

Table 1: Number of enriched response elements for differential expressed genes. Full genes with flanking regions of 10.000 nucleotides were searched for the VDRE (RRGKTCAnnRRGKTCA) and D5 RARE (RGKTSAnnnnnRGKTSA) motifs using RNAbob. Enrichment between significant differential expressed genes (basemean ≥ 10 , \log_2 FC ≥ 2 , p-value ≤ 0.05) and non-significant differential expressed genes (p-value < 0.05) was calculated using Fisher's exact test.

Treatment	Regulation	DEGs	DEGs with RE	Proportion DEGs with RE	non-DEGs	non-DEGs with RE	Proportion non-DEGs with RE	p-value
atRA on <i>A. fumigatus</i> inf.+atRA	UP	12	3	0.250	93	15	0.161	0.4598
	DOWN	59	10	0.169				1
	ALL	71	13	0.183				0.8376
atRA on <i>C. albicans</i> inf.+atRA	UP	15	4	0.267	141	17	0.121	0.2497
	DOWN	27	2	0.074				0.7427
	ALL	42	6	0.143				0.7941
atRA on <i>E. coli</i> inf.+atRA	UP	20	8	0.400	148	18	0.122	0.03024
	DOWN	33	9	0.273				0.07634
	ALL	53	17	0.321				0.01483
vitD on <i>A. fumigatus</i> inf.+vitD	UP	11	0	0.000	176	9	0.051	1
	DOWN	5	0	0.000				1
	ALL	16	0	0.000				1
vitD on <i>C. albicans</i> inf.+vitD	UP	12	0	0.000	181	6	0.033	1
	DOWN	10	0	0.000				1
	ALL	22	0	0.000				1
vitD on <i>E. coli</i> inf.+vitD	UP	5	0	0.000	140	6	0.043	1
	DOWN	14	0	0.000				1
	ALL	19	0	0.000				1
atRA on <i>A. fumigatus</i> inf.+atRA+vitD	UP	23	6	0.261	190	24	0.126	0.1432
	DOWN	28	2	0.071				0.7509
	ALL	51	8	0.157				0.6487
atRA on <i>C. albicans</i> inf.+atRA+vitD	UP	31	10	0.323	200	34	0.170	0.1626
	DOWN	36	9	0.250				0.3688
	ALL	67	19	0.284				0.1267
atRA on <i>E. coli</i> inf.+atRA+vitD	UP	15	4	0.267	153	23	0.150	0.3083
	DOWN	59	10	0.169				0.8356
	ALL	74	14	0.189				0.5743
vitD on <i>A. fumigatus</i> inf.+atRA+vitD	UP	23	1	0.043	190	9	0.047	1
	DOWN	28	1	0.036				1
	ALL	51	2	0.039				1
vitD on <i>C. albicans</i> inf.+atRA+vitD	UP	31	0	0.000	200	6	0.030	1
	DOWN	36	0	0.000				0.5956
	ALL	67	0	0.000				0.3413
vitD on <i>E. coli</i> inf.+atRA+vitD	UP	15	0	0.000	153	6	0.039	1
	DOWN	59	3	0.051				0.7131
	ALL	74	3	0.041				1
atRA on any inf.+atRA	UP	51	12	0.235	304	41	0.135	0.1512
	DOWN	98	18	0.184				0.3357
	ALL	149	30	0.201				0.1389
vitD on any inf.+vitD	UP	28	0	0.000	365	14	0.038	0.6118
	DOWN	38	1	0.026				1
	ALL	66	1	0.015				0.7102
atRA on any inf.+atRA+vitD	UP	68	15	0.221	390	60	0.154	0.3013
	DOWN	106	18	0.170				0.7674
	ALL	174	33	0.190				0.3996
vitD on any inf.+atRA+vitD	UP	68	1	0.015	390	14	0.036	0.7081
	DOWN	106	4	0.038				1
	ALL	174	5	0.029				0.8036