

# Cancer gene prioritization by integrative analysis of mRNA expression and DNA copy number data: a comparative review

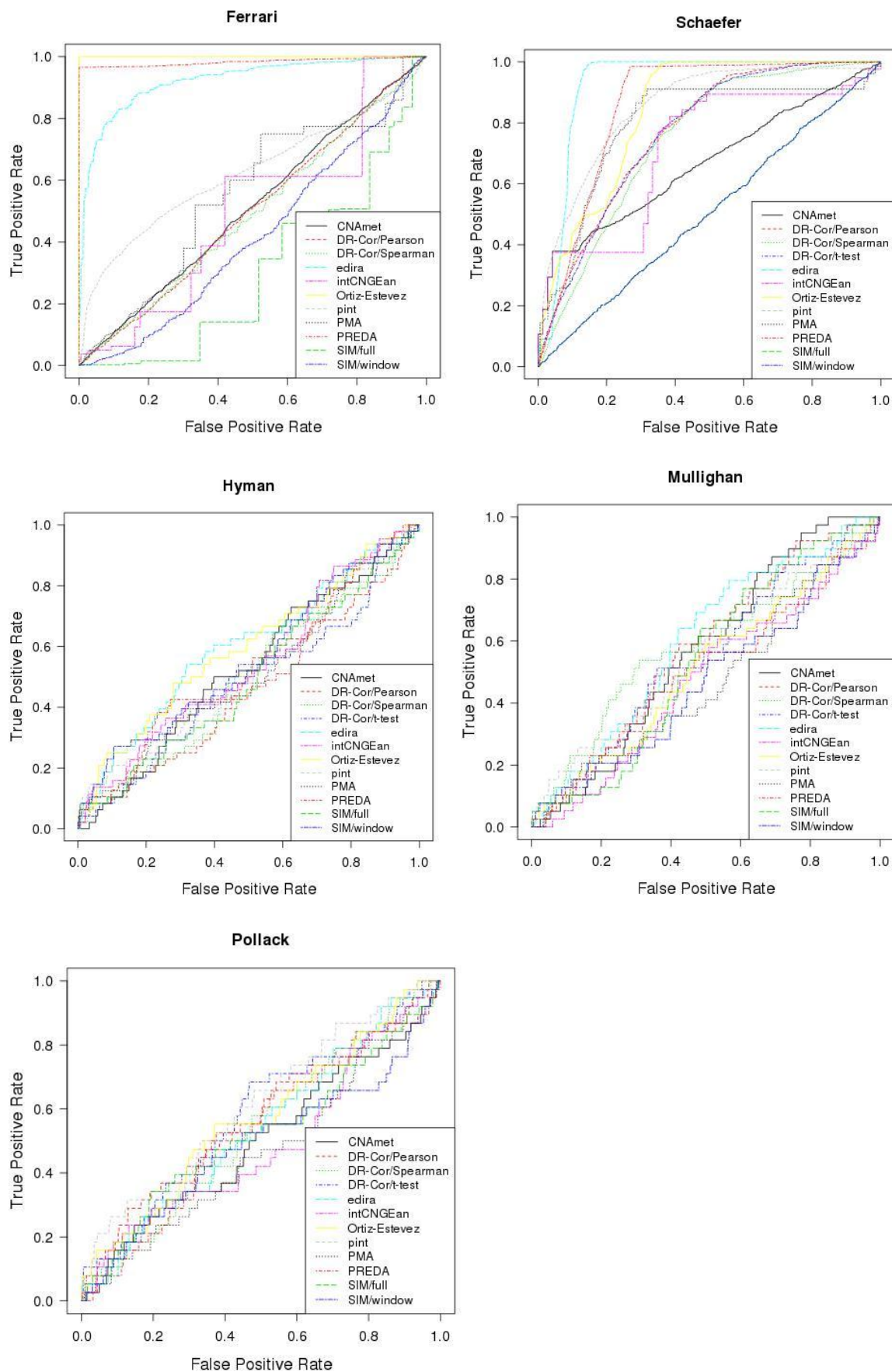
## Supplementary Material

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	Ferrari	Schaefer	Hyman	Mullighan	Pollack
CNAmet	106.96	52.34	77.44	28.38	44.99
DR-Cor/Pearson	168.50	61.11	70.26	24.39	41.41
DR-Cor/Spearman	310.52	120.40	135.04	45.08	78.41
DR-Cor/t-test	-	67.52	68.02	26.18	43.38
edira	0.41	0.23	0.22	0.11	0.15
intCNGEan	5.74	47.64	20.05	45.64	23.95
Ortiz-Estevez	0.53	2.84	0.65	1.24	1.07
pint	86.20	130.20	29.75	6.80	19.13
PMA	0.34	0.33	0.18	0.17	0.13
PREDA	79.23	155.65	59.95	360.60	106.53
SIM/full	87.51	155.96	13.63	4.77	5.14
SIM/window	19.15	171.96	2.81	1.28	1.40

**Supplementary Table 1** Running times (in minutes) for the comparison algorithms in the five benchmarking data sets.



**Supplementary Figure 1** Receiver-Operator Characteristic (ROC) curves characterize the cancer gene prioritization performance of the comparison algorithms in two simulated data sets (‘Ferrari’ and ‘Schäfer’), two breast cancer data sets (‘Hyman’ and ‘Pollack’), and one leukemia data set (‘Mullighan’) based on golden standard lists of knccustom cancer genes.