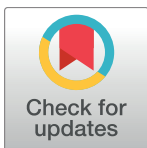


CORRECTION

# 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<sup>en</sup>” 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.



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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 <sup>a</sup>	Relative ECDF area correlation <sup>b</sup>	Relative ECDF deviation area P-value			Jaccard measure P-value		Projection test P-value		
					Close <sup>c</sup>	Far	Overlap <sup>d</sup>	N	Overlap	N		
eLRR vs. NLR genes <sup>e</sup>	256	366	3.2E-06	0.152	<0.01	✓		0.43	✓	0.44	✓	
NLR vs. eLRR genes <sup>e</sup>	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 <sup>e</sup>	622	1134	0.002	-0.054	<0.01		✓	<0.01	✓	0.21		✓
Ribosomal vs. LRR genes <sup>e</sup>	1134	622	0.289	0.021	0.21	✓		<0.01	✓	0.02		✓
LRR vs. all other genes <sup>e</sup>	622	80305	0.000	-0.261	<0.01		✓	<0.01	✓	8.9E-78		✓
All other genes vs. LRR <sup>e</sup>	80305	622	2.4E-04	0.009	<0.01	✓		<0.01	✓	1.9E-120		✓

<sup>a</sup> P values are shown for all tests in both directions, using one dataset as a query and the other one as a reference.

<sup>b</sup> ECDF: Empirical Distribution Cumulative Function

<sup>c</sup> For the relative distance test, positive and negative relative ECDF area correlation values are labeled as close and far, respectively.

<sup>d</sup> The outcome of Jaccard and projection tests is defined as overlapping or non-overlapping (N).

<sup>e</sup> 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, Kukul 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