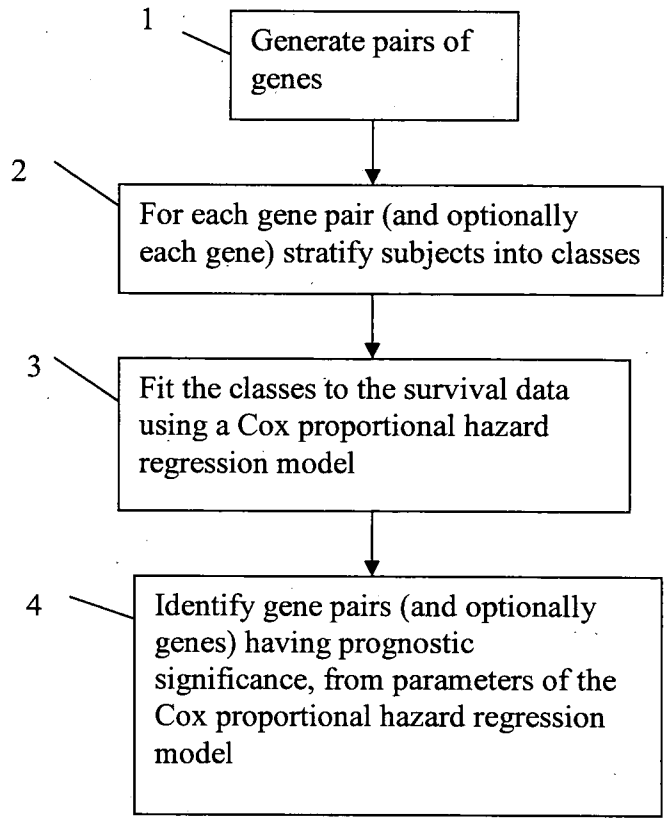
1
Generate pairs of genes
2
For each gene pair (and optionally each gene) stratify subjects into classes
3
Fit the classes to the survival data using a Cox proportional hazard regression model
4
Identify gene pairs (and optionally genes) having prognostic significance, from parameters of the Cox proportional hazard regression model

Fig. 1

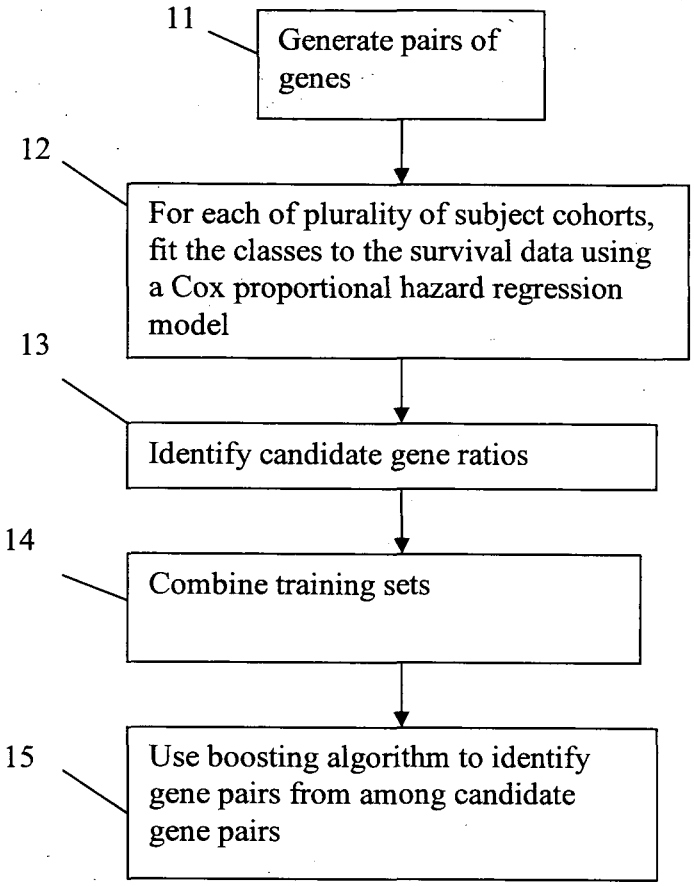
11
Generate pairs of genes
12
For each of plurality of subject cohorts, fit the classes to the survival data using a Cox proportional hazard regression model
13
Identify candidate gene ratios
14
Combine training sets
15
Use boosting algorithm to identify gene pairs from among candidate gene pairs

Fig. 2

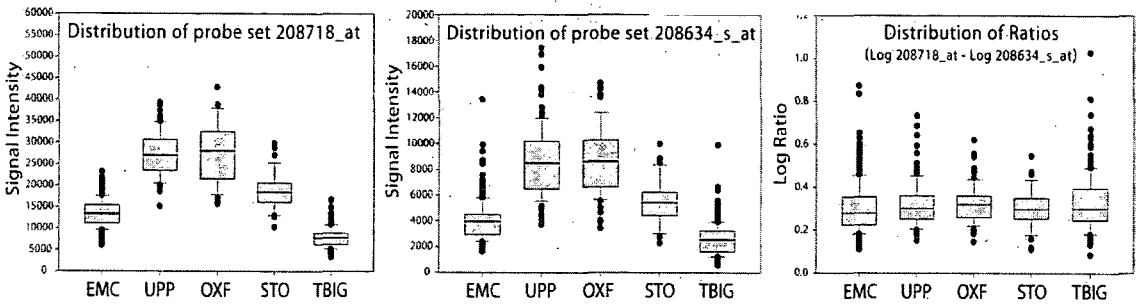

Fig. 3

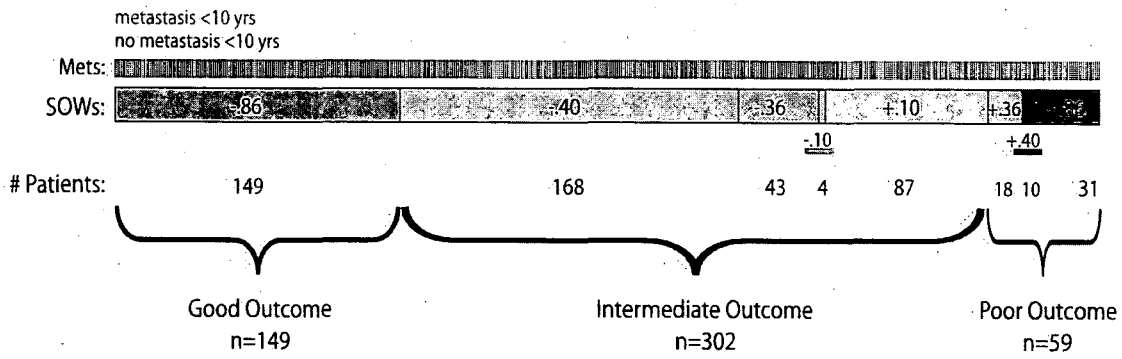

Fig. 4

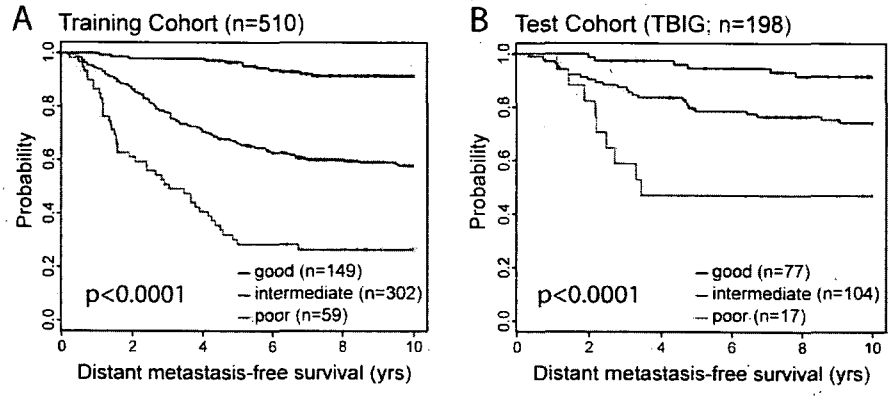

Fig. 5

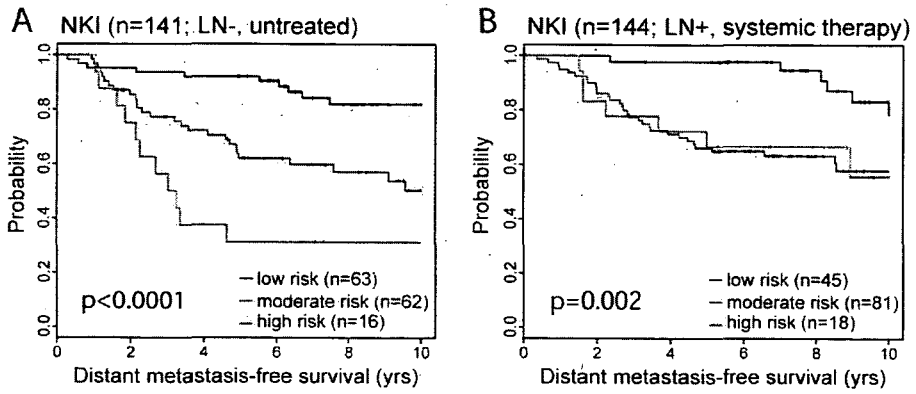
A
NKI (n=141; LN-, untreated)
Probability
0.0
0.2
0.4
0.6
0.8
1.0
0
2
4
6
8
10
Distant metastasis-free survival (yrs)
p<0.0001
low risk (n=63)
moderate risk (n=62)
high risk (n=16)
B
NKI (n=144; LN+, systemic therapy)
Probability
Distant metastasis-free survival (yrs)
p=0.002
low risk (n=45)
moderate risk (n=81)
high risk (n=18)

Fig. 6