

AU-PAGE Band	Observed m/z	Identified α -defensin	Theoretical m/z	Percent Identity
rDefa4				
1	3754.9551	Defa4	3756.51	99.96%
WT				
2	4076.2622	vDefa24-N	4079.90	99.91%
	4090.9565	vDefa24	4094.90	99.90%
	4317.0957	Defa5	4316.20	99.98%
3	4077.0854	vDefa24-N	4079.90	99.93%
	4091.0470	vDefa24	4094.90	99.91%
	4128.0332	Defa16	4134.92	99.83%
4	2475.1162	Defa20*	2475.34	99.99%
	4232.8076	vDefa23	4231.04	99.96%
	4248.2339	Defa2	4248.08	99.99%
5	4329.6270	Defa21	4330.11	99.99%
	4228.1084	vDefa23	4231.04	99.93%
	4244.2031	Defa2	4248.08	99.91%
6	4347.9673	Defa22	4344.19	99.91%
	4342.5874	Defa22	4344.19	99.96%
	Nod2^{-/-}			
7	4075.8882	vDefa24-N	4079.90	99.90%
	4092.0063	vDefa24	4094.90	99.93%
	4313.2397	Defa5	4316.20	99.93%
8	4076.0728	vDefa24-N	4079.90	99.91%
	4092.0823	vDefa24	4094.90	99.93%
	4133.0376	Defa16	4134.92	99.95%
9	2483.5461	Defa20*	2475.34	99.67%
	4230.8179	vDefa23	4231.04	99.99%
	4244.3823	Defa2	4248.08	99.91%
10	4330.0146	Defa21	4330.11	99.99%
	4229.1157	vDefa23	4231.04	99.95%
	4246.1221	Defa2	4248.08	99.95%
11	4345.3413	Defa22	4344.19	99.97%
	4346.5649	Defa22	4344.19	99.95%

Supplemental Table 2. *WT* and *Nod2^{-/-}* mice express the same set of Paneth cell α -defensins. Observed mass-to-charge (m/z) values of prominent, software-indicated mass peaks found within the expected cryptdin mass range (2499.0 to 4518.0 m/z) are tabulated in correspondence to the gel bands labeled in Fig.2E. The observed m/z values are listed in increasing value. Determination of the

cryptdin identity of individual m/z values was assisted by a comparison of the observed m/z values with the calculated m/z values of all purified and transcript- and gene-predicted cryptdin peptides based upon their oxidized, singly-protonated forms. Matches of m/z values with greater than 99.6% identity or with mass differences less than 5 Da were deemed sufficient for individual identification of mass peaks. Percent identity of m/z values was calculated from the quotient of the lesser over the greater m/z values of matched pairs. The labels vDefa23 and vDefa24 are used for various non-identical masses since there are multiple Defa23 and Defa24 variant transcripts that have yet to acquire unambiguous identifiers. Note that the identification of Defa20 was extrapolated by the presence of an m/z value that was more than 98% identical to the predicted m/z value of the doubly-protonated form of oxidized Defa20, since mass spectrometric analysis was performed outside the mass range of its predicted, singly-protonated-based m/z value (4950.69).