PLOS ONE

CORRECTION

Correction: Genomic evidence for genes encoding leucine-rich repeat receptors linked to resistance against the eukaryotic extra- and intracellular *Brassica napus* pathogens *Leptosphaeria maculans* and *Plasmodiophora brassicae*

The *PLOS ONE* Journal Staff

In Table 1, the value in the row titled "All other genes vs. LRR^{e}" and the column titled "Projection test *P*- value" should read as 1.9E-120. Please see the corrected Table 1 here. The publisher apologizes for this error.

Citation: The *PLOS ONE* Journal Staff (2018) Correction: Genomic evidence for genes encoding leucine-rich repeat receptors linked to resistance against the eukaryotic extra- and intracellular *Brassica napus* pathogens *Leptosphaeria maculans* and *Plasmodiophora brassicae*. PLoS ONE 13(8): e0202143. https://doi.org/10.1371/journal.pone.0202143

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Table 1. Summary of statistical tests used to determine genome-wide spatial correlations between extracellular receptor-like proteins (RLPs) and secreted peptides (SPs) versus intracellular nucleotide-binding leucine-rich repeat receptors (NLRs).

	Query	Reference	Relative Kolmogorov-Smirnov *P*-value[a]	Relative ECDF area correlation[b]	Relative ECDF deviation area *P*-value			Jaccard measure *P*–value			Projection test *P*–value		
						Close[c]	Far		Overlap[d]	N		Overlap	N
eLRR vs. NLR genes[e]	256	366	3.2E-06	0.152	<0.01	✓		0.43		✓	0.44	✓	
NLR vs. eLRR genes[e]	366	256	0.862	-2.2E-04	0.72		✓	0.40		✓	0.34	✓	
RLP vs. NLR genes	152	366	1.2E-04	0.141	0.01	✓		0.44	✓		0.29	✓	
NLR vs. RLP genes	366	152	0.007	0.046	0.07	✓		0.45	✓		0.24	✓	
SP vs. NLR genes	104	366	0.009	0.167	<0.01	✓		0.25	✓		0.21	✓	
NLR vs. SP genes	366	104	3.8E-04	0.064	0.02	✓		0.38	✓		0.14	✓	
SP vs. RLP genes	104	152	0.010	0.129	0.03	✓		0.12	✓		0.07	✓	
RLP vs. SP genes	152	104	8.2E-05	0.241	<0.01	✓		0.05	✓		0.06	✓	
LRR vs. ribosomal genes[e]	622	1134	0.002	-0.054	<0.01		✓	<0.01		✓	0.21		✓
Ribosomal vs. LRR genes[e]	1134	622	0.289	0.021	0.21	✓		<0.01		✓	0.02		✓
LRR vs. all other genes[e]	622	80305	0.000	-0.261	<0.01		✓	<0.01		✓	8.9E-78		✓
All other genes vs. LRR[e]	80305	622	2.4E-04	0.009	<0.01	✓		<0.01		✓	1.9E-120		✓

[a] *P* values are shown for all tests in both directions, using one dataset as a query and the other one as a reference.

[b] ECDF: Empirical Distribution Cumulative Function

[c] For the relative distance test, positive and negative relative ECDF area correlation values are labeled as close and far, respectively.

[d] The outcome of Jaccard and projection tests is defined as overlapping or non-overlapping (N).

[e] The combination of RLP and SP genes are referred to as eLRR genes. Control comparisons include those of all predicted leucine-rich repeat (LRR) genes, consisting of RLP, NLR and SP genes, to ribosomal genes or those to all other coding genes of the *Brassica napus* genome.

https://doi.org/10.1371/journal.pone.0202143.t001

Reference

1. Stotz HU, Harvey PJ, Haddadi P, Mashanova A, Kukol A, Larkan NJ, et al. (2018) Genomic evidence for genes encoding leucine-rich repeat receptors linked to resistance against the eukaryotic extra- and intracellular *Brassica napus* pathogens *Leptosphaeria maculans* and *Plasmodiophora brassicae*. PLoS ONE 13(6): e0198201. https://doi.org/10.1371/journal.pone.0198201 PMID: 29856883