

The use of genetic programming in the analysis of quantitative gene expression profiles for identification of nodal status in bladder cancer

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### **Additional File 3**

<b>Rule number</b>	<b>Classifier Rule</b>
1	$(MAP2K6 / KDR) \times (1.0 - (MAP2K6 / ICAM1)) > .71$
2	$MAP2K6 \times ((ICAM1 - KDR) / (ICAM1 \times KDR)) > .705$
3	$MAP2K6 \times ((ICAM1 - KDR) / (ICAM1 \times KDR)) > .705$
4	$(MAP2K6 / KDR) - \exp(KDR) - (MAP2K6 / ICAM1) > -.294$
5	$(MAP2K6 / KDR) \times (1.0 - (MAP2K6 / ICAM1)) > .71$
6	$ICAM1 / (MAP2K6 - KDR \times \exp(ICAM1)) > 4.092$
7	$(MAP2K6 / KDR) \times (1.0 - (MAP2K6 / ICAM1)) > .71$
8	$(MAP2K6 / KDR) - (MAP2K6 / (ICAM1 + \exp(ICAM1))) > .705$
9	$MAP2K6 \times ((ICAM1 - KDR) / (ICAM1 \times KDR)) > .69$
10	$(MAP2K6 / KDR) - (MAP2K6 / (ICAM1 \times \exp(KDR))) > .705$
11	$(MAP2K6 / KDR) - (MAP2K6 / (ICAM1 + \exp(ICAM1))) > .886$

**Meta-rule for node positive patients using the three most frequently used genes, viz. *KDR*, *MAP2K6* and *ICAM1*.**

Note that rules 1, 5 and 7 feature the same rule.