

Supplementary Table 3

## Molecular function

Transect	GO Term Accession	GO Term Name	P-value	P-value (BC)	№ Genes Obs	№ Genes Exp	Significance
BV	GO:0005125	cytokine activity	2.62E-006	3.07E-004	58	33.57	**
	GO:0004252	serine-type endopeptidase activity	1.86E-003	2.18E-001	57	40.54	*
	GO:0003700	sequence-specific DNA binding transcription factor activity	1.93E-003	2.26E-001	208	174.62	*
CZ	GO:0030414	peptidase inhibitor activity	4.56E-007	5.34E-005	44	22.72	**
	GO:0020037	heme binding	6.18E-007	7.23E-005	69	41.05	**
	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	7.27E-007	8.50E-005	36	17.59	**
	GO:0016779	nucleotidyltransferase activity	2.37E-006	2.78E-004	35	17.59	**
	GO:0003677	DNA binding	5.28E-006	6.18E-004	413	343.55	**
	GO:0004867	serine-type endopeptidase inhibitor activity	5.69E-006	6.66E-004	47	26.63	**
	GO:0008009	chemokine activity	1.76E-005	2.06E-003	26	12.71	**
	GO:0005179	hormone activity	4.55E-005	5.32E-003	43	25.41	**
	GO:0004497	monooxygenase activity	2.17E-004	2.54E-002	32	18.57	**
	GO:0046872	metal ion binding	4.80E-004	5.62E-002	677	610.14	**
GO:0009055	electron carrier activity	1.65E-003	1.93E-001	58	41.54	**	
GO:0008201	heparin binding	1.84E-003	2.15E-001	36	23.70	**	
Without X	GO:0008009	chemokine activity	2.32E-007	2.70E-005	14	3.12	**
	GO:0046872	metal ion binding	3.48E-007	4.04E-005	207	149.60	**
	GO:0030414	peptidase inhibitor activity	8.75E-006	1.02E-003	17	5.57	**
	GO:0008201	heparin binding	1.61E-005	1.86E-003	17	5.81	**
	GO:0003676	nucleic acid binding	3.35E-005	3.89E-003	104	71.00	**
	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	8.10E-005	9.39E-003	13	4.31	**
	GO:0004497	monooxygenase activity	1.49E-004	1.73E-002	13	4.55	**
	GO:0008270	zinc ion binding	2.75E-004	3.19E-002	148	113.17	**
	GO:0005507	copper ion binding	6.55E-004	7.60E-002	9	3.00	**
	GO:0004867	serine-type endopeptidase inhibitor activity	7.67E-004	8.89E-002	15	6.53	**

Supplementary Table 3

	GO:0003700	sequence-specific DNA binding transcription factor activity	2.22E-003	2.58E-001	69	49.55	**
	GO:0020037	heme binding	5.78E-003	6.70E-001	18	10.07	*
	GO:0043565	sequence-specific DNA binding	8.10E-003	9.40E-001	49	35.23	*
	GO:0009055	electron carrier activity	1.36E-002	1.00E+000	17	10.18	*
Including X	GO:0046872	metal ion binding	1.31E-005	1.50E-003	221	169.87	**
	GO:0030414	peptidase inhibitor activity	5.01E-005	5.72E-003	17	6.35	**
	GO:0003676	nucleic acid binding	7.80E-005	8.89E-003	113	80.09	**
	GO:0008201	heparin binding	8.91E-005	1.02E-002	17	6.62	**
	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	3.18E-004	3.62E-002	13	4.92	**
	GO:0004497	monooxygenase activity	5.66E-004	6.45E-002	13	5.19	**
	GO:0008270	zinc ion binding	2.57E-003	2.93E-001	158	128.43	**
	GO:0004867	serine-type endopeptidase inhibitor activity	2.94E-003	3.36E-001	15	7.44	**
	GO:0003700	sequence-specific DNA binding transcription factor activity	3.33E-003	3.80E-001	76	56.40	**

**Biological process**

Transect	GO Term Accession	GO Term Name	P-value	P-value (BC)	№ Genes Obs	№ Genes Exp	Significance
BV	GO:0006952	defense response	4.44E-012	9.73E-010	58	18.16	**
	GO:0042742	defense response to bacterium	1.04E-008	2.29E-006	44	20.06	**
	GO:0009615	response to virus	1.60E-005	3.51E-003	40	21.96	**
	GO:0006355	regulation of transcription, DNA-dependent	1.51E-004	3.31E-002	454	392.74	**
	GO:0009952	anterior/posterior pattern formation	9.26E-004	2.03E-001	34	21.12	**
CZ	GO:0006334	nucleosome assembly	0.00E+000	0.00E+000	77	30.30	**
	GO:0006396	RNA processing	5.32E-004	1.17E-001	24	13.44	**
	GO:0007417	central nervous system development	1.00E-003	2.19E-001	26	15.39	*
	GO:0001501	skeletal system development	1.54E-003	3.37E-001	30	18.81	*
	GO:0001666	response to hypoxia	2.87E-003	6.28E-001	63	46.67	*
	GO:0006351	transcription, DNA-dependent	3.13E-003	6.85E-001	130	105.80	*
hout X	GO:0006355	regulation of transcription, DNA-dependent	3.33E-008	7.12E-006	167	111.44	**
	GO:0006935	chemotaxis	1.50E-005	3.21E-003	15	4.73	*

Supplementary Table 3

With	GO:0006396	RNA processing	1.42E-003	3.04E-001	9	3.30	*
Including X	GO:0006355	regulation of transcription, DNA-dependent	3.66E-007	7.84E-005	180	126.38	**
	GO:0006935	chemotaxis	2.61E-006	5.59E-004	17	5.19	**
	GO:0007519	skeletal muscle tissue development	1.90E-004	4.07E-002	11	3.62	**
	GO:0006396	RNA processing	1.06E-003	2.28E-001	10	3.76	*
	GO:0006310	DNA recombination	2.92E-003	6.25E-001	10	4.23	*

P-value (BC): p-value after Bonferroni correction

Significance: \* FDR  $\leq$  0.1, \*\* FDR  $\leq$  0.05