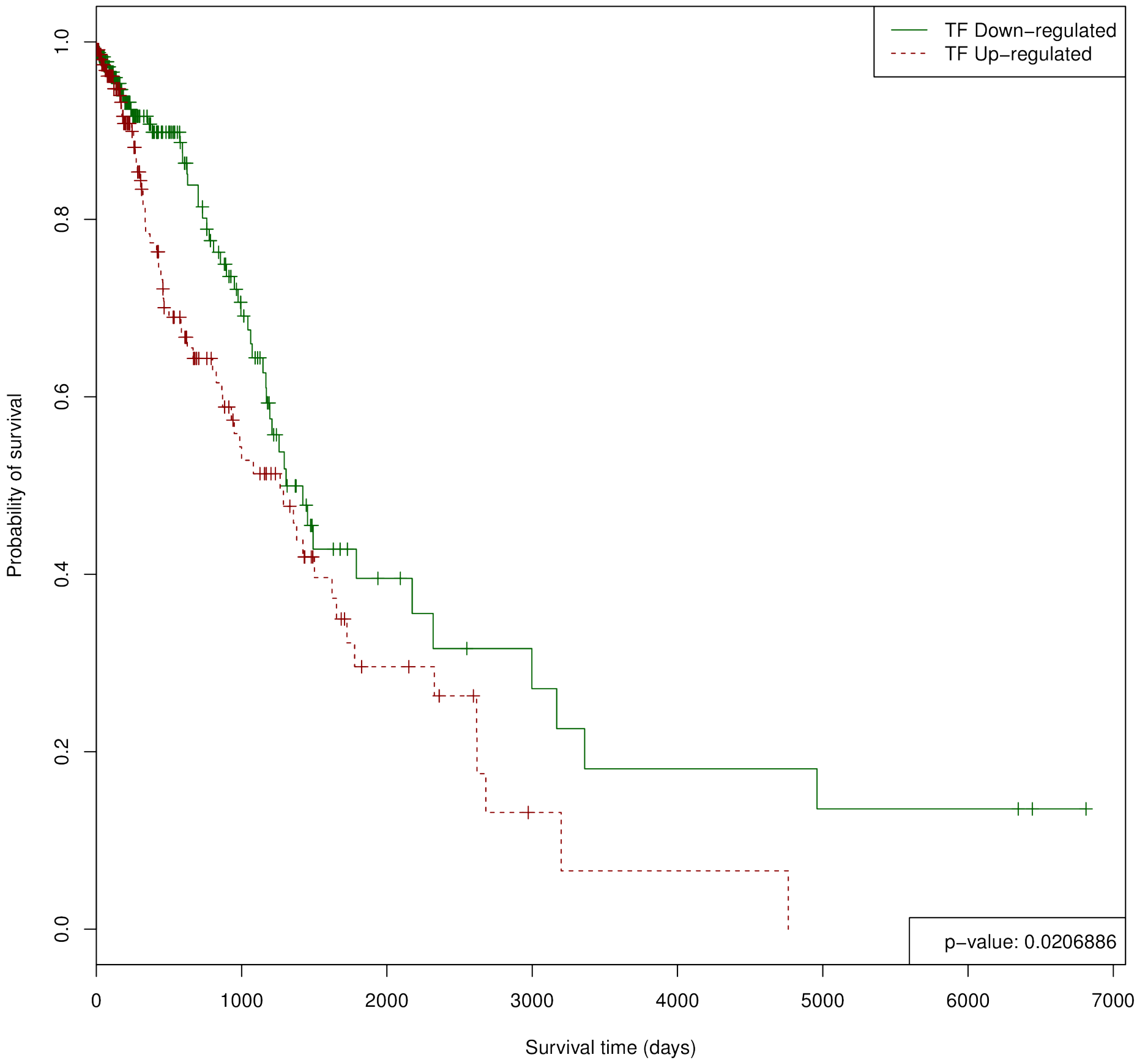
# SRF in KIRC



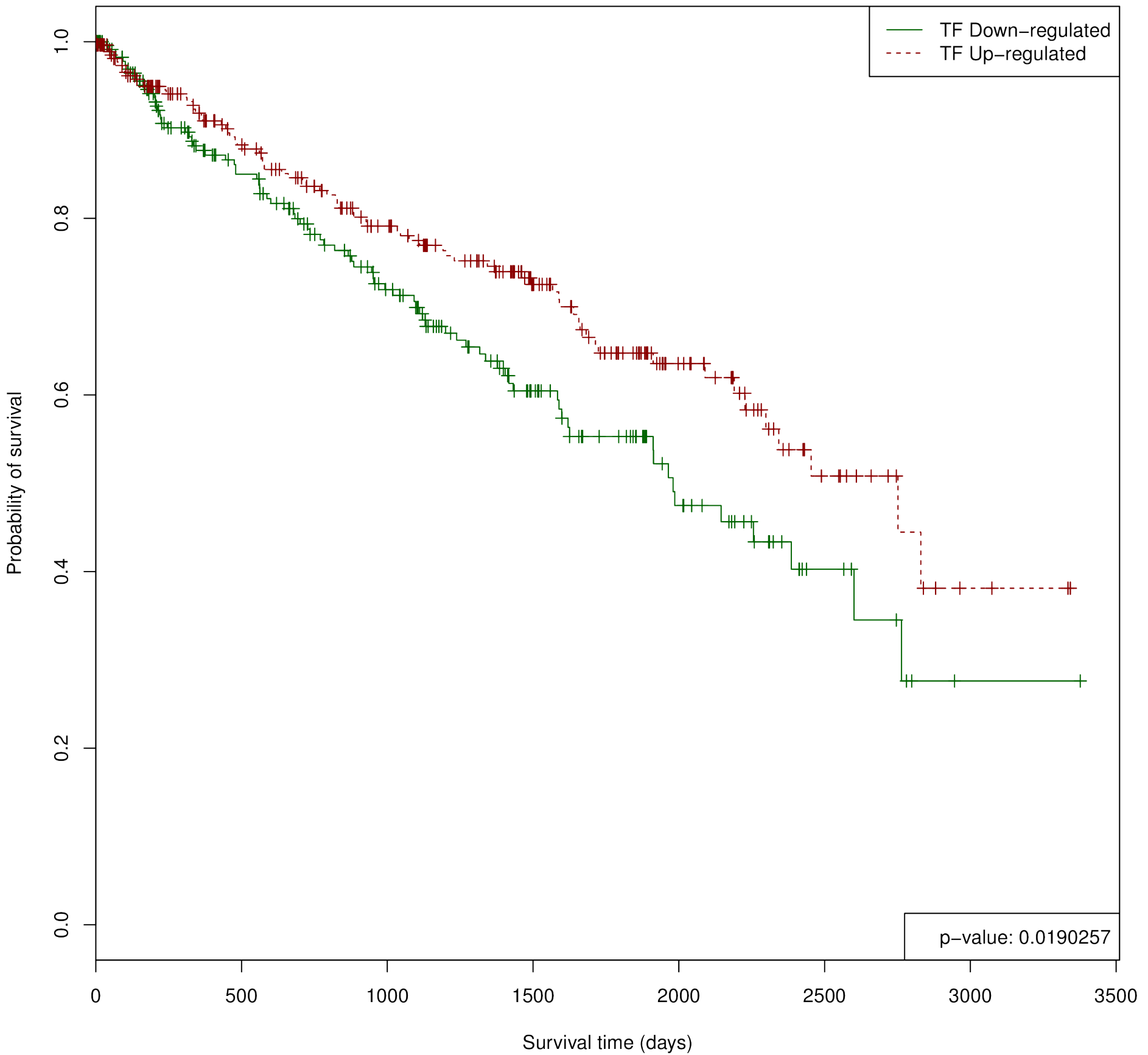
# TAL1::GATA1 in BRCA



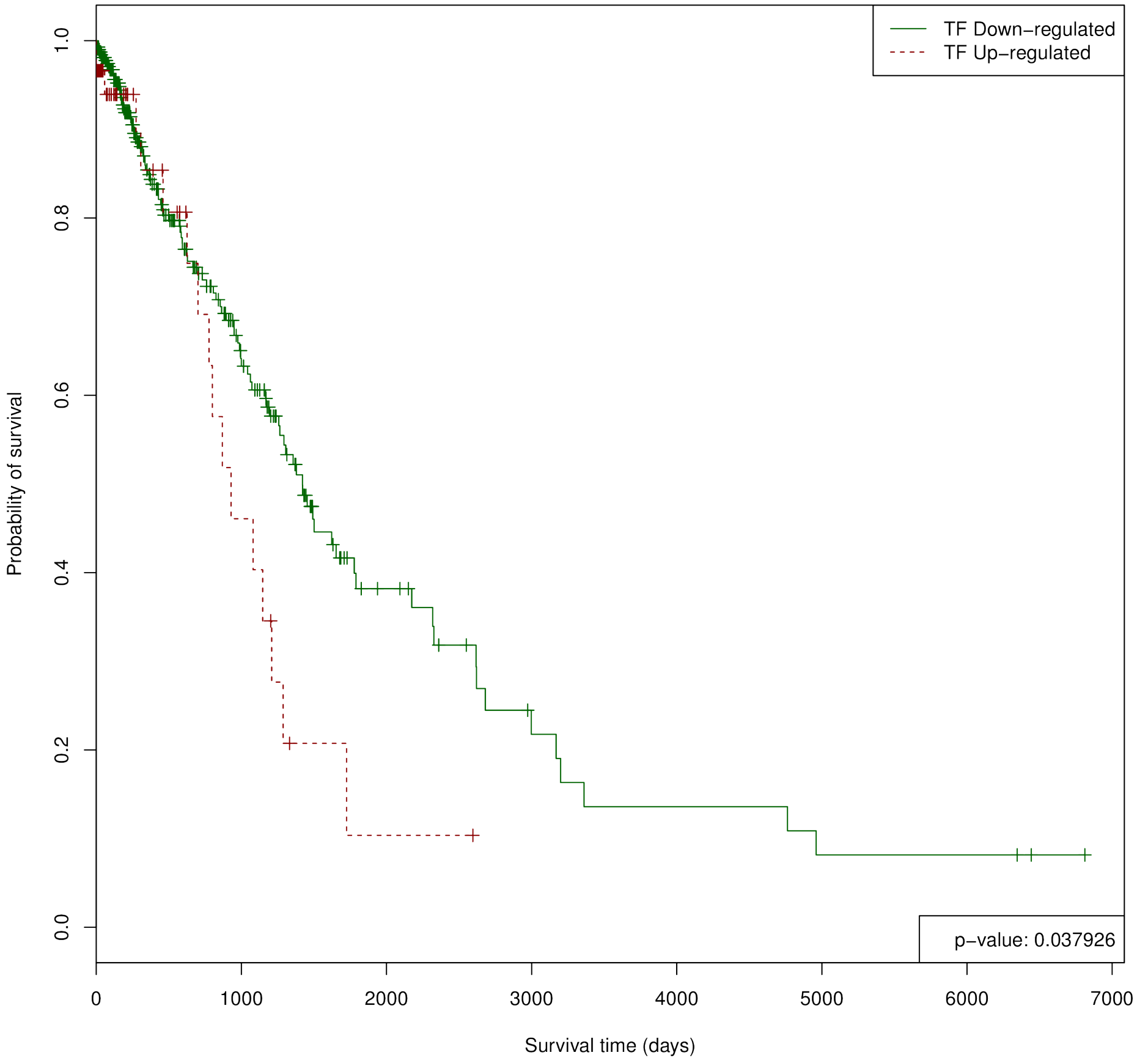
# TAL1::GATA1 in LUAD



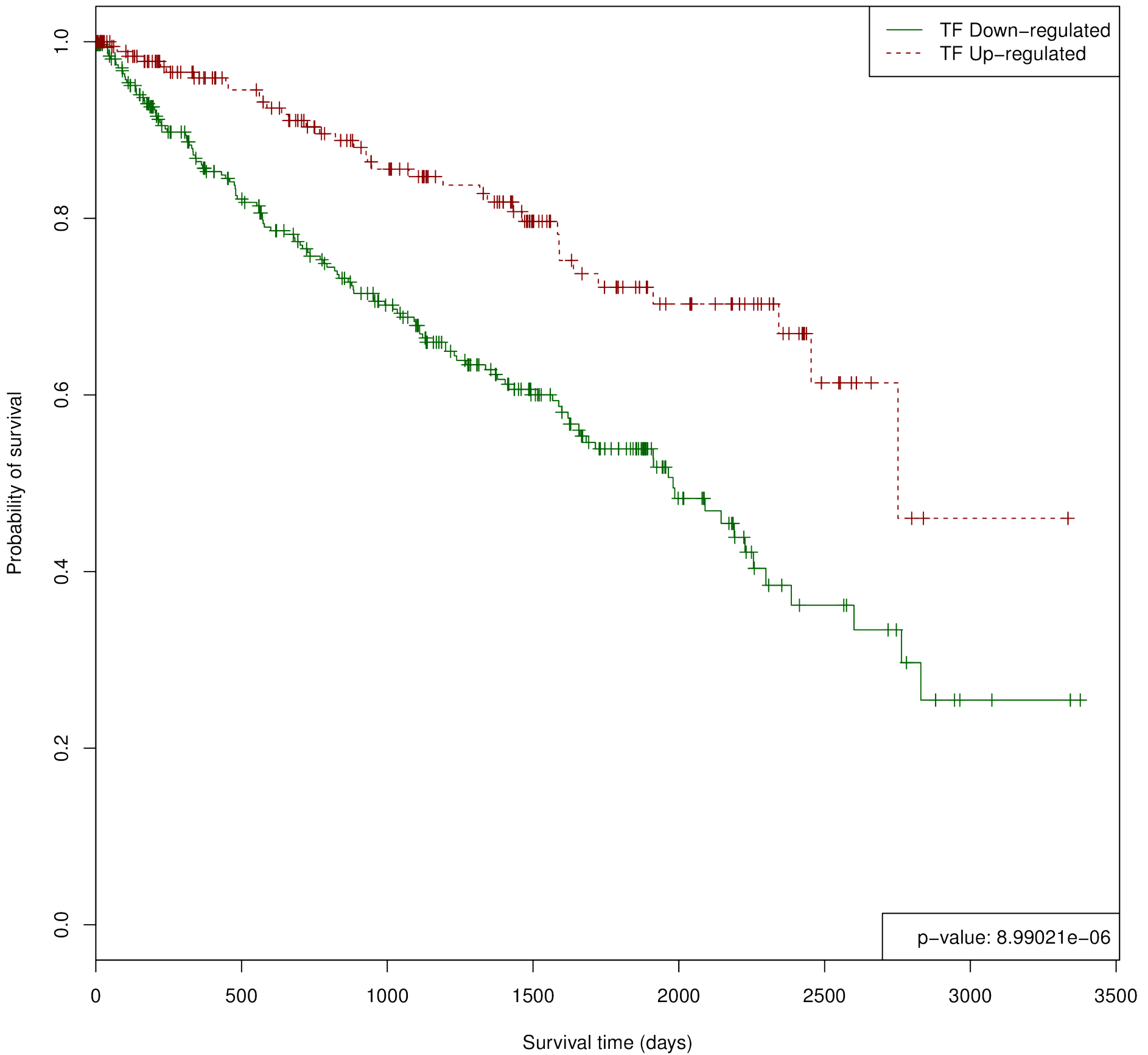
# TCF12 in KIRC



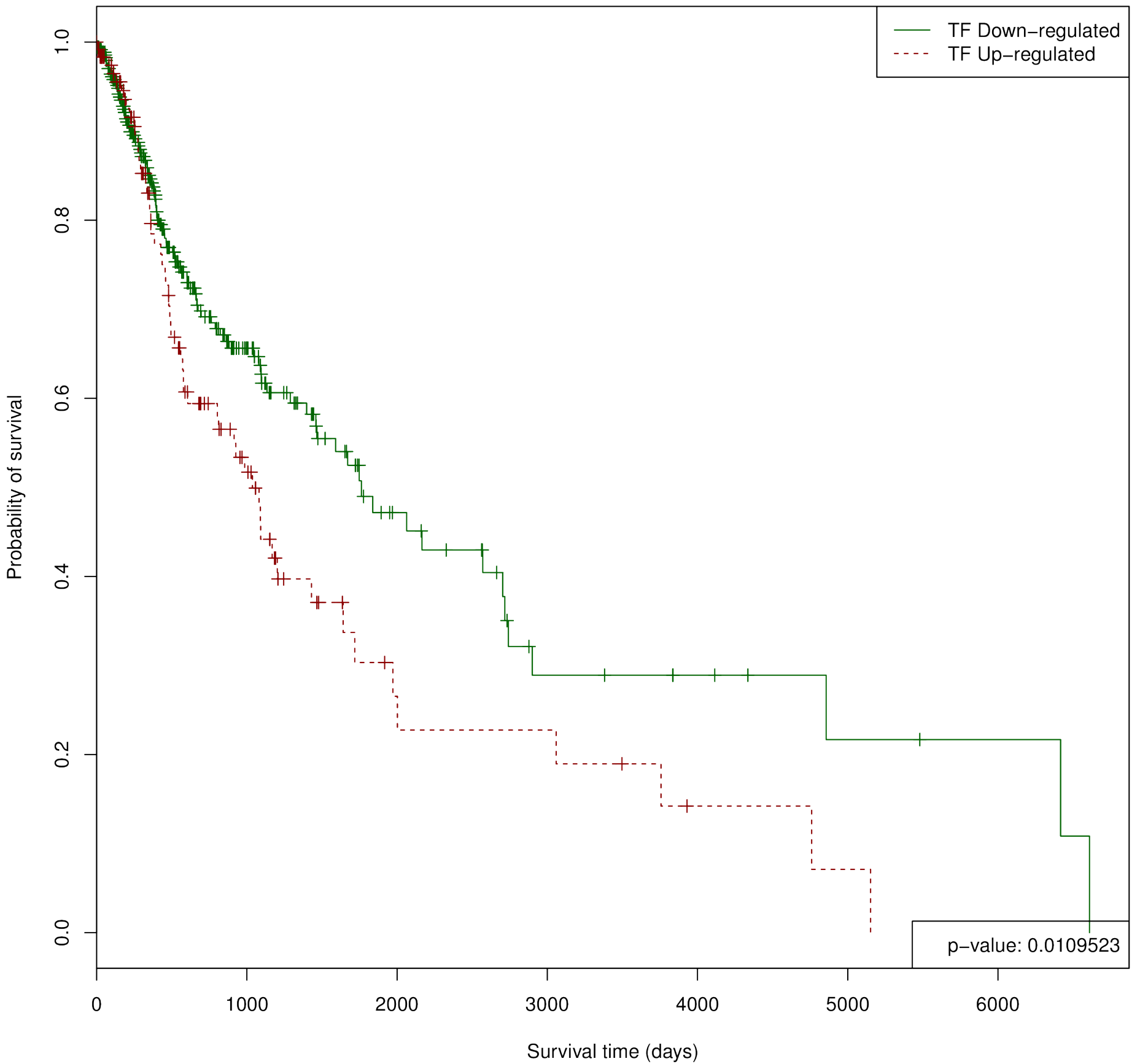
# TCF12 in LUAD



# USF1 in KIRC

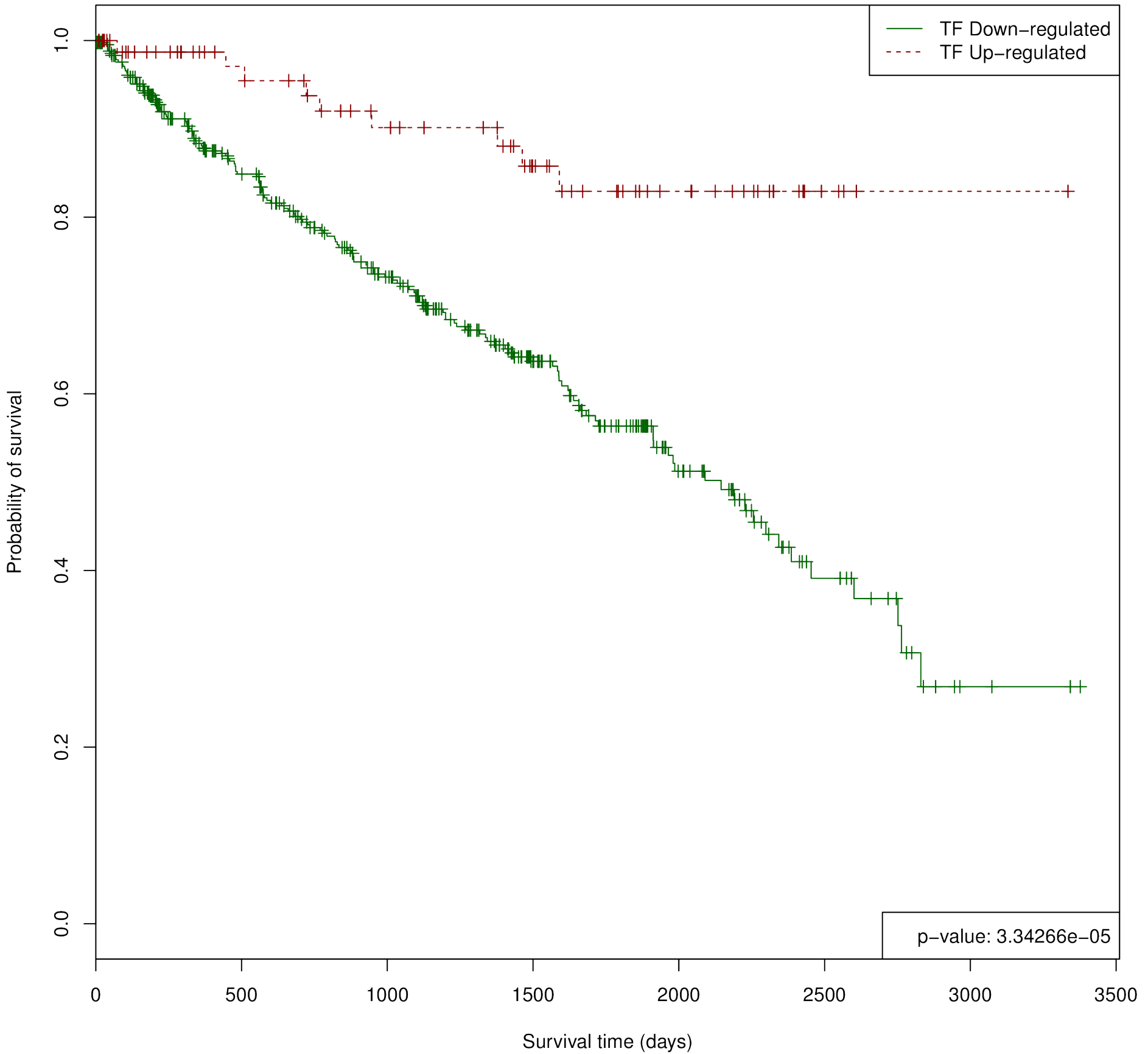


# YY1 in HNSC

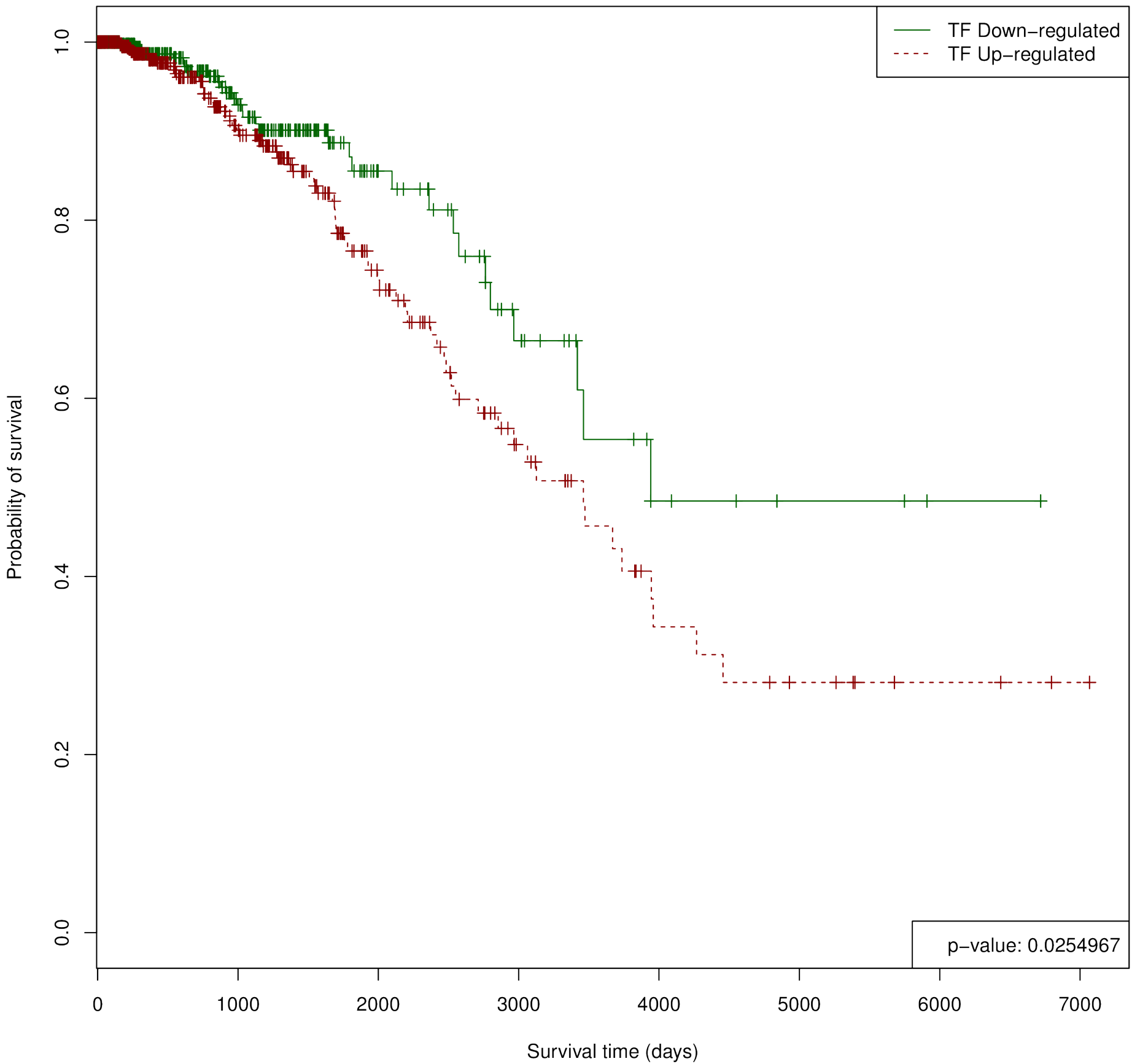




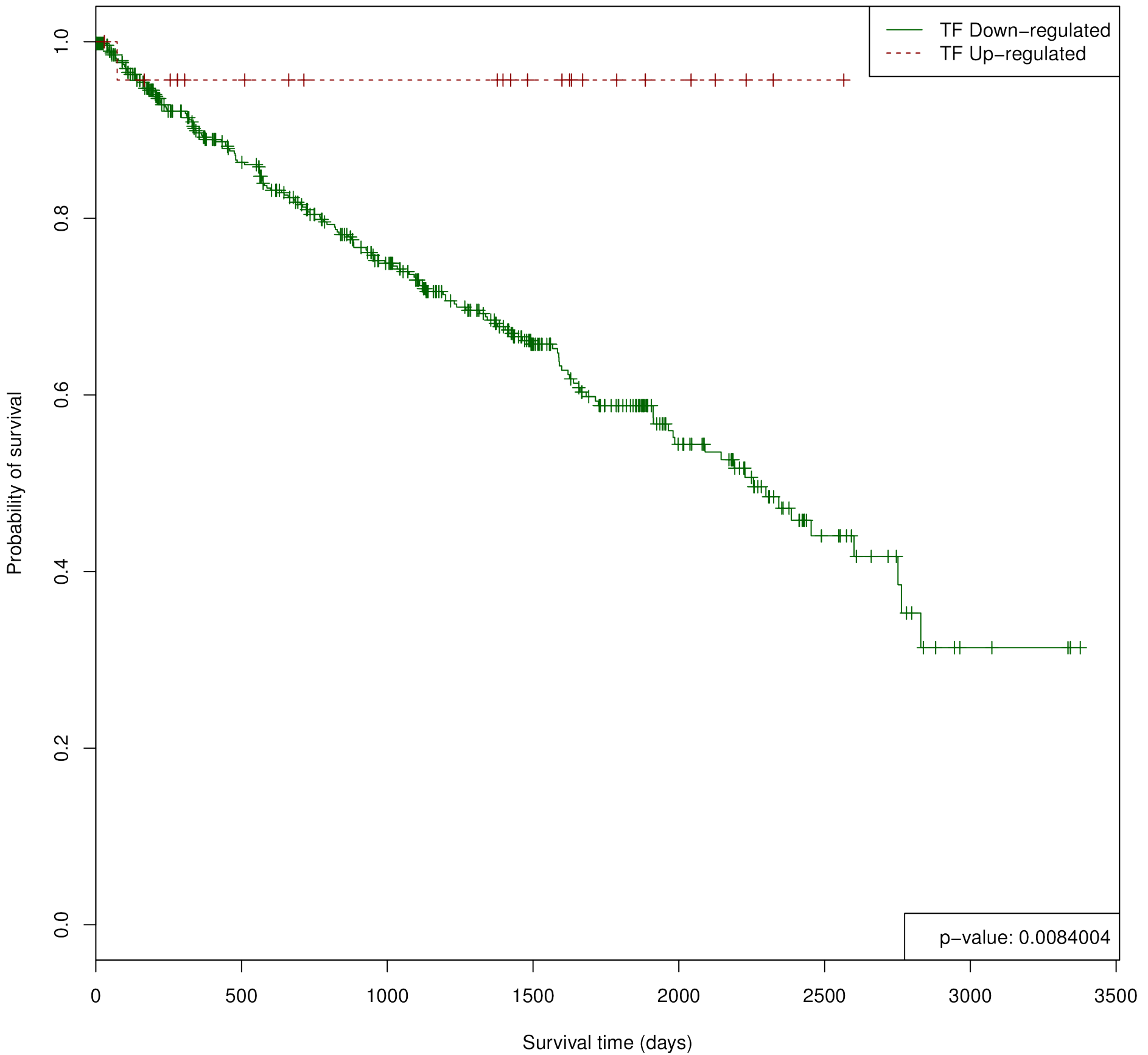
# YY1 in KIRC



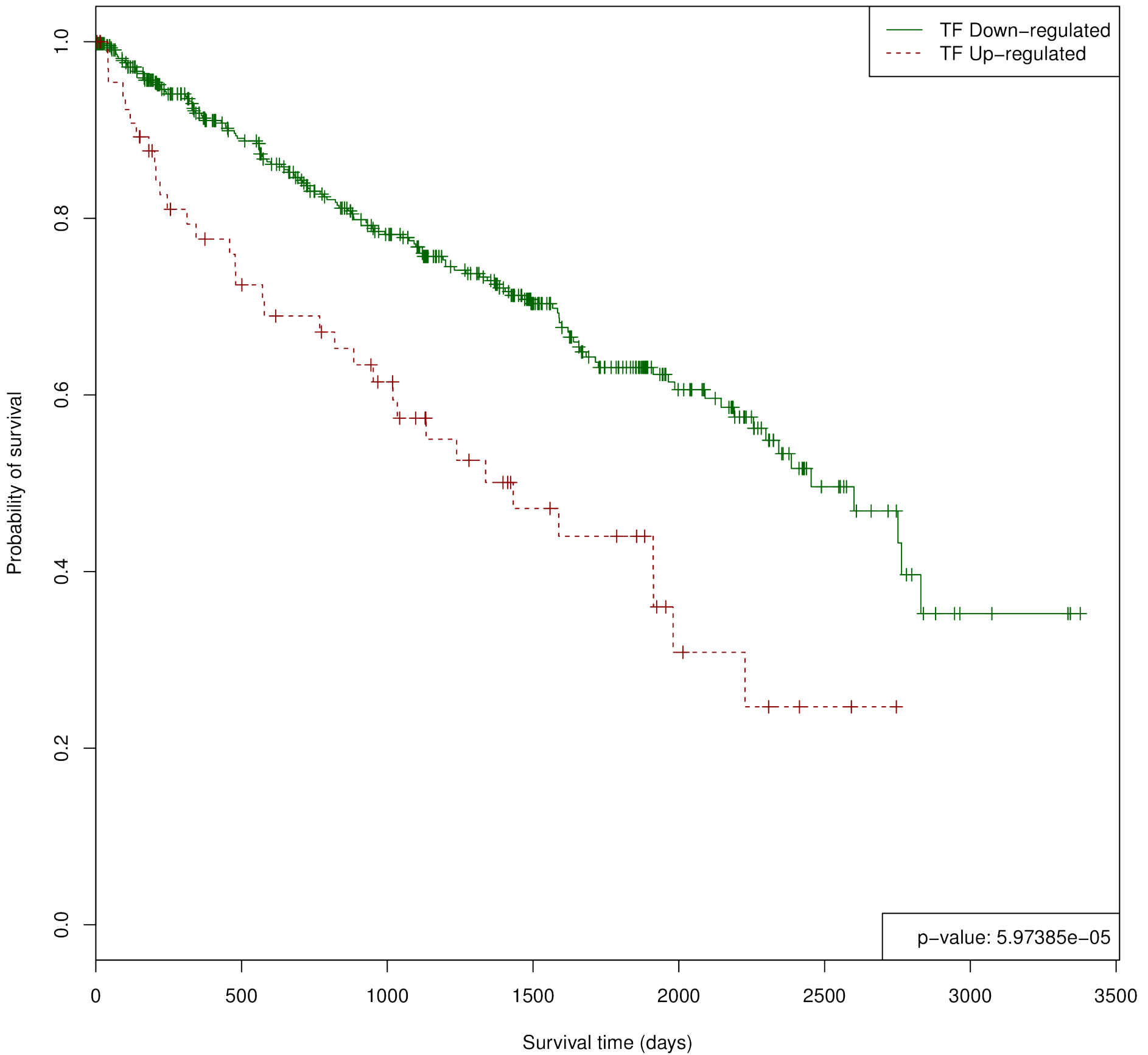
# ZBTB33 in BRCA



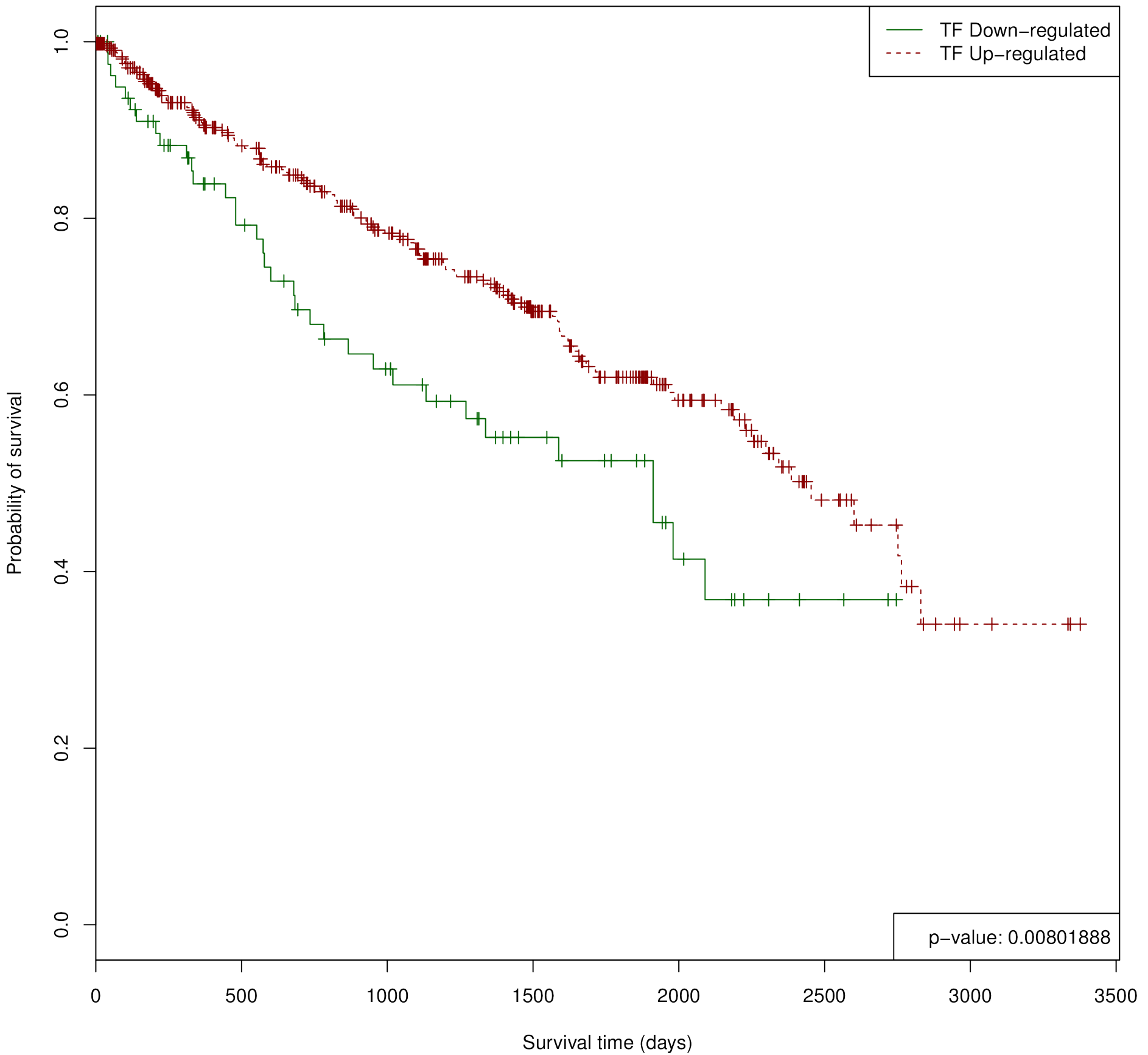
# ZBTB33 in KIRC



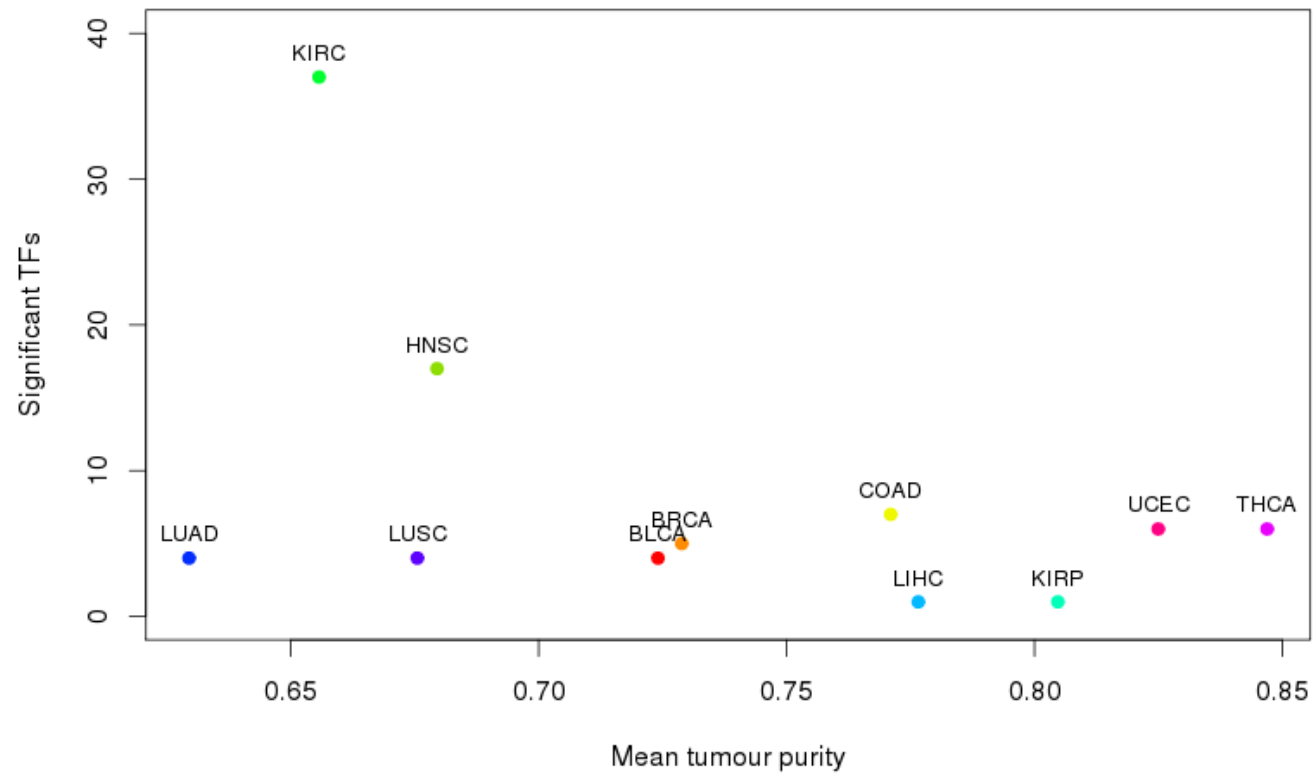
# ZEB1 in KIRC



# ZNF263 in KIRC



**Supplementary Figure 3.** Number of TF with a significant change of activity between cancers and the corresponding healthy tissue of origin a function of mean tumour purity.



**Supplementary Figure 4.** Number of TF significantly associated to survival by a K-M test as a function of the number of deceased patients.

