

		Pathogenicity	Integrase	Phage	tRNA	HEG	Transposase	Virulence	Repeats	IS
Genuine GI		27	5	130	1	36	9	2	2	3
	IslandPick	0	1	10	0	8	0	0	0	0
	IslandPath-DIMOB	0	2	58	0	10	1	0	0	0
	Sigi-HMM	16	0	5	0	6	3	0	0	0
Predicted	Alien_Hunter	<b>25</b>	<b>4</b>	65	1	23	6	2	2	3
GIS	Centroid	4	0	3	1	3	0	2	1	0
	INDeGenIUS	5	2	1	1	7	0	2	0	0
	SigHunt	0	1	15	0	1	2	0	2	0
	<b>2SigFinder</b>	<b>25</b>	<b>3</b>	<b>101</b>	<b>1</b>	<b>28</b>	<b>2</b>	<b>2</b>	<b>2</b>	<b>2</b>

Supp Table 4. Summary of functional features predicted by 2SigFinder, SIGI-HMM, Alien\_Hunter, Centroid, IslandPath-DIMOB, INDeGenIUS, SigHunt and IslandPick on detection of genomic islands in *S. enterica Typhi CT18*, and the functional features were based on the number of the related genes in the real genomic islands which are covered by more than 50% of the results of the prediction method.