

**Table 4 (supplemental data). Main indices of *EGFR* gene copy number in tumor areas used for analysis of the variability of gene copy number within individual tumor samples**

Sample	Mean	SD	Median	Min	Max	Number of tumor areas analyzed
505008i	2.74	0.00	2.74	2.74	2.74	2
00L-27072	3.63	0.32	3.60	3.33	3.96	3
01.1239.1	2.93	0.06	2.90	2.89	3.00	3
028.7785.3A	2.86	0.06	2.89	2.80	2.90	3
02B8919.3C	2.40	0.18	2.35	2.25	2.60	3
04.1113.5	1.63	0.03	1.64	1.60	1.66	3
1303540.5	1.38	0.14	1.34	1.25	1.53	3
137R71C	3.23	0.25	3.35	2.95	3.40	3
722474.5.B2	2.51	0.07	2.52	2.44	2.58	3
01W1977-2	2.34	0.17	2.33	2.16	2.56	4
02-8462-B4	2.63	0.17	2.60	2.45	2.85	4
03275374	3.21	0.34	3.18	2.84	3.64	4
667330.5	3.18	0.14	3.20	3.00	3.32	4
710248	2.54	0.22	2.60	2.24	2.73	4
566903B3	3.19	0.59	3.26	2.55	3.95	5
566903B4	2.93	0.58	3.15	2.25	3.60	5
566903B5	3.75	0.14	3.75	3.55	3.95	5
660024.3	2.64	0.15	2.65	2.40	2.78	5
674072.4	3.41	0.21	3.35	3.14	3.65	5
H2O 4249.4	3.07	0.54	3.20	2.46	3.75	5
02.2553.I	2.50	0.26	2.60	2.15	2.76	6
02P11543B9	3.64	0.33	3.48	3.35	4.10	6
1004578.6	2.76	0.18	2.78	2.50	3.02	6
1100501.8	2.84	0.15	2.82	2.63	3.02	6
17956.04A	2.89	0.16	2.88	2.70	3.11	6
98B3002.3	2.60	0.29	2.50	2.26	3.00	6
01-2296B2	2.78	0.32	2.73	2.40	3.24	8

SD: standard deviation; Min = lowest mean gene copy number observed in a single area; Max = highest mean gene copy number observed in a single area.

**Table 5 (supplemental data). Main indices of *EGFR* gene copy number in tumor samples used for analysis of the variability of gene copy number within individual patients**

Patient	Mean	SD	Median	Min	Max	Number of available blocks	Tumor sites analyzed
2	2.94	0.55	2.94	2.56	3.33	2	Primary/metastasis
15	3.07	0.65	3.07	2.61	3.53	2	Primary/primary
26	2.57	0.31	2.57	2.34	2.79	2	Primary/metastasis
28	3.02	0.32	3.02	2.80	3.25	2	Primary/metastasis
43	2.54	0.28	2.54	2.34	2.74	2	Primary/primary
56	2.89	0.31	2.89	2.67	3.11	2	Primary/primary
57	2.72	0.13	2.72	2.63	2.82	2	Primary/primary
58	2.24	0.02	2.24	2.22	2.25	2	Primary/primary
59	1.82	0.01	1.82	1.81	1.83	2	Metastasis/metastasis
69	3.47	0.27	3.47	3.28	3.67	2	Primary/metastasis
72	2.64	0.36	2.64	2.38	2.90	2	Metastasis/metastasis
13	3.13	0.80	2.78	2.56	4.04	3	Primary/primary/ metastasis
36	1.87	0.23	1.79	1.69	2.12	3	Primary/primary/ primary
41	1.85	0.11	1.91	1.72	1.91	3	Primary/primary/ primary
53	2.71	0.16	2.79	2.52	2.82	3	Primary/metastasis/ metastasis
62	2.92	0.43	2.84	2.54	3.38	3	Primary/primary/ primary
236	3.29	0.42	3.19	2.93	3.75	3	Primary/primary/ primary

SD: standard deviation; Min = lowest mean gene copy number observed in a single tumor sample; Max = highest mean gene copy number observed in a single tumor sample.

**Table 6 (supplemental data). Results obtained using the dichotomisation: “is the percentage of cells, having a GCN higher than a specific value  $r$ , higher than some percentage value  $s$ ?” as a predictor for response. Listed are all dichotomisations yielding a c-index higher than 0.60**

	<b>c-index</b>	<b>GCN (= <math>r</math>)</b>	<b>Percent of cells (= <math>s</math>)</b>
<b>1</b>	0.718710	2	56
<b>2</b>	0.710645	2	54
<b>3</b>	0.710645	2	55
<b>4</b>	0.698710	2	57
<b>5</b>	0.698710	2	58
<b>6</b>	0.694516	2	53
<b>7</b>	0.686129	3	15
<b>8</b>	0.682581	3	20
<b>9</b>	0.682581	3	21
<b>10</b>	0.682258	3	17
<b>11</b>	0.678710	1	91
<b>12</b>	0.674839	1	92
<b>13</b>	0.674194	3	16
<b>14</b>	0.670645	1	90
<b>15</b>	0.670323	3	18
<b>16</b>	0.670323	2	52
<b>17</b>	0.666774	3	22
<b>18</b>	0.662903	3	23
<b>19</b>	0.662903	3	24
<b>20</b>	0.662903	3	25
<b>21</b>	0.662903	3	26
<b>22</b>	0.662581	4	5
<b>23</b>	0.662258	1	88
<b>24</b>	0.661935	3	14
<b>25</b>	0.661935	2	40
<b>26</b>	0.661935	2	41
<b>27</b>	0.661935	2	42
<b>28</b>	0.661935	2	43
<b>29</b>	0.661935	2	44
<b>30</b>	0.659355	1	96

	<b>c-index</b>	<b>GCN (= <i>r</i>)</b>	<b>Percent of cells (= <i>s</i>)</b>
<b>31</b>	0.659032	1	93
<b>32</b>	0.659032	1	94
<b>33</b>	0.658387	3	19
<b>34</b>	0.658065	2	50
<b>35</b>	0.655484	4	11
<b>36</b>	0.654839	2	61
<b>37</b>	0.654194	2	51
<b>38</b>	0.654194	1	87
<b>39</b>	0.653871	2	39
<b>40</b>	0.653548	1	80
<b>41</b>	0.653226	3	5
<b>42</b>	0.650968	2	63
<b>43</b>	0.650968	2	64
<b>44</b>	0.650968	2	65
<b>45</b>	0.650968	2	66

GCN: gene copy number.

**Table 7 (supplemental data). Diagnostic performances obtained with 56% of polysomic cells (best percentage of polysomic cells as indicated by receiver operating characteristic curve analysis) to predict objective response**

<b>sensitivity</b>	<b>specificity</b>	<b>PPV</b>	<b>NPV</b>	<b>accuracy</b>	<b>AUC</b>
0.72	0.74194	0.52941	0.86792	0.73563	0.73097

PPV, positive predictive value; NPV, negative predictive value; AUC, area under the curve.