```
 GET DATA
  /TYPE=TXT
  /FILE="C:\Users\ldramire\Desktop\PAH_MB_genes.csv.pred.csv"
  /DELCASE=LINE
  /DELIMITERS=","
  /ARRANGEMENT=DELIMITED
  /FIRSTCASE=2
  /IMPORTCASE=ALL
  /VARIABLES=
  PAH F1.0
  ABCE1 F1.0
  ADRA2A F1.0
  ATF2 F1.0
  BCLAF1 F1.0
  TMF1 F1.0
  CYCS F1.0
  DDX18 F1.0
  FGA F1.0
  LDHA F1.0
  MAP7 F1.0
  MAPK6 F1.0
  NRAS F1.0
  NRIP1 F1.0
  PEX5 F1.0
  PPP1CC F1.0
  PTGS1 F1.0
  CD40 F1.0
  GP1BA F1.0
  HAAO F1.0
  Prediction F8.6.
CACHE.
EXECUTE.
DATASET NAME DataSet2 WINDOW=FRONT.
DATASET ACTIVATE DataSet2.
DATASET CLOSE DataSet1.
ROC Prediction BY PAH (1)
  /PLOT=CURVE(REFERENCE)
  /CRITERIA=CUTOFF(INCLUDE) TESTPOS(LARGE) DISTRIBUTION(FREE) CI(95)
  /MISSING=EXCLUDE.
```

ROC Curve

Notes

Output Created		14-AUG-2014 15:21:02
Comments		
Input	Data	C:\Users\ldramire\Desktop\PAH_MB_genes.csv.pred.csv
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	146
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the analysis.
Syntax		ROC Prediction BY PAH(1) /PLOT=CURVE(REFERENCE) /CRITERIA=CUTOFF(INCLUDE) TESTPOS(LARGE) DISTRIBUTION(FREE) CI(95) /MISSING=EXCLUDE.
Resources	Processor Time	00:00:01.06
	Elapsed Time	00:00:00.82

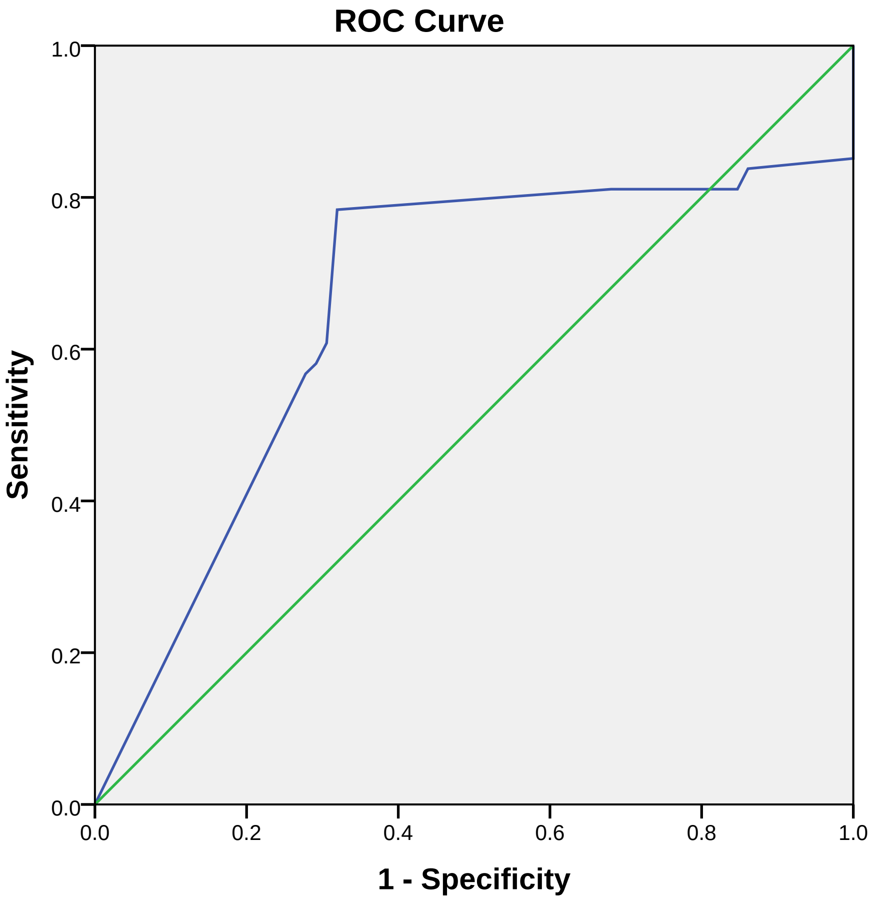
`[DataSet2]`

Case Processing Summary

PAH	Valid N (listwise)
Positive[a]	74
Negative	72

Larger values of the test result variable(s) indicate stronger evidence for a positive actual state.

a. The positive actual state is 1.



Diagonal segments are produced by ties.

Area Under the Curve

Test Result Variable(s): Prediction

Area
.657

The test result variable(s): Prediction has at least one tie between the positive actual state group and the negative actual state group. Statistics may be biased.