Cancer Epidemiology, Biomarkers & Prevention

Correction: A Computational Method to Classify Variants of Uncertain Significance Using Functional Assay Data With Application to *BRCA1*

In this article (Cancer Epidemiol Biomarkers Prev 2011;20:1078–88), which was published in the June 2011 issue of *Cancer Epidemiology, Biomarkers & Prevention* (1), all the negative values in the "$\log_e$ posterior odds" column of Table 2 were incorrectly typeset as positive values. The correct table is shown below. The publisher regrets the error.

Table 2. Table of variant-specific summaries: variant name (column 1), prior classification (column 2), posterior probability that the variant is protein damaging (column 3), and natural logarithm of the posterior odds in favor of the variant being protein damaging (column 4)

Variant	Classification	Posterior probability damaging	$\log_e$ posterior odds[a]
5673insC	Pathogenic[b]	1.0000	
del17/18	Pathogenic	1.0000	
W1837X	Pathogenic	1.0000	
WT	Neutral[c]	0.0000	
Y1853X	Pathogenic	1.0000	
A1669S	VUS	0.0625	−2.71
A1708E	VUS	1.0000	17.67
A1752P	VUS	1.0000	18.02
A1823T	VUS	0.9999	8.89
A1830T	VUS	0.0015	−6.53
C1697R	VUS	0.9999	9.50
D1546N	VUS	0.0015	−6.51
D1692N	VUS	0.0948	−2.26
E1644G	VUS	0.0016	−6.45
E1794D	VUS	0.0013	−6.62
F1662S	$VUS_{0.0001}$[d]	0.0017	−6.40
F1695L	VUS	0.0013	−6.63
G1706A	VUS	1.0000	11.85
G1706E	$VUS_{0.999}$[e]	1.0000	16.61
G1738E	VUS	0.9952	5.34
G1738R	$VUS_{0.99}$[f]	1.0000	17.39
G1788D	VUS	0.0147	−4.21
G1788V	VUS	1.0000	17.80
H1402Y	VUS	0.0032	−5.73
H1421Y	VUS	0.0017	−6.37
H1746N	VUS	0.0231	−3.74
I1766S	VUS	1.0000	16.01
K1487R	VUS	0.0045	−5.39
K1847R	VUS	0.0025	−5.98
L1407P	VUS	0.4052	−0.38

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Table 2. Table of variant-specific summaries: variant name (column 1), prior classification (column 2), posterior probability that the variant is protein damaging (column 3), and natural logarithm of the posterior odds in favor of the variant being protein damaging (column 4) (Cont'd)

Variant	Classification	Posterior probability damaging	$\log_e$ posterior odds[a]
L1564P	VUS	0.0058	−5.14
L1664P	VUS	0.0017	−6.38
L1764P	$VUS_{0.99}$	1.0000	16.85
L1844R	VUS	0.0013	−6.62
M1628T	VUS	0.0031	−5.77
M1628V	VUS	0.0031	−5.78
M1628V+S1613G	VUS	0.0026	−5.97
M1652I	VUS	0.0013	−6.63
M1689R	VUS	1.0000	16.00
M1775K	VUS	1.0000	13.37
M1775R	$VUS_{0.99}$	1.0000	17.24
M1783L	VUS	0.0013	−6.63
M1783T	VUS	0.0346	−3.33
P1614S	$VUS_{0.0001}$	0.0011	−6.82
P1771L	VUS	0.0066	−5.01
P1806A	VUS	0.0016	−6.45
P1812A	VUS	0.0050	−5.29
P1859R	$VUS_{0.0001}$	0.0013	−6.64
Q1785H	VUS	0.0012	−6.77
Q1826H	VUS	0.0031	−5.77
R1443G	VUS	0.0223	−3.78
R1495M	VUS	0.0019	−6.24
R1699L	VUS	1.0000	17.50
R1699Q	VUS	0.9987	6.65
R1699W	VUS	0.8795	1.99
R1726G	VUS	0.0013	−6.66
R1751P	VUS	1.0000	17.54
R1751Q	$VUS_{0.0001}$	0.0022	−6.11
R1753T	VUS	1.0000	17.57
R1835Q	VUS	0.0021	−6.15
S1512I	$VUS_{0.0001}$	0.0013	−6.62
S1613C	VUS	0.0012	−6.69
S1613G	$VUS_{0.0001}$	0.0009	−7.03
S1655F	VUS	0.9995	7.56
S1715N	VUS	0.9994	7.49
S1715R	VUS	0.9997	8.16
T1685I	$VUS_{0.99}$	1.0000	18.59
T1700A	VUS	0.4291	−0.29
T1720A	$VUS_{0.0001}$	0.0014	−6.59
V1534M	$VUS_{0.0001}$	0.0011	−6.81
V1665M	VUS	0.0263	−3.61
V1688del	$VUS_{0.99}$	0.9995	7.60
V1713A	VUS	1.0000	14.52
V1736A	VUS	0.9998	8.69
V1741G	VUS	0.7891	1.32

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Table 2. Table of variant-specific summaries: variant name (column 1), prior classification (column 2), posterior probability that the variant is protein damaging (column 3), and natural logarithm of the posterior odds in favor of the variant being protein damaging (column 4) (Cont'd)

Variant	Classification	Posterior probability damaging	$\log_e$ posterior odds[a]
V1804D	$VUS_{0.0001}$	0.0057	−5.17
V1809F	VUS	1.0000	17.74
V1833M	VUS	0.0017	−6.36
W1837R	VUS	1.0000	16.96
WTdelta14	VUS	0.0013	−6.67
WTdelta14+S1616G	VUS	0.0012	−6.74

[a]The posterior odds are equivalent to the Bayes Factor, Pr(Data|Damaging)/Pr(Data|Benign), because the prior distribution is uniform, and could be combined in this form with other conditionally independent data types.
[b]Known pathogenic variant ("negative control").
[c]Wild–type, known benign variant ("positive control").
[d]Variant of unknown significance (VUS) previously classified as neutral with an estimated posterior probability of pathogenicity less than 0.0001, but blinded for purposes of model evaluation.
[e]VUS previously classified as pathogenic with an estimated posterior probability greater than 0.999, but blinded for purposes of model evaluation.
[f]VUS previously classified as pathogenic with an estimated posterior probability of between 0.99 and 0.999, but blinded for purposes of model evaluation.

Reference

1. Iversen ES Jr, Couch FJ, Goldgar DE, Tavtigian SV, Monteiro ANA. A computational method to classify variants of uncertain significance using functional assay data with application to BRCA1. Cancer Epidemiol Biomarkers Prev 2011;20:1078–88.

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