THE LANCET
Microbe

Supplementary appendix

Supplement to: Pearson MS, Tedla BA, Mekonnen GG, et al. Immunomics-guided discovery of serum and urine antibodies for diagnosing urogenital schistosomiasis: a biomarker identification study. *Lancet Microbe* 2021; published online August 31. https://doi.org/10.1016/S2666-5247(21)00150-6.

Appendix and supplementary materials table of contents

Table 1. Serum and urine sample cohorts used in this study.

Country	Sample	Cohort size (*n*)	Egg burden						Study component[*]			
			Range	Heavy[&] (*n* [%])	Moderate[#] (*n* [%])	Light[^] (*n* [%])	Egg negative/ CAA positive (*n* [%])	Egg negative/ CAA negative (*n* [%])	A	E	ICT	SS
Mashonaland East province, Zimbabwe	serum	201	0·3-743	64 [31·8]	N/A	137 [68·2]	0 [0·0]	0 [0·0]	✓	✓		
Lambarene, Gabon	serum	56	0-1265	13 [23·2]	N/A	25 [44·6]	4 [7·1]	14 [25·0]	✓	✓	✓	✓
Mashonaland East province, Zimbabwe	urine	97	0-1008	31 [32·0]	N/A	59 [60·8]	6 [6·2]	1 [1·0]	✓	✓		
Lambarene, Gabon	urine	27	0-1265	5 [18·5]	N/A	12 [44·4]	0 [0·0]	10 [37·0]	✓			
Pemba/Unjuga islands, Zanzibar	urine	152	0-540	7 [4·6]	N/A	60 [39·5]	4 [2·6]	81 [53·3]		✓		
Northern Samar, The Philippines	serum	21	24-5616	134 [58·3]	54 [23·5]	42 [18·3]	0 [0·0]	0 [0·0]				✓
Gondar, Ethiopia	serum	230	10-650	3 [14·3]	8 [38·1]	10 [43·5]	0 [0·0]	0 [0·0]				✓
Cairns, Australia	urine	15	-	-	-	-	-	-	✓	✓		
Leiden, The Netherlands	serum	10	-	-	-	-	-	-	✓	✓	✓	✓

[*] A = array, E = ELISA, ICT = immunochromatographic test, SS = species specificity.

[&] For *S. haematobium* infection, heavy egg burden ≥50 eggs/10 ml urine; for *S. mansoni* and *S. japonicum* infection, heavy egg burden >400 eggs per gram faeces.

[#] As per WHO guidelines, *S. haematobium* infection is grouped into only heavy or light egg burden; for *S. mansoni* and *S. japonicum* infection, moderate egg burden = 101-400 eggs per gram faeces.

[^] For *S. haematobium* infection, light egg burden = 1-49 eggs/10 ml urine; for *S. mansoni* and *S. japonicum* infection, light egg burden = 1-100 eggs per gram faeces.

Table 2. Top 20 antigens with significantly higher IgG responses in the serum and urine of infected versus non-infected individuals.

Antigen (WBPS14[$] Accession)	Description[#]	*P* value	fdr[*]	Selection method for array inclusion[^]
Serum				
MS3_10186	IPSE[#]	3·2 x 10^{-22}	2·5 x 10^{-20}	bioinformatic
MS3_10385	neuroserpin[#]	3·2 x 10^{-20}	1·6 x 10^{-17}	proteomic (T, AES, EV)
MS3_02553	saposin containing protein[#]	1·1 x 10^{-17}	3·8 x 10^{-15}	proteomic (T, EV)
MS3_09207	hemoglobinase (C13 family)[#]	4·2 x 10^{-17}	1·0 x 10^{-14}	proteomic (EV)
MS3_09198	CD63 antigen[#]	2·9 x 10^{-16}	5·8 x 10^{-14}	proteomic (T, EV)
MS3_07972	ferritin, heavy polypeptide 1	7·1 x 10^{-16}	1·2 x 10^{-13}	proteomic (AES, EV)
MS3_01370	CD63 antigen	3·1 x 10^{-15}	3·8 x 10^{-13}	proteomic (T, EV)
MS3_05950	16 kDa calcium-binding protein[#]	1·0 x 10^{-13}	1·0 x 10^{-11}	proteomic (T, AES, EES)
MS3_06828	calcium-binding mitochondrial carrier protein SCaMC-1	1·3 x 10^{-12}	1·0 x 10^{-10}	proteomic (T)
MS3_01658	phospholipase D3	5·5 x 10^{-11}	4·2 x 10^{-9}	proteomic (AES, EV)
MS3_06368	5'-AMP-activated protein kinase subunit beta-1	6·9 x 10^{-11}	4·7 x 10^{-9}	bioinformatic
MS3_07892	guanine nucleotide-binding protein subunit beta	1·5 x 10^{-10}	9·5 x 10^{-9}	proteomic (T)
MS3_01466	band 7 protein	6·4 x 10^{-10}	3·5 x 10^{-8}	bioinformatic
MS3_00180	putative programmed cell death protein	8·4 x 10^{-10}	4·4 x 10^{-8}	proteomic (T, EV)
MS3_08105	peptidyl-prolyl cis-trans isomerase B	1·1 x 10^{-9}	5·7 x 10^{-8}	bioinformatic
MS3_06193	PUR-alpha-like protein[#]	1·8 x 10^{-9}	8·5 x 10^{-8}	proteomic (AES)
MS3_09175	aquaporin-3 (AQP-3)	3·4 x 10^{-9}	1·5 x 10^{-7}	proteomic (T, EV)
MS3_09779	cathepsin B-like peptidase (C01 family)	7·6 x 10^{-9}	3·0 x 10^{-7}	proteomic (EV)
MS3_09828	Rho GDP-dissociation inhibitor 2	9·3 x 10^{-9}	3·3 x 10^{-7}	bioinformatic
MS3_10252	steroid dehydrogenase, putative	1·2 x 10^{-8}	4·3 x 10^{-7}	bioinformatic
Urine				
MS3_10385	neuroserpin[#]	4·2 x 10^{-11}	4·2 x 10^{-11}	proteomic (T,A ES, EV)

MS3_06193	PUR-alpha-like protein[#]	1·8 x 10^{-7}	1·8 x 10^{-7}	proteomic (AES)
MS3_10186	IPSE/alpha[#]	1·8 x 10^{-7}	1·8 x 10^{-7}	bioinformatic
MS3_02553	saposin containing protein[#]	4·3 x 10^{-6}	4·3 x 10^{-6}	proteomic (T, EV)
MS3_01466	band 7 protein	3·5 x 10^{-8}	3·5 x 10^{-8}	bioinformatic
MS3_07702	troponin T	2·0 x 10^{-5}	2·0 x 10^{-5}	proteomic (T, AES, EV)
MS3_04688	zinc finger CDGSH domain-containing protein 1	7·7 x 10^{-5}	7·7 x 10^{-5}	proteomic (T)
MS3_00996	sh3 domain grb2-like protein B1 (endophilin B1)	8·6 x 10^{-5}	8·6 x 10^{-5}	proteomic (T, AES, EV)
MS3_09198	CD63 antigen[#]	8·6 x 10^{-5}	8·6 x 10^{-5}	proteomic (T, EV)
MS3_07481	fimbrin, putative	1·2 x 10^{-3}	1·2 x 10^{-3}	proteomic (T, AES, EV)
MS3_09207	hemoglobinase (C13 family)[#]	1·3 x 10^{-3}	1·3 x 10^{-3}	proteomic (EV)
MS3_07178	putative ferritin	2·3 x 10^{-3}	2·3 x 10^{-3}	proteomic (T, AES, EES, EV)
MS3_05950	16 kDa calcium-binding protein[#]	3·6 x 10^{-3}	3·6 x 10^{-3}	proteomic (T, AES, EES)
MS3_02428	cytochrome b-c1 complex subunit 7	3·6 x 10^{-3}	3·6 x 10^{-3}	proteomic (T)
MS3_00180	putative programmed cell death protein	3·7 x 10^{-3}	3·7 x 10^{-3}	proteomic (T, EV)
MS3_01257	BC026374 protein (S09 family)	4·1 x 10^{-3}	4·1 x 10^{-3}	bioinformatic
MS3_01857	paramyosin isoform 1	4·5 x 10^{-3}	4·5 x 10^{-3}	Proteomic (EES)
MS3_04820	putative zinc transporter	4·5 x 10^{-3}	4·5 x 10^{-3}	bioinformatic
MS3_03509	protein jagged-1b	4·9 x 10^{-3}	4·9 x 10^{-3}	bioinformatic
MS3_09779	cathepsin B-like peptidase (C01 family)[#]	5·1 x 10^{-3}	5·1 x 10^{-3}	proteomic (EV)

[$] WormBase ParaSite online database, version 14 https://parasite.wormbase.org/Schistosoma_haematobium_prjna78265/Info/Index/

[#] hits common to serum and urine.

[*] false discovery rate.

^proteins for array inclusion selected from bioinformatic analysis of second-generation *S. mansoni* array[12] or proteomic analysis of *S. haematobium* T,[17] ES,[17] EES,[17] SEA[17] or EV.[16]

T = adult tegument, AES = adult excretory/secretory products, EES = egg excretory/secretory products, SEA = soluble egg antigen, EV = adult extracellular vesicles.

Table 3. Subset of arrayed antigens inducing an antibody signature[#] able to most effectively discriminate between infected and non-infected populations using sera or urine.

Antigen (WBPS14[$] accession)	Description	Serum IgG response			Urine IgG response		
		Fold change[^]	Infected (%)*	AUC[&] (95% CI)	Fold change[^]	Infected (%)*	AUC[&] (95% CI)
MS3_10385	neuroserpin[+]	47·47	81·07	0·88 (0·83-0·92)	90·02	91·15	0·93 (0·85-1·00)
MS3_10186	IPSE	14·59	95·47	0·88 (0·83-0·92)	50·96	87·61	0·88 (0·80-0·97)
MS3_06193	PUR-alpha-like protein	8·58	53·09	0·71 (0·64-0·79)	29·67	79·65	0·83 (0·75-0·91)
MS3_01466	band 7 protein	3·71	66·26	0·69 (0·62-0·75)	12·18	52·21	0·75 (0·66-0·84)
MS3_05950	16 kDa calcium-binding protein	4·18	69·55	0·76 (0·70-0·82)	5·64	56·64	0·72 (0·62-0·82)
MS3_09198	CD63 antigen[+]	4·81	95·88	0·79 (0·73-0·85)	7·39	91·15	0·83 (0·73-0·92)
MS3_09779	cathepsin B-like peptidase (C01 family)[+]	8·85	32·92	0·84 (0·76-0·93)	2·56	26·55	0·66 (0·55-0·76)
MS3_07972	ferritin, heavy polypeptide 1[+]	13·33	55·97	0·86 (0·80-0·92)	2·36	45·13	0·65 (0·54-0·76)
MS3_09207	hemoglobinase (C13 family)[+]	5·31	30·45	0·78 (0·71-0·84)	2·97	34·51	0·68 (0·57-0·78)
MS3_01370	CD63 antigen[+]	4·53	32·51	0·78 (0·71-0·84)	2·23	38·05	0·66 (0·56-0·77)

[#] A minimum of four antigens is predicted to achieve the most effective discrimination between infected and non-infected populations using sera or urine.

[$] WormBase ParaSite online database, version 14 https://parasite.wormbase.org/Schistosoma_haematobium_prjna78265/Info/Index/

[+] Antigens were identified from proteomic analysis of *S. haematobium* EVs.[16]

[^] mean of the $\log_2$-transformed fold change of the signal intensity between the infected and non-infected population

* Percentage of infected population samples (positive by egg microscopy or CAA) that are positive by array probing.

[&] Area under the curve (AUC) value determined from receiver-operator characteristic (ROC) curve analysis of the IgG response to each antigen.

Table 4: Diagnostic accuracy of antigens using serum of individuals from *Schistosoma haematobium*-endemic populations determined by ELISA.

Antigen	AUC in cohort (95% CI)		
	Zimbabwe	Gabon	All
MS3_10385	0·79 (0·68-0·91)	0·83 (0·71-0·95)	0·80 (0·70-0·91)
MS3_10186	0·85 (0·78-0·92)	0·98 (0·94-1·00)	0·88 (0·82-0·94)
MS3_09198	0·82 (0·73-0·91)	0·86 (0·75-0·96)	0·82 (0·74-0·91)
MS3_01370	0·93 (0·88-0·98)	0·95 (0·88-1·00)	0·93 (0·89-0·97)
Sh-TSP2	0·97 (0·94-1·00)	1·00 (1·00-1·00)	0·98 (0·95-1·00)
Sh-SEA	0·97 (0·94-0·99)	1·00 (1·00-1·00)	0·97 (0·95-1·00)

Table 5: Diagnostic accuracy of antigens using urine of individuals from *Schistosoma haematobium*-endemic populations determined by ELISA.

Antigen	AUC in cohort (95% CI)		
	Zimbabwe	Zanzibar	All
MS3_10385	0·95 (0·90-0·99)	0·57 (0·46-0·69)	0·78 (0·71-0·86)
MS3_10186	0·96 (0·92-1·00)	0·66 (0·55-0·77)	0·69 (0·62-0·77)
MS3_09198	0·94 (0·90-0·98)	0·66 (0·51-0·81)	0·78 (0·67-0·88)
MS3_01370	0·89 (0·82-0·96)	0·69 (0·56-0·82)	0·81 (0·72-0·89)
Sh-TSP2	0·98 (0·96-1·00)	0·93 (0·87-0·99)	0·96 (0·93-0·99)
Sh-SEA	0·77 (0·68-0·87)	0·82 (0·68-0·95)	0·79 (0·69-0·90)

Materials and Methods

Ethical Statement

Ethical approval for collection of samples from individuals from Zimbabwe was obtained by the Medical Research Council of Zimbabwe. Urine samples from this country were collected as part of a previous study investigating the diagnostic potential of host-exposed *S. haematobium* proteomes[1] (approval MRCZ/A/1710). Sample collection from individuals from Gabon was approved by the Comite de Ethique Regional Independent de Lambarene (protocol no. 06/08). The Zanzibar Medical Research Ethics Committee in Stonetown, Zanzibar (ZAMREC; reference no. ZAMREC 0003/Sept/011), the Ethikkommission beider Basel (EKBB) in Basel, Switzerland (reference no. 236/11) and the Institutional Review Board of the University of Georgia in Athens, GA, USA (project no. 2012-10138-0) approved the collection of samples from Zanzibar as part of a recently concluded five-year study on urogenital schistosomiasis elimination[2]. Collection of *Schistosoma japonicum*-infected samples was approved by the Institutional Review Board of the Research Institute for Tropical Medicine, Department of Health Manila, the Philippines (Institutional Review Board Numbers 2012-13-0 and 2015-12) and the Human Research Ethics Committee, QIMR Berghofer Medical Research Institute, Brisbane, Australia (Ethics Approval: Project P524). Collection of *Schistosoma mansoni*-infected samples was approved by the Institutional Review Board of the University of Gondar, Ethiopia.

Study design and cohorts

On collection, all serum and urine samples were stratified based on egg burden as determined by microscopy analysis of urine samples (high, ≥50 eggs per 10 ml urine; or light, 1-49 eggs per 10 ml urine). Egg-negative samples were further tested for the presence of CAA using the up-converting phosphor lateral flow CAA assay[3] and were classified as being egg negative/CAA positive or egg negative/CAA negative. Serum and urine samples from individuals from non-endemic areas were used as non-endemic negative controls. Protein arrays were probed with serum and urine samples from individuals from the *S. haematobium*-endemic regions of Mashonaland East province, Zimbabwe and Lambarene, Gabon. Validation of array results was conducted by ELISA using the same cohorts of serum samples from Zimbabwe and Gabon and the same cohort of urine samples from Zimbabwe only (the Gabon urine cohort had been exhausted from array probing). Additional ELISA validation was performed using urine samples from individuals from Pemba and Unjuga islands, Zanzibar, sites of a recent five-year study into *S. haematobium* elimination. Immunochromatographic test evaluation was performed with serum samples from the Gabon cohort (the Zimbabwe cohort had been exhausted from ELISA validation) (table 1).

S. haematobium protein array feature selection and construction

The primary criterion for the selection of proteins to be included on the *S. haematobium* protein array was the presence of the protein in surface and secreted proteomes of the parasite as these molecules are likely to be exposed to the host upon infection, and their cognate antibodies contained within the immune repertoire of infected individuals. Accordingly, proteins present in the adult *S. haematobium* tegument, soluble excretory/secretory products (ES) and EVs, ES from the egg stage,[1,4] and *S. haematobium* orthologues of proteins present in the *S. mansoni* schistosomula tegument proteome[5] (650 proteins in total) were selected for the array. The remaining ~350 proteins (for a ~1,000 feature array) consisted of *S. haematobium* orthologues of select proteins featured on the next generation *S. mansoni* proteome array[6]. Open reading frames (minus predicted signal peptides and flanked by 20 bp sequences corresponding to the recombination sites of the pXI array expression vector[7] to facilitate cloning by homologous recombination) for all selected proteins (table s1) were codon optimised for expression in *E. coli* and commercially synthesised and cloned in pUC57 by either Twist Bioscience (sequences < 1.8 kb) or ProteinCT (sequences > 1.8 kb). Synthesised genes were PCR amplified by primers corresponding to the pXI recombination sites and cloned into pXI, in-frame with the vector's 5' HA and 3' HIS tag-encoding sequences, using *in vivo* recombination[8]. Proteins encoded by each purified plasmid were expressed *in vitro* (RTS 100 *E. coli* HY kit – 5 Prime, MD, USA) according to the manufacturer's instructions and printed onto eight-pad nitrocellulose-coated AVID glass slides (Grace Biolabs, OR, USA) with an Omnigrid 100 microarray printer (Genomic Solutions, Ann Arbor, MI, USA). Vector containing no insert was similarly "expressed" and printed (in multiple locations) to act as a negative control and multiple empty spots were left on each pad to serve as background controls. Purified human IgG, anti-human IgG and parasite extracts (*S. haematobium* adult- and egg-stage ES products, soluble egg antigen and adult-stage tritonX-100-soluble extract) were also printed as positive controls. Expression quality control was assessed by detection of N-terminal HA and C-terminal HIS tags as previously described[7].

Probing of *S. haematobium* protein arrays with human sera and urine

Serum IgG responses to arrayed antigens were determined by probing with human serum (1:50 in array blocking buffer/10% *E. coli* lysate) as previously described[7] with the exception that an anti-human IgG-Qdot conjugate (1:100 in array blocking buffer) was used as the secondary/detection antibody and so tertiary incubation with a separate detection reagent was not needed. Urine IgG responses were determined by probing arrays in the same way except that human urine samples were first concentrated 15-fold and buffer-exchanged into PBS before being diluted 1:5 in array blocking buffer/10% *E. coli* lysate and applied to the arrays.

S. haematobium **protein array data analysis and bioinformatics**

Datasets generated from probing arrays with serum and urine were analysed separately. After substracting slide backgrounds, the signal intensity (SI) of each spot was background corrected using the "group average" method, where the mean SI of the negative control (empty vector) spots were subtracted from the SI of each protein spot. Corrected SIs were then transformed using the variance stabilizing normalization (vsn) method[7] in GMine (http://cgenome.net/gmine) using the VSN Bioconductor package.[9] Proteins were defined as IgG reactive if the mean of the transformed SI for all infected individuals was greater than the mean plus 1.5 standard deviations (SD) of the transformed SI of all non-endemic negative individuals. Significance differences between mean antibody responses in the infected versus non-infected groups were determined by Student's t-test and p values adjusted for multiple statistical comparisons. Receiver-operating characteristic (ROC) curves and area under curve (AUC) values were generated for each significantly reactive antibody response using the ROCR R package and the proteins inducing those responses were ranked in order of significance.

Antibody signature identification

A set of antigens capable of producing an antibody signature which could most effectively discriminate between infected and non-infected individuals, using either serum or urine as the diagnostic fluid, was identified. Firstly, for each dataset, all antigens inducing an antibody response that was significantly upregulated (after correction for multiple testing) between the infected and non-infected populations were selected (serum, n = 208; urine, n = 45). From these, antigens inducing antibody responses with a frequency of positivity (reactivity) in less than 30% of the infected population (serum, n = 178; urine, n = 7) and more than 30% of the non-infected population (serum, n = 9; urine, n = 13) were also excluded. Antigens in these trimmed datasets (serum, n = 21; urine, n = 25) were sorted by greatest to least fold change in mean SI between the infected and non-infected populations and frequency of reactivity in the infected population. The top antigens in each dataset were used to build a support vector machine classifier, the performance of which was evaluated by Monte Carlo cross-validation. Iteratively, 15 samples were randomly selected as the training set and the remaining samples were used as the test set. The model was then fit to the training data, and the predictive accuracy of the model in classifying samples as infected or non-infected was assessed using the testing set. This process was repeated 4 times. The predictive performance of the model was then evaluated by averaging the ROC curves across all 4 Monte Carlo cross-validation runs.

Selection of EV-derived TSPs

TSPs present in the *S. haematobium* EV proteome were sorted by abundance (peptide spectrum counting), and the most abundant TSPs with homologues of diagnostic efficacy reported in the literature (n=3) were selected for further assessment.

Recombinant protein production in *E. coli*

Eight antigens, selected from the immune signature and EV proteomic set (MS3_10385, MS3_10186, MS3_06193, MS3_01466, MS3_05950, MS3_09198, MS3_01370 and *Sh*-TSP-2), were cloned into the *Nde*I and *Xho*I sites of the pET41a *E. coli* expression vector, such that the N-terminal GST tag was removed, to prevent the detection of non-specific immune responses upon ELISA validation of recombinant proteins. Pilot expression experiments showed *Sh*-TSP-2 to be expressed in soluble form and all other antigens to be expressed in insoluble form. Expression of MS3_06193, MS3_01466 and MS3_05950 were at levels too low to warrant further development. Large-scale protein expression was induced for 24 h in *E. coli* BL21(DE3) by addition of 1 mM Isopropyl beta-D-1-thiogalactopyranoside (IPTG) using standard methods. Cultures were harvested by centrifugation (8,000 *g* for 20 min at 4°C), re-suspended in 50 ml lysis buffer (50 mM sodium phosphate, pH 8.0, 300 mM NaCl, 40 mM imidazole) and stored at -80°C. Cell pellets were lysed by three freeze-thaw cycles at -80°C and 42°C followed by sonication on ice (10 × 5 s pulses [70% amplitude] with 30 s rest periods between each pulse) with a Qsonica Sonicator. Insoluble material was pelleted by centrifugation at 20,000 *g* for 20 min at 4°C. The supernatant was discarded (except for the *Sh*-TSP-2 lysate, where the supernatant was kept and the insoluble material discarded) and inclusion bodies (IBs) were washed twice by resuspension in 30 ml of lysis buffer followed by centrifugation at 20,000 *g* for 20 min at 4°C. IBs were then solubilized sequentially by resuspension in 25 ml lysis buffers containing either 2 M, 4 M or 8 M urea, end-over-end mixing overnight at 4°C and centrifugation at 20,000 *g* for 20 min at 4°C. Finally, supernatants containing solubilized IBs were diluted 1:4 in lysis buffer containing 8M urea and filtered through a 0.22 μm membrane (Millipore). Solubilized IBs were purified by immobilized metal affinity chromatography (IMAC) by loading onto a prepacked 1 ml His-Trap HP column (GE Healthcare) equilibrated with lysis buffer containing 8M urea at a flow rate of 1 ml/min using an AKTA-pure-25 FPLC (GE Healthcare). After washing with 20 ml lysis buffer containing 8M urea, bound Histagged proteins were eluted using the same buffer with a stepwise gradient of 50-250 mM imidazole (50 mM steps). The supernatant containing *Sh*-TSP2 was similarly purified except that buffers did not contain urea. Fractions containing recombinant proteins (as determined by SDS-PAGE) were pooled and concentrated using Amicon Ultra-15 centrifugal devices with a 3 kDa MWCO and quantified using the Pierce BCA Protein Assay kit. The final concentration of each protein was adjusted to 1 mg/ml and proteins were aliquoted and stored at -80°C.

ELISA validation of serum and urine IgG responses

The same serum samples used to probe the protein microarrays (Zimbabwe and Gabon cohorts) were used to measure IgG responses against each antigen by indirect ELISA. Microlon high-binding 96-well microtiter ELISA plates (Greiner) were incubated overnight at 4°C with protein (either MS3_10385, MS3_10186, MS3_09198, MS3_01370 or *Sh*-TSP-2 - 2 µg/ml in 0.1 M $Na_2CO_3/NaHCO_3$, pH 9.6) and, after washing with PBST, the plates were blocked for 2 hours at RT with 100 µl of PBST/5% BSA. Fifty microliters of sera (1:50 in PBST/1% BSA) were added to the wells and incubated overnight at 4°C, then the plates were washed with PBST and 100 µl of goat anti-human IgG-HRP (Sigma, 1:5000 in PBST) was added to the plates. Plates were incubated for 1 hour at RT, washed with PBST and developed with 3,3',5,5'-tetramethylbenzidine. Plates were read at a wavelength of 405 nm on a POLARstar Omega (BMG Labtech) microplate reader. Urine IgG responses to each antigen were measured in the same way (using the Zimbabwe cohort of samples used to probe the arrays as well as the Zanzibar cohort of samples) except that plates were blocked in PBST/5% skimmed milk powder and urine samples were diluted 1:10 in PBST. Urine IgG responses to multiple antigens were performed in the same way and plates were coated with 2 µg/ml of each antigen mixture. Assays were performed in triplicate and blank-corrected values were plotted using Graphpad Prism 7. Reactivity cutoffs were determined as the average plus 3SD of the values of the non-endemic negative group. ROC curves were also generated using Graphpad Prism 7 and significant differences between mean antibody responses of each infected group and the non-infected group was determined by Student's t-test, $*p \leq 0.05$, $**p \leq 0.01$, $***p \leq 0.001$, $****p \leq 0.0001$.

Analysis of species specificity

Sera from Kato-Katz- and SEA-positive cohorts of individuals from areas endemic for *S. japonicum* (Northern Samar, The Philippines; n=21)[10] or *S. mansoni* (Gondar, Ethiopia; n=230)[11] only were tested by ELISA (as described previously in this study) to determine their reactivity with MS3_01370 or *Sh*-TSP-2, the two topperforming antigens by ELISA. For each antigen tested, the Gabon cohort of serum samples from *S. haematobium* infected individuals were used as positive controls.

Pilot development of PoC-ICTs

For PoC test development, a lateral flow ICT was commercially designed (Serve Science, Bangkok, Thailand) (figure s1). The conjugate pad was coated with 10 OD of gold-conjugated mouse anti-human IgG (to capture any human IgG present in the applied serum). Either recombinant (1.0 mg/ml) MS3_01370.1 or *Sh*-TSP2 (the two antigens with greatest diagnostic capacity as determined by ELISA) were sprayed at the test line (to capture any antigen-specific human IgG/anti-human IgG gold-conjugate complex) and 1.0 mg/ml anti-mouse IgG was sprayed at the control line (to capture anti-human IgG gold-conjugate and serve as an internal validation). To test samples with the ICT, 5 µl of serum (diluted 1:10 in buffer BS-007) was applied to the sample reservoir, 3 drops (approximately 100 µl) of buffer BS-007 was applied to the sample reservoir and the test was read after 15 mins. For each strip, a band at the test and control lines was considered a positive result, a band at the control line only was considered a negative result and a test was considered invalid if there was no band at the control line. Band intensity on positive tests were scored on a four-point scale from most (+4) to least (+1) intense. A score of 0 was given for a negative result. Test results were confirmed by two independent and blinded examiners.

References

1. Sotillo J, Pearson MS, Becker L, et al. In-depth proteomic characterization of *Schistosoma haematobium*: Towards the development of new tools for elimination. *PLoS Negl Trop Dis* 2019; **13**(5): e0007362.

2. Knopp S, Person B, Ame SM, et al. Evaluation of integrated interventions layered on mass drug administration for urogenital schistosomiasis elimination: a cluster-randomised trial. *Lancet Glob Health* 2019; **7**(8): e1118-e29.

3. de Dood CJ, Hoekstra PT, Mngara J, et al. Refining diagnosis of *Schistosoma haematobium* infections: antigen and antibody detection in urine. *Front Immunol* 2018; **9**: 2635.

4. Mekonnen GG, Tedla BA, Pickering D, et al. *Schistosoma haematobium* extracellular vesicle proteins confer protection in a heterologous model of schistosomiasis. *Vaccines (Basel)* 2020; **8**(3).

5. Sotillo J, Pearson M, Becker L, Mulvenna J, Loukas A. A quantitative proteomic analysis of the tegumental proteins from *Schistosoma mansoni* schistosomula reveals novel potential therapeutic targets. *Int J Parasitol* 2015; **45**(8): 505-16.

6. de Assis RR, Ludolf F, Nakajima R, et al. A next-generation proteome array for *Schistosoma mansoni*. *Int J Parasitol* 2016; **46**(7): 411-5.

7. Gaze S, Driguez P, Pearson MS, et al. An immunomics approach to schistosome antigen discovery: antibody signatures of naturally resistant and chronically infected individuals from endemic areas. *PLoS Pathog* 2014; **10**(3): e1004033.

8. Davies DH, Liang X, Hernandez JE, et al. Profiling the humoral immune response to infection by using proteome microarrays: high-throughput vaccine and diagnostic antigen discovery. *Proc Natl Acad Sci U S A* 2005; **102**(3): 547-52.

9. Proietti C, Zakrzewski M, Watkins TS, et al. Mining, visualizing and comparing multidimensional biomolecular data using the Genomics Data Miner (GMine) Web-Server. *Sci Rep* 2016; **6**: 38178.

10. Cai P, Weerakoon KG, Mu Y, et al. A parallel comparison of antigen candidates for development of an optimized serological diagnosis of *Schistosomiasis japonica* in the Philippines. *EBioMedicine* 2017; **24**: 237-46.

11. Amare B, Moges B, Fantahun B, et al. Micronutrient levels and nutritional status of school children living in Northwest Ethiopia. *Nutr J* 2012; **11**: 108.

Table S1: antigens used in construction of the S. haematobium protein microarray

Antigen (WBPS14* Accession)	Description	Predicted SP?#	Selection method for array inclusion^
2008-Sh-TSP2	Tetraspanin 2	Yes	proteomic (T, EV)
MS3_00004	Lysosomal alpha-glucosidase	Yes	proteomic (AES, SEA, EV)
MS3_00006	Pre-mRNA-splicing factor 38B	No	bioinformatic
MS3_00047	14-3-3 epsilon	No	proteomic (T, AES, EES, SEA, EV)
MS3_00048	putative reticulon/nogo	No	proteomic (T, EV)
MS3_00054	TWiK family of potassium channels protein 18	Yes	bioinformatic
MS3_00066	putative sperm nuclear basic protein PL-I isoform PLIb	No	bioinformatic
MS3_00076	Deoxyhypusine hydroxylase	No	bioinformatic
MS3_00143	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	No	proteomic (T)
MS3_00147	eukaryotic translation initiation factor 5A	No	proteomic (T, AES, EV)
MS3_00148	Peptidase S1 S6 chymotrypsin Hap active site	Yes	bioinformatic
MS3_00151	Prenylcysteine oxidase 1	No	proteomic (T)
MS3_00178	Small nuclear ribonucleoprotein-associated protein B	No	bioinformatic
MS3_00180	putative programmed cell death protein	No	proteomic (T, EV)
MS3_00183	Calcium-binding EF-hand,domain-containing protein	No	proteomic (EES, SEA)
MS3_00187	Guanine nucleotide-binding protein G(o) subunit alpha	No	proteomic (T, EV)
MS3_00196	Protein NDRG3	No	proteomic (T, EV)
MS3_00203	Pro-neuregulin-2, membrane-bound isoform	Yes	bioinformatic
MS3_00223	Oxalate:formate antiporter	No	proteomic (EV)
MS3_00242	Signal recognition particle protein 19	No	bioinformatic
MS3_00257	Regulator of microtubule dynamics protein 1	No	proteomic (T, AES)
MS3_00277	cAMP-dependent protein kinase type II regulatory subunit	No	proteomic (T, AES, EES, SEA, EV)
MS3_00286	aldo-keto reductase family 1, member B4 (aldose reductase)	No	proteomic (T, AES, EES, SEA)
MS3_00287	40S ribosomal protein S6	Yes	bioinformatic
MS3_00294	cytochrome b5 reductase 1	No	proteomic (T)
MS3_00312	optic atrophy 1-like protein, opa1	No	proteomic (T)
MS3_00316	Ubiquitin-conjugating enzyme E2 G1	No	bioinformatic
MS3_00353	rab-related GTP-binding protein	No	bioinformatic
MS3_00361	putative alpha-actinin	No	proteomic (T, AES, EV)
MS3_00383	putative dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase	No	bioinformatic
MS3_00403	tar DNA-binding protein, putative	No	bioinformatic
MS3_00404	Density-regulated protein	No	proteomic (EV)
MS3_00405	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	No	bioinformatic
MS3_00412	putative endophilin B1	No	proteomic (T, EV)
MS3_00413	60S ribosomal protein L8	No	bioinformatic
MS3_00440	pyruvate dehydrogenase (lipoamide)	No	bioinformatic
MS3_00447	Homeobox protein abdominal-B	No	bioinformatic

MS3_00449	SJCHGC08006 protein	No	bioinformatic
MS3_00450	Mxi neural development protein	No	bioinformatic
MS3_00452	Lysosomal Pro-X carboxypeptidase	No	proteomic (AES, EV)
MS3_00494	putative 40s ribosomal protein S18	No	bioinformatic
MS3_00498	hypotheticial protein	No	bioinformatic
MS3_00499	Tissue alpha-L-fucosidase	No	proteomic (AES, SEA)
MS3_00504	ER membrane protein complex subunit 7	Yes	bioinformatic
MS3_00508	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	No	proteomic (T, SEA)
MS3_00560	AChain A, Uridine phosphorylase	No	proteomic (SEA, EV)
MS3_00569	G2/mitotic-specific cyclin-B2	No	bioinformatic
MS3_00604	Ribosomal Protein, Small subunit	No	bioinformatic
MS3_00610	Ester hydrolase C11orf54-like protein	No	proteomic (AES, EES, SEA)
MS3_00625	NADH dehydrogenase (ubiquinone) flavoprotein 1	No	bioinformatic
MS3_00663	Aspartate aminotransferase, cytoplasmic	No	proteomic (T, AES, SEA)
MS3_00665	putative camp-regulated phosphoprotein	No	bioinformatic
MS3_00668	Replication protein A 70 kDa DNA-binding subunit	No	bioinformatic
MS3_00670	SJCHGC09518 protein	No	bioinformatic
MS3_00676	Persulfide dioxygenase ETHE1, mitochondrial	No	proteomic (T, AES)
MS3_00702	ribosomal protein S16	No	bioinformatic
MS3_00703	Tricarboxylate transport protein	No	bioinformatic
MS3_00719	putative palmitoyltransferase ZDHHC12	No	bioinformatic
MS3_00756	Sodium/potassium-transporting ATPase subunit alpha	No	proteomic (T, EV)
MS3_00769	Transmembrane protein 50A	No	bioinformatic
MS3_00779	cellular nucleic acid-binding protein	No	bioinformatic
MS3_00785	T-complex protein 1 subunit gamma	No	proteomic (T, AES, EES, SEA, EV)
MS3_00787	Ectonucleoside triphosphate diphosphohydrolase 1	No	proteomic (T, AES, EV)
MS3_00800	Serine/threonine-protein kinase haspin	No	bioinformatic
MS3_00805	Alanine aminotransferase 2	No	proteomic (AES)
MS3_00808	Polyadenylate-binding protein 2	No	bioinformatic
MS3_00812	Splicing factor U2AF 35 kDa subunit	No	bioinformatic
MS3_00844	putative cystinosin	Yes	bioinformatic
MS3_00850	protein kinase	No	bioinformatic
MS3_00859	Fibrillin 2	No	bioinformatic
MS3_00862	thioredoxin peroxidase	No	proteomic (AES, EES, SEA, EV)
MS3_00876	Neuronal calcium sensor 2	No	bioinformatic
MS3_00880	Glioma pathogenesis-related protein 1 precursor	No	proteomic (T, AES)
MS3_00881		Yes	proteomic (EES)
MS3_00886	putative syntenin	No	proteomic (T, EV)
MS3_00891	GLIPR1-like protein 1	No	proteomic (T)
MS3_00900	Guanylate kinase	No	proteomic (EES)

MS3_00931	putative nascent polypeptide associated complex alpha subunit (nac alpha)	No	proteomic (EV)
MS3_00934	F-box only protein isoform 1	No	bioinformatic
MS3_00939	PI-PLC X domain-containing protein 1	No	bioinformatic
MS3_00996	sh3 domain grb2-like protein B1 (endophilin B1)	No	proteomic (T, AES, EV)
MS3_01001	vesicle-associated membrane protein 2	No	bioinformatic
MS3_01004	COX assembly mitochondrial protein 1	No	bioinformatic
MS3_01014	intraflagellar transport protein 20	No	bioinformatic
MS3_01016	Alpha-tocopherol transfer protein-like	No	proteomic (EV)
MS3_01030	Activin receptor type-2A	No	bioinformatic
MS3_01049	Alpha-tocopherol transfer protein-like	No	proteomic (EV)
MS3_01051	Synaptophysin (Major synaptic vesicle protein p38)	No	bioinformatic
MS3_01053	tropomyosin, putative	No	bioinformatic
MS3_01095	putative smirv1 protein	Yes	proteomic (T, EV)
MS3_01096	Universal stress protein	No	proteomic (T, SEA, EV)
MS3_01104	Heterogeneous nuclear ribonucleoprotein A1, A2/B1 homolog	No	proteomic (EES)
MS3_01105	Universal stress protein	No	bioinformatic
MS3_01114	hypothetical protein MS3_01114	No	bioinformatic
MS3_01124	small subunit ribosomal protein S2e	No	bioinformatic
MS3_01141	tRNA-splicing endonuclease subunit Sen2	No	proteomic (EV)
MS3_01153	putative tetraspanin-CD63 receptor	No	proteomic (EV)
MS3_01160	Stomatin-like protein 2, mitochondrial	No	proteomic (T)
MS3_01193	putative pre-mRNA-processing ATP-dependent RNA helicase prp5	No	bioinformatic
MS3_01218	putative RNA-binding protein 18	No	bioinformatic
MS3_01240	syntaxin, putative	No	proteomic (EV)
MS3_01245	activator protein 4 (ap4), putative	No	bioinformatic
MS3_01257	BC026374 protein (S09 family)	Yes	bioinformatic
MS3_01261	Phosphoenolpyruvate carboxykinase [GTP]	No	proteomic (T, AES, EES, SEA, EV)
MS3_01262	SJCHGC09353 protein	No	bioinformatic
MS3_01274	ribosomal protein L7a	No	bioinformatic
MS3_01276	putative phosphatidylcholine transfer protein	No	bioinformatic
MS3_01286	putative copii-coated vesicle membrane protein P24	Yes	bioinformatic
MS3_01289	1-pyrroline-5-carboxylate dehydrogenase	No	proteomic (T, EES)
MS3_01302	Deoxyhypusine synthase	No	proteomic (AES)
MS3_01313	SJCHGC04069 protein	No	bioinformatic
MS3_01318	putative merlin/moesin/ezrin/radixin	No	proteomic (AES, EV)
MS3_01328	DnaJ subfamily C member 28	No	bioinformatic
MS3_01333	RutC family protein	No	bioinformatic
MS3_01337	Universal stress protein	No	proteomic (T)
MS3_01339	putative ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c isoform 2a precursor	No	bioinformatic
MS3_01348	High mobility group protein DSP1	No	bioinformatic

MS3_01353	basigin related	No	bioinformatic
MS3_01364	Tropomyosin isoform 2	No	proteomic (AES, EES, SEA)
MS3_01365	putative Bax inhibitor-1	No	bioinformatic
MS3_01370	CD63 antigen	No	proteomic (T, EV)
MS3_01386	Protein diaphanous 2	No	proteomic (T)
MS3_01406	putative mitochondrial import receptor subunit tom22	No	proteomic (T)
MS3_01422	rna-binding ras-gap sh3 binding protein related	No	bioinformatic
MS3_01425	PC3-like endoprotease variant A	No	proteomic (T, AES)
MS3_01435	Ribosomal protein L11	No	bioinformatic
MS3_01445	putative transformer-2 protein	No	bioinformatic
MS3_01466	Band 7 protein	No	bioinformatic
MS3_01478	polymorphic mucin variant	No	proteomic (EES)
MS3_01483	proteasome (prosome macropain) subunit alpha type 4	No	proteomic (SEA, EV)
MS3_01504	SJCHGC00710 protein	No	proteomic (T, EV)
MS3_01516	gynecophoral canal protein	No	proteomic (AES)
MS3_01527	High mobility group protein DSP1	No	proteomic (EES)
MS3_01542	acetyl-CoA C-acetyltransferase	No	proteomic (AES)
MS3_01558	Protein YIPF6	No	bioinformatic
MS3_01585	PDZ and LIM domain protein Zasp	No	bioinformatic
MS3_01597	Deoxyribodipyrimidine photo-lyase	No	bioinformatic
MS3_01600	Histone H2A	No	bioinformatic
MS3_01611	putative malate dehydrogenase	No	bioinformatic
MS3_01627	T-complex protein 1 subunit eta	No	proteomic (EES, EV)
MS3_01636	putative lysosome-associated membrane glycoprotein	No	proteomic (EV)
MS3_01643	putative lysosome-associated membrane glycoprotein	No	bioinformatic
MS3_01650	Adenylate kinase	No	proteomic (T, AES, EES, EV)
MS3_01653	Ras-related protein Rap-1b	No	proteomic (T, EV)
MS3_01658	Phospholipase D3	No	proteomic (ES, EV)
MS3_01664	Glycosyltransferase 1 domain-containing protein isoform 4	No	bioinformatic
MS3_01668	putative zinc finger protein	No	bioinformatic
MS3_01686	Minor histocompatibility antigen H13	No	bioinformatic
MS3_01693	Proteinase inhibitor I25, cystatin,domain-containing protein	Yes	bioinformatic
MS3_01705	cathepsin F (C01 family)	No	bioinformatic
MS3_01710	Small nuclear ribonucleoprotein Sm D3	No	bioinformatic
MS3_01749	Putative aminopeptidase W07G4.4	No	proteomic (T, SEA, EV)
MS3_01761	putative histone H2A.1	No	bioinformatic
MS3_01764	putative tropomyosin	No	proteomic (AES, EES, SEA)
MS3_01771	signalase (S26 family)	No	bioinformatic
MS3_01775	putative DNA-binding protein	No	bioinformatic
MS3_01777	putative elongation factor 1-gamma	No	proteomic (SEA)

MS3_01780	Eukaryotic initiation factor 4A	No	bioinformatic
MS3_01833	putative cystoskeletal protein tektin	No	proteomic (EES)
MS3_01840	Hypothetical Schistosoma spp. protein UPF0506	No	proteomic (T, EV)
MS3_01852	Zinc finger protein ZPR1	Yes	proteomic (T)
MS3_01857	Paramyosin isoform 1	No	proteomic (EES)
MS3_01870	CCR4-NOT transcription complex subunit 7	No	bioinformatic
MS3_01871	14-3-3 epsilon 2	No	proteomic (T, EV)
MS3_01898	CD36-like class B scavenger receptor	No	proteomic (EV)
MS3_01899	Prolyl endopeptidase	No	proteomic (AES)
MS3_01902	putative 40s ribosomal protein S4	No	bioinformatic
MS3_01905	putative tetraspanin	No	proteomic (EV)
MS3_01922	putative actin	No	proteomic (T, AES, EES, SEA, EV)
MS3_01934	putative carbonic anhydrase	No	proteomic (T, EV)
MS3_01937	Hypothetical Schistosoma spp. protein UPF0506	No	bioinformatic
MS3_01938	Proliferating cell nuclear antigen	No	bioinformatic
MS3_01952	Annexin A13 (Annexin XIII)	No	proteomic (T, AES, EV)
MS3_01964	putative annexin	No	proteomic (T, AES, EV)
MS3_01972	Leptin receptor overlapping transcript-like 1	No	bioinformatic
MS3_01983	putative ATPase inhibitor isoform 2	No	proteomic (T)
MS3_01988	Voltage-dependent anion-selective channel protein 2	No	proteomic (T)
MS3_02001	putative tumor protein d52	No	proteomic (EES)
MS3_02027	20S proteasome subunit alpha 7	No	proteomic (AES, EES)
MS3_02041	Protein BUD31 homolog	No	bioinformatic
MS3_02044	Casein kinase I isoform gamma-1	No	proteomic (EV)
MS3_02048	Receptor expression-enhancing protein 5	No	proteomic (T)
MS3_02050	Ras-related protein RABA2a	No	proteomic (EV)
MS3_02085	Mitochondrial import receptor subunit TOM70	No	proteomic (T)
MS3_02086	Cytochrome c	No	proteomic (T, AES, EES, SEA)
MS3_02087	Acidic leucine-rich nuclear phosphoprotein 32-related protein (ANP32/acidic nuclear phosphoprotein-like protein)	No	proteomic (EV)
MS3_02088	Netrin receptor DCC	No	bioinformatic
MS3_02136	malate dehydrogenase	No	proteomic (T)
MS3_02141	putative 60s ribosomal protein L13a	No	bioinformatic
MS3_02155	Proteasomal ubiquitin receptor ADRM1	No	bioinformatic
MS3_02157	Protein max	No	bioinformatic
MS3_02160	Tubulin beta-2C chain	No	bioinformatic
MS3_02162	putative placenta-specificprotein 8 protein (C15 protein) (Onzin)	No	proteomic (T, AES, EV)
MS3_02172	Tumor suppressor candidate 3 (Protein N33)	Yes	bioinformatic
MS3_02176	Microsomal glutathione S-transferase 3	No	proteomic (T)
MS3_02202	ribosomal protein S10	No	bioinformatic
MS3_02234	putative tfiid subunit	No	bioinformatic

MS3_02237	ring finger protein 168	No	bioinformatic
MS3_02256	SJCHGC08335 protein	No	proteomic (AES)
MS3_02275	Putative BTB/POZ domain-containing protein	No	proteomic (EES)
MS3_02289	Corepressor interacting with RBPJ 1	No	bioinformatic
MS3_02307	putative isocitric dehydrogenase subunit alpha	No	proteomic (T, EES)
MS3_02314	tubulin alpha-1A chain	No	proteomic (T, AES, EES, SEA, EV)
MS3_02318	gamma-glutamyltransferase-like protein 3 (T03 family)	No	proteomic (T, EV)
MS3_02343	V-type proton ATPase subunit B	No	proteomic (EV)
MS3_02346	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	No	proteomic (AES, EV)
MS3_02356	DM9 domain-containing protein	No	proteomic (EV)
MS3_02359	DM9 domain-containing protein	No	proteomic (T, AES, EV)
MS3_02368	SAR1 gene homolog B	No	proteomic (T)
MS3_02375	Ras-related protein Rab-30	No	proteomic (T, EV)
MS3_02393	SUZ domain-containing protein 1	No	bioinformatic
MS3_02396	Pleckstrin homology domain-containing family B member 2	No	bioinformatic
MS3_02407	SJCHGC06436 protein	No	proteomic (EES)
MS3_02425	Enolase	No	proteomic (T, AES, EES, SEA, EV)
MS3_02428	Cytochrome b-c1 complex subunit 7	No	proteomic (T)
MS3_02442	putative polyadenylate binding protein	No	bioinformatic
MS3_02453	Microtubule-associated protein RP/EB family member 1	No	bioinformatic
MS3_02460	Sorting nexin-3	No	bioinformatic
MS3_02465	actin beta/gamma 1	No	proteomic (T, AES, EV)
MS3_02474	hypothetical protein MS3_02474	No	bioinformatic
MS3_02476	SJCHGC00797 protein	No	proteomic (T, AES, EV)
MS3_02486	SJCHGC02563 protein	No	proteomic (T, AES, EV)
MS3_02489	SJCHGC06012 protein	No	bioinformatic
MS3_02494	SJCHGC01166 protein	No	proteomic (T, AES, EV)
MS3_02499	putative serpin	No	proteomic (AES)
MS3_02504	ATPase, H+ transporting, lysosomal accessory protein 1	No	proteomic (T, EV)
MS3_02538	Alanine aminotransferase 2	No	bioinformatic
MS3_02539	prominin (prom) protein, putative	No	proteomic (T, EV)
MS3_02545	putative glucose transport protein	No	proteomic (T, AES, EV)
MS3_02553	saposin containing protein	No	proteomic (T, EV)
MS3_02593	putative cytosolic purine 5-nucleotidase	No	proteomic (EV)
MS3_02637	SJCHGC06845 protein	Yes	bioinformatic
MS3_02641	ribosomal protein S8	No	bioinformatic
MS3_02653	60S ribosomal protein L26	No	bioinformatic
MS3_02674	SJCHGC09134 protein	Yes	proteomic (AES, EV)
MS3_02681	Transmembrane protein 256-like protein	No	bioinformatic
MS3_02685	putative prohibitin	No	proteomic (T, EES)

MS3_02688	97 kDa heat shock protein	No	proteomic (T, EES, SEA, EV)
MS3_02690	synaptotagmin, putative	No	proteomic (T)
MS3_02709	Tropinone reductase 2	No	bioinformatic
MS3_02734	O-acetyl-ADP-ribose deacetylase MACROD2	No	proteomic (T, AES)
MS3_02747	putative fatty acid binding protein	No	proteomic (EES)
MS3_02752	dihydrolipoamide dehydrogenase	No	proteomic (AES, EES, SEA)
MS3_02758	Solute carrier family 2, facilitated glucose transporter member 2	No	bioinformatic
MS3_02787	Mitochondrial import receptor subunit TOM34	No	proteomic (EV)
MS3_02802	ceramide kinase	No	bioinformatic
MS3_02804	small subunit ribosomal protein S30e	No	bioinformatic
MS3_02805	Saposin-like,IPR008139 Saposin B,domain-containing protein	No	proteomic (AES, EV)
MS3_02807	proteasome subunit alpha 6 (T01 family)	No	proteomic (EES, SEA, EV)
MS3_02838	AN1-type zinc finger protein 6 (Zinc finger A20 domain-containing protein 3)	No	proteomic (T, AES, EES, SEA, EV)
MS3_02855	putative selenoprotein T	No	bioinformatic
MS3_02856	Fructose-bisphosphate aldolase isoform 3	No	proteomic (T, AES, EES, SEA, EV)
MS3_02899	SLIT and NTRK-like protein 2	No	proteomic (AES)
MS3_02928	putative serine/threonine-protein phosphatase PP2A regulatory subunit	No	proteomic (T, AES)
MS3_02944	Extracellular superoxide dismutase [Cu-Zn] precursor	Yes	bioinformatic
MS3_02951	Putative adenosylhomocysteinase 3	No	bioinformatic
MS3_02952	DnaJ subfamily B member 9 isoform 2	Yes	bioinformatic
MS3_02954	putative dtdp-glucose 4-6-dehydratase	No	bioinformatic
MS3_02991	V-type H+-transporting ATPase subunit E	No	proteomic (EV)
MS3_02999	Galectin-3-binding protein A	No	proteomic (EES)
MS3_03041	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	No	bioinformatic
MS3_03047	Tektin-4	No	proteomic (EES)
MS3_03054	chaperonin containing TCP1, subunit 5 (epsilon)	No	proteomic (SEA)
MS3_03079	nalp (nacht, leucine rich repeat and pyrin domain containing)-related	No	proteomic (EV)
MS3_03084	putative beta thymosin	No	proteomic (T, AES)
MS3_03091	putative pdz and lim domain protein	No	bioinformatic
MS3_03096	glucose-6-phosphate isomerase	No	proteomic (T, AES, EES, SEA, EV)
MS3_03101	Peptidyl-glycine alpha-amidating monooxygenase	No	bioinformatic
MS3_03119	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	No	bioinformatic
MS3_03127	Putative actin-interacting protein 1	No	proteomic (AES, SEA, EV)
MS3_03130	putative tRNA(His) guanylyltransferase	Yes	bioinformatic
MS3_03140	40S ribosomal protein S3A, putative	No	bioinformatic
MS3_03171	Ribosomal protein S15Aa	No	proteomic (EES, SEA)
MS3_03192	25 kDa integral membrane protein	No	bioinformatic
MS3_03193	tetraspanin TE736	No	bioinformatic
MS3_03206	ATP:ADP antiporter	No	proteomic (T, EES)
MS3_03226	Leucine-rich repeat-containing protein 57	No	proteomic (T)

MS3_03231	H/ACA ribonucleoprotein complex subunit 2	No	bioinformatic
MS3_03269	SJCHGC05509 protein	No	bioinformatic
MS3_03270	putative phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	No	bioinformatic
MS3_03295	putative atp synthase beta subunit	No	proteomic (T, EES)
MS3_03301	putative atp synthase beta subunit	No	proteomic (T, EES, SEA)
MS3_03304	Translocon-associated protein subunit delta	No	proteomic (T, EV)
MS3_03350	DEP domain-containing protein 5	No	bioinformatic
MS3_03372	syntaxin-binding protein 1	No	proteomic (EV)
MS3_03381	Tubulin beta chain	No	proteomic (T, AES)
MS3_03385	putative rna binding motif protein 4,lark	No	proteomic (AES)
MS3_03400	Stress protein DDR48 (DNA damage-responsive protein 48)	Yes	bioinformatic
MS3_03405	eggshell precursor protein	No	bioinformatic
MS3_03406	Pro-His-rich protein	No	bioinformatic
MS3_03417	Major egg antigen	No	proteomic (T, EV)
MS3_03419	integral membrane G protein-coupled receptor isoform 2	No	bioinformatic
MS3_03420	Major egg antigen	No	proteomic (AES)
MS3_03424	putative elongation factor ts	No	bioinformatic
MS3_03427	Major egg antigen	No	proteomic (AES)
MS3_03429	putative protease	Yes	bioinformatic
MS3_03443	ADP-ribosylation factor 4-like	No	proteomic (T)
MS3_03453	Katanin p60 ATPase-containing subunit A-like 2	No	proteomic (EV)
MS3_03461	low-density lipoprotein receptor (ldl)	Yes	bioinformatic
MS3_03509	Protein jagged-1b	Yes	bioinformatic
MS3_03511	putative sj-Ts4 protein	No	bioinformatic
MS3_03513	glutathione peroxidase, putative	No	proteomic (SEA)
MS3_03534	UTP--glucose-1-phosphate uridylyltransferase	No	proteomic (SEA)
MS3_03558	chloride intracellular channel 4	Yes	proteomic (AES, EV)
MS3_03569	Protein transport protein Sec61 subunit alpha-like 1	No	bioinformatic
MS3_03571	putative cationic amino acid transporter	No	bioinformatic
MS3_03576	Y+L amino acid transporter 2	No	bioinformatic
MS3_03577	ribosomal protein S14	No	bioinformatic
MS3_03599	ribosomal protein L27	No	bioinformatic
MS3_03603	SJCHGC06759 protein	Yes	bioinformatic
MS3_03615	putative elongation factor tu (ef-tu)	No	proteomic (T)
MS3_03618	Mitochondrial inner membrane protein OXA1L	No	bioinformatic
MS3_03625	Ubiquitin-conjugating enzyme E2 G2	No	bioinformatic
MS3_03641	ribosomal protein S8	No	bioinformatic
MS3_03655	nervana 2	No	proteomic (T, EV)
MS3_03662	sugar nucleotide epimerase related	No	bioinformatic
MS3_03695	Rab effector MyRIP	No	proteomic (T)

MS3_03726	Stromal membrane-associated protein 1	No	proteomic (EV)
MS3_03768	putative tensin	No	proteomic (T)
MS3_03775	Transketolase	No	proteomic (T, AES, EES, SEA, EV)
MS3_03776	Mitochondrial deoxynucleotide carrier	No	bioinformatic
MS3_03789	family T2 unassigned peptidase (T02 family)	Yes	bioinformatic
MS3_03800	hypotheticial protein	No	proteomic (T)
MS3_03802	Transitional endoplasmic reticulum ATPase	No	proteomic (T, AES, EES, SEA, EV)
MS3_03814	EF-hand domain-containing protein 1	No	proteomic (EES, SEA)
MS3_03817	putative cationic amino acid transporter	No	bioinformatic
MS3_03818	MIT domain-containing protein isoform 3	No	proteomic (T)
MS3_03824	ribosomal protein L10a	No	bioinformatic
MS3_03853	osteopetrosis associated transmembrane	No	bioinformatic
MS3_03856	SJCHGC05495 protein	No	bioinformatic
MS3_03863	Golgi to ER traffic protein 4-like protein	No	bioinformatic
MS3_03872	Putative complexin-1	No	proteomic (EES)
MS3_03918	Transmembrane 9 superfamily protein member 4	No	bioinformatic
MS3_03933	Severin	No	proteomic (T, AES, EV)
MS3_03937	putative gelsolin	No	proteomic (T, AES, EES, SEA, EV)
MS3_03938	ras-like protein 3	No	proteomic (T, EV)
MS3_03963	dynein light chain type 1	No	bioinformatic
MS3_03973	putative sm29	No	proteomic (T, AES, EV)
MS3_03976	14-3-3 protein, putative	No	proteomic (T, AES, EV)
MS3_03977	14-3-3 protein, putative	No	proteomic (T, AES, EES, SEA, EV)
MS3_03979	putative vesicle-associated membrane protein (vamp)	No	proteomic (AES)
MS3_03988	receptor for activated PKC, putative	No	bioinformatic
MS3_03992	putative growth hormone inducible transmembrane protein	No	bioinformatic
MS3_04011	Co-chaperone protein isoform 1	No	proteomic (EV)
MS3_04025	Vacuolar H ATPase	No	bioinformatic
MS3_04053	Neuronal acetylcholine receptor subunit alpha-2	Yes	proteomic (EV)
MS3_04063	adenylosuccinate lyase	No	proteomic (SEA)
MS3_04083	putative glypican	No	bioinformatic
MS3_04100	Palmitoyl-protein thioesterase 1	No	proteomic (AES)
MS3_04117	SJCHGC02809 protein	No	bioinformatic
MS3_04147	hypothetical protein MS3_04147	Yes	bioinformatic
MS3_04157	hypothetical protein MS3_04157	Yes	bioinformatic
MS3_04158	Clumping factor A precursor (Fibrinogen-binding protein A) (Fibrinogen receptor A), putative	No	proteomic (T, AES)
MS3_04178	ubiquinol-cytochrome c reductase cytochrome c1 subunit	No	proteomic (T)
MS3_04179	THO complex subunit 4	No	bioinformatic
MS3_04193	Phosphopantetheine-binding,domain-containing protein	No	proteomic (T)
MS3_04206	ATP synthase subunit O, mitochondrial	No	proteomic (T)

MS3_04221	26S proteasome non-ATPase regulatory subunit 10	No	bioinformatic
MS3_04225	Aspartate aminotransferase, mitochondrial	No	proteomic (T, EES, SEA)
MS3_04227	Egg protein CP3842	Yes	bioinformatic
MS3_04261	Ribosomal Protein, Small subunit	No	bioinformatic
MS3_04262	Histone H1B	Yes	bioinformatic
MS3_04266	SJCHGC06358 protein	No	proteomic (EV)
MS3_04267	Globin-3	No	proteomic (EES, SEA)
MS3_04268	hypothetical protein MS3_04268	No	proteomic (EV)
MS3_04269	Cercarial stage-specific protein isoform 2	No	bioinformatic
MS3_04275	putative tegumental protein	No	proteomic (T, EV)
MS3_04276	SJCHGC06242 protein	No	proteomic (T, AES, EV)
MS3_04279	Saposin B domain-containing protein	No	proteomic (AES)
MS3_04285	Peptidyl-prolyl cis-trans isomerase	No	proteomic (T, AES, EES, SEA, EV)
MS3_04286	Hematopoietic lineage cell-specific protein isoform 1	No	bioinformatic
MS3_04307	fatty acid binding protein	No	proteomic (T, AES, EES, SEA, EV)
MS3_04311	putative annexin	No	proteomic (AES, SEA)
MS3_04342	citrate synthase	No	proteomic (T, AES, EES, SEA)
MS3_04347	ER degradation-enhancing alpha-mannosidase-like protein 2	No	proteomic (EV)
MS3_04355	Ras-related protein Ral-A	No	proteomic (T, EV)
MS3_04364	putative small nuclear ribonucleoprotein Sm D2	No	bioinformatic
MS3_04375	Zinc finger, C2H2-type domain-containing protein	No	bioinformatic
MS3_04386	Isochorismatase domain-containing protein 2, mitochondrial	No	proteomic (T)
MS3_04437	putative DNA double-strand break repair rad50 ATPase	Yes	proteomic (AES)
MS3_04449	Adenosylhomocysteinase A	No	proteomic (AES, EES, SEA, EV)
MS3_04453	Basic-leucine zipper (BZIP) transcription factor, domain-containing protein isoform 1	No	bioinformatic
MS3_04474	hypothetical protein MS3_0018310	No	proteomic (T, AES, EV)
MS3_04493	putative mitochondrial import receptor subunit TOM40 homolog	No	proteomic (T)
MS3_04499	NADH dehydrogenase (ubiquinone) Fe-S protein 8	No	bioinformatic
MS3_04526	subfamily T1A non-peptidase homologue (T01 family)	No	proteomic (AES, EES, SEA, EV)
MS3_04540	RuvB-like protein 2	No	bioinformatic
MS3_04550	glyoxalase I	No	proteomic (T, AES, SEA)
MS3_04559	Eukaryotic translation initiation factor 5	No	bioinformatic
MS3_04564	Growth hormone-regulated TBC protein 1-A	No	proteomic (EV)
MS3_04582	6-phosphofructokinase	No	proteomic (T)
MS3_04584	6-phosphofructokinase	No	proteomic (T, AES, EV)
MS3_04595	Programmed cell death 6-interacting protein	No	proteomic (T, AES, SEA, EV)
MS3_04598	putative annexin	No	proteomic (EV)
MS3_04609	putative 26S proteasome non-ATPase regulatory subunit 11	No	bioinformatic
MS3_04617	Lysosomal protective protein	Yes	proteomic (AES, EV)
MS3_04642	Glutathione S-transferase omega-1 isoform 1	No	proteomic (EES)

MS3_04646	Omega-amidase NIT2	No	proteomic (AES, SEA)
MS3_04680	Ras-related protein Rab-14	No	proteomic (T)
MS3_04688	Zinc finger CDGSH domain-containing protein 1	No	proteomic (T)
MS3_04717	ribosomal protein related	Yes	proteomic (SEA)
MS3_04767	putative vesicular amine transporter	No	bioinformatic
MS3_04774	Cathepsin L-like proteinase precursor	No	proteomic (EV)
MS3_04778	Phosphoglycerate kinase	No	proteomic (T, AES, EES, SEA, EV)
MS3_04781	Ribosomal protein L9	No	bioinformatic
MS3_04799	Armadillo repeat-containing protein 1	No	bioinformatic
MS3_04800	hypothetical protein MS3_04800, partial	Yes	bioinformatic
MS3_04817	SJCHGC02432 protein	No	bioinformatic
MS3_04820	putative zinc transporter	Yes	bioinformatic
MS3_04827	Ubiquinone biosynthesis protein COQ7-like protein	No	bioinformatic
MS3_04873	putative prefoldin subunit 2	No	bioinformatic
MS3_04887	putative UDP-galactose-4-epimerase	No	proteomic (T, SEA, EV)
MS3_04896	S-phase kinase-associated protein 1	No	bioinformatic
MS3_04920	Mastin precursor	Yes	proteomic (EV)
MS3_04932	1,4-alpha-glucan-branching enzyme isoform 2	No	proteomic (AES, EES, EV)
MS3_04962	Interferon-related developmental regulator 1	No	bioinformatic
MS3_04981	hydroxymethylbilane synthase	No	proteomic (EV)
MS3_05000	putative sodium/potassium-transporting ATPase subunit beta-3	No	proteomic (T, EV)
MS3_05002	Rabenosyn-5	No	bioinformatic
MS3_05011	Secreted Protein Acidic and Cysteine Rich	Yes	bioinformatic
MS3_05016	Xaa-Pro dipeptidase	No	proteomic (AES)
MS3_05024	Syntaxin-binding protein 1	No	proteomic (T)
MS3_05026	putative actin-depolymerizing factor	No	proteomic (AES, SEA)
MS3_05034	Voltage-dependent anion-selective channel protein 2	No	proteomic (T, EES)
MS3_05038	Ubiquitin-fold modifier 1	No	proteomic (AES, EES)
MS3_05040	ADIPOR-like receptor	No	bioinformatic
MS3_05047	Calmodulin	No	proteomic (AES, EES, SEA)
MS3_05050	Innexin unc-7	No	bioinformatic
MS3_05077	Guanine nucleotide-binding protein subunit beta	No	proteomic (EV)
MS3_05125	hypothetical protein MS3_05125	No	proteomic (T, AES, EV)
MS3_05126	Eukaryotic translation initiation factor 1A	No	bioinformatic
MS3_05142	Ribosomal protein L24	No	bioinformatic
MS3_05150	putative sarcoplasmic calcium-binding protein (SCP)	No	proteomic (T, AES, SEA, EV)
MS3_05157	tetraspanin, putative	No	proteomic (EV)
MS3_05170	putative bcl-2 homologous antagonist/killer (bak)	No	proteomic (T)
MS3_05192	programmed cell death, putative	No	bioinformatic
MS3_05203	UPF0764 protein C16orf89 isoform 4	Yes	bioinformatic

MS3_05213	RNA-binding protein 12	No	proteomic (EES)
MS3_05216	cysteine protease inhibitor	No	proteomic (T, EES)
MS3_05219	putative tyrosine 3-monooxygenase	No	bioinformatic
MS3_05222	asparaginyl-tRNA synthetase	No	proteomic (EV)
MS3_05226	tetraspanin, putative	No	proteomic (AES, EV)
MS3_05230	small subunit ribosomal protein S17	No	bioinformatic
MS3_05252	DM9 domain-containing protein	No	proteomic (T, AES)
MS3_05280	Histone H3.3	No	bioinformatic
MS3_05283	Adenylosuccinate synthetase	No	proteomic (AES, SEA)
MS3_05284	Ubiquitin-conjugating enzyme E2 R2	No	bioinformatic
MS3_05289	putative tetraspanin 18, isoform 1	No	proteomic (EV)
MS3_05322	family S9 non-peptidase homologue (S09 family)	No	proteomic (T)
MS3_05326	Acetylcholinesterase	No	bioinformatic
MS3_05332	putative beta-galactosidase	Yes	proteomic (AES)
MS3_05337	Allatostatin-A receptor	Yes	bioinformatic
MS3_05350	Formin-binding protein 1	No	proteomic (EV)
MS3_05351	Dynein light chain	No	proteomic (T, AES, EV)
MS3_05352	putative dynein light chain	No	proteomic (EV)
MS3_05360	Coiled-coil domain-containing protein 25	No	bioinformatic
MS3_05370	SJCHGC02540 protein	Yes	bioinformatic
MS3_05387	putative arf gtpase-activating protein	No	bioinformatic
MS3_05389	putative p30 dbc protein	No	bioinformatic
MS3_05391	putative 40s ribosomal protein S9	No	bioinformatic
MS3_05425	14 kDa subunit splicing factor 3b	No	bioinformatic
MS3_05427	Charged multivesicular body protein	No	bioinformatic
MS3_05437	Serine/threonine-protein phosphatase	No	proteomic (T)
MS3_05447	Synaptosomal-associated protein 25	No	proteomic (EV)
MS3_05465	Isocitrate dehydrogenase [NADP], mitochondrial	No	bioinformatic
MS3_05484	fragile X related 1, frx1	No	bioinformatic
MS3_05495	Lysophospholipid acyltransferase 5	No	proteomic (T)
MS3_05496	Solute carrier family 43 member 3	No	bioinformatic
MS3_05516	AChain A, Purine-nucleoside Phosphorylase	No	proteomic (EES, SEA)
MS3_05520	putative methylthioadenosine phosphorylase	No	proteomic (AES)
MS3_05530	Rab GDP dissociation inhibitor alpha	No	proteomic (T, AES, EES, SEA, EV)
MS3_05539	folylpolyglutamate synthase	No	bioinformatic
MS3_05555	venom allergen-like (VAL) 7 protein	No	bioinformatic
MS3_05586	plasma membrane calcium-transporting atpase,putative	No	proteomic (T)
MS3_05587	Plasma membrane calcium-transporting ATPase 2	No	bioinformatic
MS3_05595	porphobilinogen synthase	No	proteomic (AES, SEA)
MS3_05600	Four and a half LIM domains protein 2	No	bioinformatic

MS3_05602	putative prothymosin alpha-B	No	bioinformatic
MS3_05614	Neuronal calcium sensor 2	No	bioinformatic
MS3_05631	Taurocyamine kinase	No	proteomic (T, AES, EES, SEA, EV)
MS3_05639	putative ribosomal protein L13	No	bioinformatic
MS3_05646	hypotheticial protein	Yes	bioinformatic
MS3_05676	Cytosolic Fe-S cluster assembly factor NARFL	Yes	bioinformatic
MS3_05677	Activator of 90 kDa heat shock protein ATPase homolog 1	No	proteomic (T, EV)
MS3_05686	Eukaryotic translation initiation factor 3 subunit J-B	No	proteomic (T)
MS3_05715	hypothetical protein MS3_05715	No	proteomic (T, EV)
MS3_05718	Myosin-2 essential light chain	No	proteomic (SEA, EES)
MS3_05730	putative endoplasmin	No	bioinformatic
MS3_05734	Proteasome subunit alpha type-7-like	No	proteomic (SEA, EV)
MS3_05735	16 kDa calcium-binding protein isoform 2	No	proteomic (T, AES, EV)
MS3_05739	hypothetical protein MS3_05739	No	bioinformatic
MS3_05748	zinc finger protein, putative	No	bioinformatic
MS3_05754	Guanine nucleotide-binding protein G(q) subunit alpha	No	bioinformatic
MS3_05761	protein FAM50	No	bioinformatic
MS3_05836	putative phospholipid-transporting ATPase IIB	No	proteomic (EV)
MS3_05837	SJCHGC09124 protein	No	bioinformatic
MS3_05896	putative 60s ribosomal protein L23a	No	bioinformatic
MS3_05908	Ubiquitin-conjugating enzyme E2 L3	No	proteomic (T, AES)
MS3_05910	putative rab5	No	proteomic (T, EV)
MS3_05911	Dynein light chain 2, cytoplasmic	No	proteomic (EES, SEA, EV)
MS3_05913	putative tensin	No	proteomic (T, AES)
MS3_05939	putative Lysosomal Pro-X carboxypeptidase precursor	Yes	proteomic (AES, EV)
MS3_05945	TATA box-binding protein-associated factor RNA polymerase I subunit A	No	bioinformatic
MS3_05950	16 kDa calcium-binding protein	No	proteomic (T, AES, EES)
MS3_05952	Tegument antigen	No	proteomic (AES, EV)
MS3_05953	Rho-related GTP-binding protein isoform 1	No	proteomic (T, EV)
MS3_05958	Antigen Sm21.7	No	proteomic (T, AES, EES, SEA, EV)
MS3_05959	Tegument antigen	No	proteomic (T, AES, EV)
MS3_05960	Tegument antigen	No	proteomic (AES, EES, SEA, EV)
MS3_05976	putative rab	No	proteomic (T, EV)
MS3_05999	phosphoglycerate kinase 1	No	proteomic (T, AES, EES, SEA, EV)
MS3_06009	Proteasome subunit alpha type-2	No	proteomic (SEA, EV)
MS3_06022	putative eukaryotic translation initiation factor 2 gamma subunit (eif-2-gamma)	No	bioinformatic
MS3_06069	Store-operated calcium entry-associated regulatory factor	No	proteomic (T)
MS3_06075	F-actin-capping protein subunit beta	No	proteomic (EV)
MS3_06080	Alpha-soluble NSF attachment protein	No	proteomic (EV)
MS3_06101	apoferritin-2	Yes	proteomic (AES, EV)

MS3_06108	Fasciclin-1 isoform 2	No	bioinformatic
MS3_06112	SJCHGC07210 protein	Yes	bioinformatic
MS3_06125	serpin, putative	No	proteomic (EV)
MS3_06126	sulfide quinone reductase, putative	No	proteomic (T)
MS3_06147	putative aldehyde dehydrogenase	No	proteomic (T)
MS3_06149	DnaJ subfamily B member 4	No	proteomic (AES, EES)
MS3_06161	ATPase, H+ transporting, lysosomal, V0 subunit c	No	bioinformatic
MS3_06167	Dynein assembly factor with WDR repeat domains 1	No	bioinformatic
MS3_06193	PUR-alpha-like protein	No	proteomic (AES)
MS3_06211	SJCHGC04876 protein	No	bioinformatic
MS3_06214	hypothetical protein MS3_06214	Yes	bioinformatic
MS3_06223	Acyl-coenzyme A thioesterase 8	No	proteomic (AES, SEA)
MS3_06243	Eukaryotic translation initiation factor 6	No	bioinformatic
MS3_06248	SJCHGC06557 protein	No	proteomic (AES, EV)
MS3_06257	Exocyst complex component 5	No	bioinformatic
MS3_06258	Glutamine--tRNA ligase	No	bioinformatic
MS3_06276	20S proteasome subunit beta 4	No	proteomic (AES)
MS3_06283	Dexamethasone-induced Ras-related protein 1	No	bioinformatic
MS3_06296	Splicing factor 3B subunit 2	No	bioinformatic
MS3_06299	Transmembrane protein isoform 3	No	bioinformatic
MS3_06327	transmembrane-lke protein isoform 1	Yes	bioinformatic
MS3_06347	putative gtp-binding protein rit	No	bioinformatic
MS3_06348	Mitochondrial-processing peptidase subunit beta	No	proteomic (T, EES, SEA)
MS3_06368	5'-AMP-activated protein kinase subunit beta-1	No	bioinformatic
MS3_06380	Adenylyl cyclase-associated protein 1	No	proteomic (T, SEA, EV)
MS3_06400	Epididymal secretory protein E1 precursor (Niemann Pick type C2 protein homolog)	Yes	bioinformatic
MS3_06403	Golgi SNAP receptor complex member 1	No	bioinformatic
MS3_06424	Translocator protein	No	bioinformatic
MS3_06430	putative mitochondrial ATP synthase B chain	No	proteomic (T)
MS3_06431	putative tropomodulin	No	bioinformatic
MS3_06449	putative mitochondrial 39S ribosomal protein L27 (L27mt) (MRP-L27)	No	bioinformatic
MS3_06462	Universal stress protein	No	proteomic (T)
MS3_06468	putative membrane protein isoform 1	No	bioinformatic
MS3_06471	Translationally-controlled tumor protein homolog	No	proteomic (AES, EV)
MS3_06482	AChain A, Glutathione S-transferase 28 Kda	No	proteomic (T, AES, EES, SEA, EV)
MS3_06488	RecQ-mediated genome instability protein 1	No	bioinformatic
MS3_06500	isocitrate dehydrogenase (NAD+)	No	bioinformatic
MS3_06507	putative 6-phosphogluconate dehydrogenase	No	proteomic (AES, SEA, EV)
MS3_06532	Hormone receptor 4 (dHR4), putative	Yes	bioinformatic
MS3_06538	SJCHGC05602 protein	Yes	bioinformatic

MS3_06539	G1/S-specific cyclin-D2	No	bioinformatic
MS3_06551	EH domain-containing protein 1	No	proteomic (EV)
MS3_06559	Kynurenine--oxoglutarate transaminase 3	No	proteomic (T, AES)
MS3_06583	ng-dimethylarginine dimethylaminohydrolase	No	proteomic (T, AES, EES, EV)
MS3_06592	hydroxyacylglutathione hydrolase	No	proteomic (T, AES, SEA)
MS3_06608	nardilysin (M16 family)	No	proteomic (T)
MS3_06649	putative dna repair protein xp-E	No	proteomic (AES)
MS3_06668	ribosomal protein L35	No	bioinformatic
MS3_06669	T-complex protein 1 subunit zeta	No	proteomic (EV)
MS3_06677	Dehydrogenase/reductase SDR family member 1	No	bioinformatic
MS3_06680	putative mannose-6-phosphate isomerase	No	proteomic (AES)
MS3_06690	putative rassf	No	bioinformatic
MS3_06704	Alpha-1, 3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform 2	No	bioinformatic
MS3_06707	lipase maturation factor	No	proteomic (T)
MS3_06719	putative phosphoglucomutase	No	proteomic (SEA)
MS3_06729	putative dual-specificity phosphatase	No	bioinformatic
MS3_06732	Ubiquitin-60S ribosomal protein L40	No	proteomic (EES)
MS3_06736	family C2 unassigned peptidase (C02 family)	No	proteomic (AES)
MS3_06740	Stromal cell-derived factor 2	Yes	bioinformatic
MS3_06745	eukaryotic translation elongation factor 1 beta 2	No	proteomic (AES)
MS3_06746	ADP-ribose pyrophosphatase, mitochondrial precursor	No	proteomic (AES, EES, SEA)
MS3_06748	Tubulin beta-2C chain	No	proteomic (T, AES, EES, EV)
MS3_06769	60S ribosome subunit biogenesis protein NIP7	No	bioinformatic
MS3_06789	ATP synthase, subunit d	Yes	bioinformatic
MS3_06798	Retinol dehydrogenase 14	No	proteomic (T, AES, EV)
MS3_06807	SJCHGC01113 protein	No	bioinformatic
MS3_06825	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	No	proteomic (T)
MS3_06828	Calcium-binding mitochondrial carrier protein SCaMC-1	No	proteomic (T)
MS3_06832	3'(2'), 5'-bisphosphate nucleotidase	No	proteomic (T, AES, SEA, EV)
MS3_06834	putative succinate dehydrogenase	No	bioinformatic
MS3_06868	La-related protein 6	No	bioinformatic
MS3_06877	Long-chain-fatty-acid--CoA ligase 5	No	bioinformatic
MS3_06889	NADH dehydrogenase (ubiquinone) Fe-S protein 7	No	bioinformatic
MS3_06898	Protein MEMO1	No	proteomic (AES)
MS3_06914	proteasome (prosome macropain) subunit beta type 4	No	proteomic (AES, SEA)
MS3_06918	Protein DJ-1	No	proteomic (T, AES, EES, SEA, EV)
MS3_06928	T-complex protein 1 subunit delta	No	proteomic (AES, SEA, EV)
MS3_06944	putative profilin splice variant 4	No	proteomic (T, EV)
MS3_06947	X-box-binding protein	No	bioinformatic
MS3_06950	Three prime repair exonuclease 1	No	bioinformatic

MS3_06979	putative growth factor receptor-bound protein	No	bioinformatic
MS3_06994	ribosomal protein L28	No	bioinformatic
MS3_07002	SJCHGC06187 protein	No	bioinformatic
MS3_07010	1-acyl-sn-glycerol-3-phosphate o-acyltransferase	No	bioinformatic
MS3_07037	Zinc finger with UFM1-specific peptidase domain protein	No	bioinformatic
MS3_07045	Dehydrogenase/reductase SDR family member 1	No	proteomic (T)
MS3_07061	Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase	No	bioinformatic
MS3_07096	SJCHGC06267 protein	No	bioinformatic
MS3_07105	Mitogen-activated protein kinase 3	No	proteomic (EV)
MS3_07125	cytochrome c oxidase subunit IV	No	proteomic (T)
MS3_07126	Exosome complex component RRP41	No	bioinformatic
MS3_07156	acyl-CoA:glycerol-3-phosphate acyltransferase	No	bioinformatic
MS3_07158	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	No	proteomic (SEA)
MS3_07178	putative ferritin	No	proteomic (T, AES, EES, EV)
MS3_07195	Ribosomal protein S11	No	bioinformatic
MS3_07213	SJCHGC01055 protein	No	bioinformatic
MS3_07231	ornithine--oxo-acid transaminase	No	proteomic (EES, SEA)
MS3_07273	Lamin-B receptor	No	bioinformatic
MS3_07280	protein kiaa0174, putative	No	bioinformatic
MS3_07294	venom allergen-like (VAL) 28 protein	Yes	proteomic (EES, SEA)
MS3_07299	Protein canopy 4	Yes	bioinformatic
MS3_07304	Protein jagunal 1	No	bioinformatic
MS3_07337	putative dolichyl-diphosphooligosaccharide-protein glycosyltransferase	Yes	bioinformatic
MS3_07345	Inorganic pyrophosphatase	No	proteomic (T, AES, EES, SEA, EV)
MS3_07347	SJCHGC01026 protein	No	proteomic (EV)
MS3_07363	Heterogeneous nuclear ribonucleoprotein K	No	proteomic (AES, EES)
MS3_07370	actin beta/gamma 1	No	proteomic (AES)
MS3_07372	Phosphatase 2A inhibitor I2PP2A	No	proteomic (AES, EES, EV)
MS3_07374	Actin alpha cardiac muscle 1	No	proteomic (EV)
MS3_07390	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	No	bioinformatic
MS3_07395	Vesicular integral-membrane protein isoform 3	No	bioinformatic
MS3_07403	Glutamine synthetase	No	proteomic (SEA)
MS3_07405	putative immunoglobulin domain superfamily (sensory guidance protein)	No	proteomic (AES)
MS3_07406	putative deferrochelatase/peroxidase YfeX	No	bioinformatic
MS3_07411	putative deferrochelatase/peroxidase YfeX	No	proteomic (T)
MS3_07419	putative spfh domain protein 1 precursor	No	bioinformatic
MS3_07420	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	Yes	bioinformatic
MS3_07422	hypothetical protein MS3_07422	No	proteomic (EV)
MS3_07464	F-type H+-transporting ATPase subunit alpha	No	proteomic (T, EES, SEA)
MS3_07465	Prostatic acid phosphatase	No	proteomic (AES, EV)

MS3_07467	putative atp synthase alpha subunit mitochondrial	No	proteomic (T, EES)
MS3_07473	putative marvel-containing potential lipid raft-associated protein	No	proteomic (T, EV)
MS3_07481	fimbrin, putative	No	proteomic (T, AES, EV)
MS3_07487	putative succinate dehydrogenase	No	proteomic (T)
MS3_07509	putative cop-coated vesicle membrane protein P24 (emp24/gp25l family)	Yes	bioinformatic
MS3_07520	putative 26s proteasome non-ATPase regulatory subunit	No	bioinformatic
MS3_07531	Peroxiredoxin, Prx3	No	proteomic (T, AES, SEA)
MS3_07565	SJCHGC01333 protein	No	bioinformatic
MS3_07569	tetraspanin, putative	No	bioinformatic
MS3_07587	programmed cell death protein, putative	No	bioinformatic
MS3_07590	Reticulon-4-interacting protein 1-like protein, mitochondrial	No	bioinformatic
MS3_07593	Sorcin	No	proteomic (EV)
MS3_07594	Immunoglobulin-like domain-containing protein	Yes	proteomic (T, AES, EV)
MS3_07600	rab11, putative	No	proteomic (EV)
MS3_07606	phosphoglycerate mutase	No	proteomic (T, AES, EES, SEA, EV)
MS3_07612	40S ribosomal protein	No	bioinformatic
MS3_07617	putative map kinase phosphatase	No	proteomic (EV)
MS3_07637	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 10	No	bioinformatic
MS3_07650	hypothetical protein MS3_07650	No	bioinformatic
MS3_07651	Ubiquitin-conjugating enzyme E2-24 kDa	No	bioinformatic
MS3_07685	FChain F, Histone H4	No	proteomic (AES, EES, SEA, EV)
MS3_07686	Histone H4	No	proteomic (AES, EV)
MS3_07693	putative titin	No	proteomic (T, AES)
MS3_07702	Troponin T	No	proteomic (T, AES, EV)
MS3_07716	phosphatidylinositol transfer protein	No	bioinformatic
MS3_07729	putative hsp40, subfamily A, members 1,2,4	No	proteomic (T, EV)
MS3_07737	histone H2A	No	proteomic (EES)
MS3_07738	MEG-8 family	No	bioinformatic
MS3_07757	Casein kinase II subunit alpha	No	proteomic (EV)
MS3_07763	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	No	proteomic (T)
MS3_07795	IQ domain-containing protein G	No	bioinformatic
MS3_07799	Reticulon-4 (Neurite outgrowth inhibitor)	No	bioinformatic
MS3_07816	E3 ubiquitin-protein ligase	No	bioinformatic
MS3_07822	SJCHGC04172 protein	Yes	bioinformatic
MS3_07823	egg protein CP391S-like protein	Yes	bioinformatic
MS3_07824	putative centromere protein A (cenp-A) (centromere autoantigen A)	No	bioinformatic
MS3_07831	putative shc transforming protein	No	proteomic (EV)
MS3_07854	putative rab-2,4,14	No	proteomic (T, EV)
MS3_07874	26S proteasome non-ATPase regulatory subunit 12	No	bioinformatic
MS3_07885	rab-related GTP-binding protein	No	bioinformatic

MS3_07892	Guanine nucleotide-binding protein subunit beta	No	proteomic (T)
MS3_07905	adenylate cyclase isoform 1	No	proteomic (T)
MS3_07918	hypothetical protein MS3_07918	No	bioinformatic
MS3_07944	Spliceosome RNA helicase DDX39B	No	bioinformatic
MS3_07968	cell division control protein 45	No	proteomic (EV)
MS3_07972	ferritin, heavy polypeptide 1	No	proteomic (AES, EV)
MS3_07988	putative ef hand containing protein	Yes	proteomic (AES)
MS3_07994	hypotherical protein	No	bioinformatic
MS3_08000	glycerol-3-phosphate dehydrogenase 1	No	proteomic (T, AES, SEA, EV)
MS3_08004	Calcyphosin-like protein	No	bioinformatic
MS3_08008	aminoacylase (M20 family)	No	proteomic (AES, EES, SEA)
MS3_08019	putative immunophilin	No	proteomic (AES, EES, SEA)
MS3_08024	cathepsin B	No	proteomic (T, AES)
MS3_08037	putative ribonuclease z, chloroplast	No	proteomic (AES)
MS3_08042	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	No	bioinformatic
MS3_08059	Ferritin-1 heavy chain	No	proteomic (AES, SEA, EV)
MS3_08087	putative dead box ATP-dependent RNA helicase	No	bioinformatic
MS3_08094	putative secretory carrier membrane protein	No	bioinformatic
MS3_08105	Peptidyl-prolyl cis-trans isomerase B	Yes	bioinformatic
MS3_08144	TM2 domain-containing protein 3	No	bioinformatic
MS3_08157	Trematode Eggshell Synthesis domain containing protein	Yes	bioinformatic
MS3_08158	Trematode Eggshell Synthesis domain containing protein	Yes	bioinformatic
MS3_08159	Trematode Eggshell Synthesis domain containing protein	Yes	bioinformatic
MS3_08160	Proactivator polypeptide	No	proteomic (AES, EES, EV)
MS3_08161	Female-specific protein 800	Yes	bioinformatic
MS3_08162	RNA-binding protein EWS	No	bioinformatic
MS3_08169	Casein kinase II subunit beta	No	bioinformatic
MS3_08176	Adenylate kinase isoenzyme 6 isoform 1	No	bioinformatic
MS3_08178	hypothetical protein MS3_08178	No	proteomic (AES)
MS3_08210	Survival of motor neuron-related-splicing factor 30	No	bioinformatic
MS3_08216	putative transaldolase isoform 1	No	proteomic (T, AES, SEA)
MS3_08220	eukaryotictranslation initiation factor,putative	No	proteomic (EV)
MS3_08262	Cell division control protein 42-like protein	No	proteomic (T)
MS3_08276	Basement membrane-specific heparan sulfate proteoglycan core protein	No	proteomic (AES)
MS3_08283	putative glypican	Yes	bioinformatic
MS3_08337	putative cation-transporting atpase worm	No	bioinformatic
MS3_08361	Elongation factor 2	No	proteomic (T, AES, EES, SEA, EV)
MS3_08366	putative crp1/csrp1/crip1	No	proteomic (T, AES)
MS3_08391	putative talin	No	bioinformatic
MS3_08398	NADH dehydrogenase ubiquinone 1 beta	No	bioinformatic

MS3_08399	T-complex protein 1 subunit theta	No	proteomic (EES, EV)
MS3_08413	Zinc finger and BTB domain-containing protein	No	bioinformatic
MS3_08415	Coatomer subunit epsilon	No	bioinformatic
MS3_08432	phosphatase 2C	No	bioinformatic
MS3_08440	Cathepsin K	No	proteomic (AES)
MS3_08444	Tegument antigen	No	bioinformatic
MS3_08446	Tegument antigen	No	proteomic (T, AES, EV)
MS3_08450	Putative aminopeptidase W07G4.4	No	proteomic (T, AES, EES, EV)
MS3_08455	COP9 signalosome complex subunit 7b	No	bioinformatic
MS3_08460	AChain A, Thioredoxin Peroxidase	No	proteomic (EES, SEA, EV)
MS3_08472	Calreticulin	Yes	proteomic (T, EES, SEA)
MS3_08479	eukaryotic translation elongation factor 1 alpha 2	No	proteomic (T, AES, EES, SEA, EV)
MS3_08480	High affinity cationic amino acid transporter 1	No	proteomic (T)
MS3_08498	Cathepsin C	Yes	proteomic (SEA, EV)
MS3_08503	venom allergen-like (VAL) 6 protein	No	proteomic (T, AES, EV)
MS3_08504	venom allergen-like (VAL) 6 protein	No	proteomic (T, AES)
MS3_08509	ATP-dependent RNA helicase DED1	No	bioinformatic
MS3_08530	peptidylprolyl isomerase	No	proteomic (T, AES, EES, EV)
MS3_08533	GTP-binding nuclear protein Ran	No	bioinformatic
MS3_08539	H/ACA ribonucleoprotein complex subunit 1	No	bioinformatic
MS3_08593	putative guanine nucleotide-binding protein beta 5 (G protein beta5)	No	bioinformatic
MS3_08607	putative zinc finger protein	No	proteomic (T, EV)
MS3_08613	mitogen-activated protein kinase kinase 1	No	proteomic (EV)
MS3_08618	Ribosomal protein S5a	No	bioinformatic
MS3_08625	putative annexin	No	bioinformatic
MS3_08636	calcineurin B	No	bioinformatic
MS3_08655	LIM domain-containing protein unc-97	No	bioinformatic
MS3_08663	Serine/threonine-protein kinase NIM1	No	proteomic (EV)
MS3_08689	Synaptic vesicle membrane protein VAT-1-like protein	No	proteomic (T, AES, EV)
MS3_08692	Pre-mRNA-processing factor 19	No	bioinformatic
MS3_08717	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	No	bioinformatic
MS3_08723	Annexin A7	No	proteomic (T, AES, EV)
MS3_08725	putative annexin	No	proteomic (T, AES, EV)
MS3_08726	putative ribosomal protein S2, eukaryotic and archaeal form	No	bioinformatic
MS3_08727	SJCHGC09795 protein	No	bioinformatic
MS3_08737	Kazal-type serine protease inhibitor domain-containing protein 1	Yes	bioinformatic
MS3_08776	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	No	bioinformatic
MS3_08805	Protein C20orf11 homolog	No	bioinformatic
MS3_08808	proteasome (prosome, macropain) subunit, beta type 5	No	proteomic (EES, EV)
MS3_08811	putative ribosomal protein L4	No	bioinformatic

MS3_08823	Transmembrane protein 85	No	bioinformatic
MS3_08826	Alcohol dehydrogenase class-3	No	proteomic (AES)
MS3_08839	putative 60s ribosomal protein L6	No	proteomic (AES)
MS3_08840	AP-2 complex subunit sigma	No	bioinformatic
MS3_08871	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	No	bioinformatic
MS3_08891	Mitochondrial carnitine/acylcarnitine carrier protein	No	proteomic (T)
MS3_08903	putative poly(p)/ATP NAD kinase	No	bioinformatic
MS3_08907	alkaline phosphatase	No	proteomic (T)
MS3_08925	Aldehyde dehydrogenase X, mitochondrial	No	proteomic (EES, SEA, EV)
MS3_08926	60 kDa heat shock protein, mitochondrial	No	proteomic (T, EES, SEA, EV)
MS3_08929	hypotherical protein	No	bioinformatic
MS3_08937	Pyruvate kinase PKM	No	proteomic (T, AES, EES, SEA, EV)
MS3_08943	hypothetical protein MS3_0013354	No	bioinformatic
MS3_08945	Dipeptidyl peptidase 3	No	bioinformatic
MS3_08953	Golgi phosphoprotein 3	No	bioinformatic
MS3_08954	dihydropyrimidinase (M38 family)	No	proteomic (EV)
MS3_08975	DnaJ subfamily C member 5	No	bioinformatic
MS3_08996	Cytochrome C Oxidase	No	proteomic (EES)
MS3_08999	Vesicle-associated membrane protein 8	No	proteomic (EV)
MS3_09000	chmp1 (chromatin modifying protein) (charged multivesicular body protein), putative	No	bioinformatic
MS3_09070	alkaline phosphatase	Yes	proteomic (T, EV)
MS3_09073	phosphatidylcholine-sterol acyltransferase (lecithin-cholesterol acyltransferase)/ Phospholipase A	No	bioinformatic
MS3_09076	Ectonucleoside triphosphate diphosphohydrolase 4	No	proteomic (T, EV)
MS3_09086	Glycogenin-1 isoform 2	No	proteomic (SEA, EV)
MS3_09089	putative ATP-dependent RNA helicase ddx6	No	bioinformatic
MS3_09110	putative rac gtpase	No	proteomic (T)
MS3_09119	eukaryotictranslation initiation factor,putative	No	bioinformatic
MS3_09124	Nucleotide exchange factor SIL1	No	bioinformatic
MS3_09128	L-2-hydroxyglutarate dehydrogenase, mitochondrial	No	bioinformatic
MS3_09160	putative arginine/serine-rich splicing factor	No	bioinformatic
MS3_09161	Thymidylate kinase	No	proteomic (AES)
MS3_09175	Aquaporin-3 (AQP-3)	No	proteomic (T, EV)
MS3_09188	SJCHGC04269 protein	No	bioinformatic
MS3_09190	Geranylgeranyl pyrophosphate synthase	No	proteomic (T, AES)
MS3_09198	CD63 antigen	No	proteomic (T, EV)
MS3_09207	hemoglobinase (C13 family)	Yes	proteomic (EV)
MS3_09229	NudC domain-containing protein 2	No	bioinformatic
MS3_09231	Guanine nucleotide-binding protein subunit beta	No	proteomic (EV)
MS3_09233	superoxide dismutase 1, soluble	No	proteomic (T, AES)
MS3_09240	Protein l(2)37Cc	No	proteomic (T)

MS3_09253	hypotheticial protein	Yes	proteomic (AES, EV)
MS3_09271	60S ribosomal protein L14, putative	No	bioinformatic
MS3_09273	Regulator of nonsense transcripts 3A	No	bioinformatic
MS3_09274	KH domain-containing, RNA-binding, signal transduction-associated protein 1	No	proteomic (EES)
MS3_09276	transcription elongation factor B, polypeptide 2	No	proteomic (AES)
MS3_09283	ribosomal protein L3	No	bioinformatic
MS3_09286	putative adenylate kinase 1	No	proteomic (T, EES)
MS3_09287	putative uv excision repair protein rad23	No	bioinformatic
MS3_09290	putative pyruvate dehydrogenase	No	proteomic (T, SEA)
MS3_09296	Cysteine desulfurase	No	proteomic (T)
MS3_09305	adenine phosphoribosyltransferase	No	proteomic (AES, EV)
MS3_09333	Charged multivesicular body protein 2a (Chromatin-modifying protein 2a)	No	bioinformatic
MS3_09353	Histone H1-delta	No	proteomic (EES)
MS3_09371	putative nebulin	No	proteomic (AES)
MS3_09396	Complement C1q tumor necrosis factor-related protein 3	No	bioinformatic
MS3_09406	23 kDa integral membrane protein	No	bioinformatic
MS3_09415	putative cop-coated vesicle membrane protein P24 (emp24/gp25l family)	No	bioinformatic
MS3_09426	hypothetical protein MS3_09426	No	bioinformatic
MS3_09427	Receptor-type tyrosine-protein phosphatase gamma	No	bioinformatic
MS3_09434	V-type proton ATPase subunit F	No	proteomic (EV)
MS3_09443	Synaptosomal-associated protein 25	No	bioinformatic
MS3_09457	putative succinate dehydrogenase iron-sulfur protein	Yes	proteomic (T)
MS3_09465	Methionine aminopeptidase 1D, chloroplastic/mitochondrial	No	bioinformatic
MS3_09473	histidine triad nucleotide binding protein 1	No	proteomic (AES, EES, SEA)
MS3_09489	Stress-70 protein isoform 1	No	proteomic (T, SEA)
MS3_09510	Phosphate carrier protein, mitochondrial precursor	No	proteomic (T, EES)
MS3_09521	putative clathrin coat adaptor ap3 medium chain	No	bioinformatic
MS3_09536	putative flotillin-1	No	bioinformatic
MS3_09546	synaptic glycoprotein sc2 related	No	bioinformatic
MS3_09569	subfamily C1A unassigned peptidase (C01 family)	Yes	bioinformatic
MS3_09613	hypothetical protein MS3_09613	No	proteomic (EV)
MS3_09619	putative carbonyl reductase	No	proteomic (EES)
MS3_09620	carbonyl reductase 1	No	proteomic (T, AES)
MS3_09626	serine/threonine-protein phosphatase 4 regulatory subunit 2	No	bioinformatic
MS3_09632	ATP synthase gamma subunit	No	bioinformatic
MS3_09634	Ras-related protein Rab-3C	No	proteomic (T)
MS3_09638	putative ATP-dependent RNA helicase DHX36	No	bioinformatic
MS3_09640	putative myosin-10 (Myosin heavy chain, nonmuscle IIb)	No	proteomic (EV)
MS3_09644	long-chain-fatty-acid--CoA ligase	No	proteomic (T)
MS3_09652	Type 2 phosphatidylinositol 4,5-bisphosphate 4-phosphatase	No	proteomic (EV)

MS3_09662	Vacuolar-sorting protein isoform 2	No	bioinformatic
MS3_09682	thioredoxin 1	No	proteomic (T, EES, SEA)
MS3_09683	Zinc finger DBF type isoform 2	No	bioinformatic
MS3_09684	Bone marrow proteoglycan	Yes	bioinformatic
MS3_09690	putative kunitz-type protease inhibitor	Yes	bioinformatic
MS3_09691	putative small subunit ribosomal protein S27Ae	No	bioinformatic
MS3_09692	Protein FAM98A	No	bioinformatic
MS3_09698	CD9-like protein Sm-TSP-1	No	bioinformatic
MS3_09700	Iron/zinc purple acid phosphatase-like protein	No	proteomic (AES)
MS3_09735	putative ribonuclease t2	No	proteomic (EES, SEA)
MS3_09739	High affinity copper uptake protein 1	No	proteomic (EV)
MS3_09744	Ribosome-binding protein 1 (Ribosome receptor protein) (mRRp), putative	No	bioinformatic
MS3_09778	cathepsin B-like peptidase (C01 family)	No	proteomic (AES)
MS3_09779	cathepsin B-like peptidase (C01 family)	Yes	proteomic (EV)
MS3_09780	10 kDa heat shock protein, mitochondrial	No	proteomic (T, AES, EES, SEA)
MS3_09793	putative chromobox protein	No	bioinformatic
MS3_09810	steroid dehydrogenase, putative	No	proteomic (T)
MS3_09826	Protein FAM136A	No	bioinformatic
MS3_09828	Rho GDP-dissociation inhibitor 2	No	bioinformatic
MS3_09829	THO complex subunit 3	No	bioinformatic
MS3_09846	20 kDa calcium-binding protein	No	proteomic (AES, EES, SEA, EV)
MS3_09865	Coatomer subunit delta	No	bioinformatic
MS3_09879	3-hydroxyacyl-CoA dehydrogenase type-2	No	bioinformatic
MS3_09903	Thimet oligopeptidase	No	proteomic (T, AES, EES)
MS3_09942	putative rab-18	No	bioinformatic
MS3_09952	26S proteasome regulatory subunit T4	No	bioinformatic
MS3_09958	putative Stress-induced-phosphoprotein 1	No	proteomic (T, EES, SEA, EV)
MS3_09961	eupitrilysin (M16 family)	No	proteomic (SEA)
MS3_09970	complement inhibitory receptor	No	bioinformatic
MS3_09993	bestrophin-related protein	No	bioinformatic
MS3_10002	putative alpha-galactosidase/alpha-n-acetylgalactosamini da se	No	proteomic (EES, SEA)
MS3_10017	AChain A, Thioredoxin Glutathione Reductase	No	proteomic (AES, SEA)
MS3_10022	Proteasome assembly chaperone 2	No	bioinformatic
MS3_10028	Cytochrome b561	No	bioinformatic
MS3_10036	Neutral ceramidase	No	proteomic (EV)
MS3_10044	Eukaryotic translation initiation factor 3 subunit G	No	bioinformatic
MS3_10083	SJCHGC02513 protein	No	bioinformatic
MS3_10085	thioredoxin 1	No	proteomic (T, AES, EES, SEA, EV)
MS3_10116	60S ribosomal protein L23	No	bioinformatic
MS3_10138	Glycine receptor subunit alpha-3	Yes	bioinformatic

MS3_10141	glyceraldehyde 3-phosphate dehydrogenase	No	proteomic (SEA, EV)
MS3_10148	lipopolysaccharide-induced tumor necrosis factor-alpha factor	No	bioinformatic
MS3_10161	GTP-binding protein ypt2	No	proteomic (T)
MS3_10177	Eukaryotic translation initiation factor 3 subunit F	No	bioinformatic
MS3_10184	Gamma-crystallin related domain-containing protein	Yes	proteomic (T, AES, EES, SEA)
MS3_10186	putative interleukin-4-inducing protein precursor	Yes	bioinformatic
MS3_10187	disulfide-isomerase ER-60 precursor (ERP60)	No	proteomic (T, AES, EES, SEA)
MS3_10188	protein kinase	No	bioinformatic
MS3_10193	Ras-related protein Rab-2B	No	proteomic (T, EV)
MS3_10194	Charged multivesicular body protein 5	No	proteomic (EV)
MS3_10209	Major egg antigen	No	proteomic (T, AES, EES, SEA, EV)
MS3_10221	Transmembrane emp24 domain-containing protein 4 precursor	Yes	bioinformatic
MS3_10225	transcript=A_05711 gene=A_05711	No	bioinformatic
MS3_10249	Proteasome subunit beta type-7	No	proteomic (EV)
MS3_10252	steroid dehydrogenase, putative	Yes	bioinformatic
MS3_10288	putative tpa_exp: ORF3	No	bioinformatic
MS3_10292	Zinc finger CCCH domain-containing protein 3	No	bioinformatic
MS3_10297	ribosomal protein L30	No	bioinformatic
MS3_10305	DNA mismatch repair protein Msh2	No	bioinformatic
MS3_10345	putative alpha-galactosidase/alpha-n-acetylgalactosaminidase	No	proteomic (EES, SEA)
MS3_10378	26S proteasome regulatory subunit S3, putative	No	bioinformatic
MS3_10385	Estrogen-regulated protein EP45 precursor	Yes	proteomic (T, AES, EV)
MS3_10397	60S acidic ribosomal protein P0	No	bioinformatic
MS3_10421	40S ribosomal protein S12	No	bioinformatic
MS3_10423	putative phospholipid-transporting ATPase IA	No	bioinformatic
MS3_10440	Endonuclease/exonuclease/phosphatase family domain-containing protein 1	No	bioinformatic
MS3_10459	nucleoside diphosphate kinase homolog 5-like	No	bioinformatic
MS3_10471	putative atp-dependent RNA helicase	No	bioinformatic
MS3_10472	putative n-acetyltransferase	No	bioinformatic
MS3_10475	seryl-tRNA synthetase	No	bioinformatic
MS3_10485	GPI-anchored membrane protein 1	No	bioinformatic
MS3_10486	Ras-related protein RABH1b	No	proteomic (T)
MS3_10489	Eukaryotic translation initiation factor 4H	No	bioinformatic
MS3_10492	putative ribosomal protein L31	No	bioinformatic
MS3_10493	tyrosinase precursor	No	bioinformatic
MS3_10499	hypothetical protein MS3_10499, partial	No	bioinformatic
MS3_10510	putative l-lactate dehydrogenase	No	proteomic (T, AES, SEA, EV)
MS3_10513	putative ribosomal protein L15	No	bioinformatic
MS3_10572	T-complex protein 1 subunit alpha	No	proteomic (T, EES, SEA, EV)
MS3_10588	Alkaline phosphatase	No	proteomic (EES, EV)

MS3_10590	importin alpha 3,4, putative	No	proteomic (EV)
MS3_10591	hypothetical protein MS3_10591, partial	No	proteomic (EV)
MS3_10600	Ribosomal protein S19a	No	bioinformatic
MS3_10607	hypothetical protein MS3_10607	No	bioinformatic
MS3_10619	AFG3-like protein 2	No	bioinformatic
MS3_10671	Gamma-soluble NSF attachment protein	No	proteomic (EV)
MS3_10687	Cathepsin B-like cysteine proteinase	No	bioinformatic
MS3_10713	putative heat shock protein 70 (hsp70)	Yes	proteomic (T, AES, EES, SEA, EV)
MS3_10721	von Willebrand factor A domain-containing protein	No	proteomic (AES, EV)
MS3_10729	cytochrome c oxidase subunit III	No	bioinformatic
MS3_10736	calponin-related protein	No	proteomic (T, AES)
MS3_10753	putative triosephosphate isomerase	No	proteomic (T, AES, EES, SEA, EV)
MS3_10772	Glycoside hydrolase subgroup catalytic core	No	proteomic (EV)
MS3_10785	4-hydroxybutyrate coenzyme A transferase	No	proteomic (T, SEA)
MS3_10803	putative phospholipid-transporting ATPase IIB	No	proteomic (T)
MS3_10811	Proteinase inhibitor I32, inhibitor of apoptosis,domain-containing protein	No	bioinformatic
MS3_10816	glutamate dehydrogenase, putative	No	proteomic (T, EES, SEA)
MS3_10820	cercarial elastase (S01 family)	Yes	bioinformatic
MS3_10847	Histone H2B	No	proteomic (EES, EV)
MS3_10898	putative ubx domain containing protein	No	proteomic (EES)
MS3_10900	putative adenosine kinase	No	bioinformatic
MS3_10931	serpin, putative	No	proteomic (T, AES, EV)
MS3_10935	SJCHGC06112 protein	No	bioinformatic
MS3_10943	ubiquitin-conjugating enzyme E2 F	No	bioinformatic
MS3_10956	putative neuroendocrine protein 7b2	Yes	bioinformatic
MS3_10998	nucleoside-diphosphate kinase	No	proteomic (T, AES, SEA)
MS3_11045	putative heterogeneous nuclear ribonucleoprotein k	No	bioinformatic
MS3_11059	putative heat shock protein	No	proteomic (T, AES, EES, EV)
MS3_11074	small subunit ribosomal protein S27	No	bioinformatic
MS3_11076	sugar nucleotide epimerase related	No	bioinformatic
MS3_11077	SJCHGC02796 protein	No	bioinformatic
MS3_11103	Four and a half LIM domains protein 2	No	bioinformatic
MS3_11139	Ras-related C3 botulinum toxin substrate 1	No	proteomic (T, EV)
MS3_11161	putative glutaredoxin, grx	No	bioinformatic
MS3_11226	Major vault protein	No	proteomic (AES, SEA, EV)
MS3_11239	putative plasminogen activator inhibitor 1 RNA-binding protein	No	bioinformatic
MS3_11247	Lysine--tRNA ligase	No	bioinformatic
MS3_11250	Heterogeneous nuclear ribonucleoproteins A2/B1 isoform 1	No	proteomic (EES)
MS3_11273	Aquaporin-9 (AQP-9) (Small solute channel 1)	No	proteomic (T)
MS3_11280	putative alpha-galactosidase/alpha-n-acetylgalactosamini da se	No	proteomic (AES, EV)

MS3_11293	heat shock 70kDa protein 1/2/6/8	No	proteomic (T, AES, EES, SEA, EV)
MS3_11376	Clathrin heavy chain 1 isoform 3	No	bioinformatic
MS3_11411	putative heat shock protein 70	No	proteomic (T, AES, EES, SEA, EV)
MS3_11428	Major egg antigen	No	proteomic (T)
MS3_11429	large subunit ribosomal protein L7e	No	bioinformatic
MS3_11432	Actin alpha cardiac muscle 1	No	proteomic (AES, EES)
MS3_11484	neuroblast differentiation-associated AHNAK-like	No	proteomic (AES, EES, SEA)
MS3_11509	putative 60s ribosomal protein L12	No	bioinformatic
MS3_11526	putative programmed cell death	No	proteomic (EES)
MS3_11537	SJCHGC07871 protein	No	proteomic (T, AES)
MS3_11544	glutathione S-transferase 26 kDa	No	proteomic (AES)
No hits	tetraspanin family isoform 2	No	bioinformatic
No hits	NF-YA subunit	No	bioinformatic
No hits	pre-mRNA processing protein prp39-related protein	No	bioinformatic
No hits	Uncharacterised protein	No	bioinformatic
No hits	fascin, putative	No	proteomic (AES)
No hits	putative SAM pointed domain containing ets transcription factor	No	bioinformatic
No hits	ribosomal protein L18	No	bioinformatic

*WormBase ParaSite online database, version 14 https://parasite.wormbase.org/Schistosoma_haematobium_prjna78265/Info/Index/

antigen sequences were interrogated for the predicted presence of a signal peptide (http://www.cbs.dtu.dk/services/SignalP-4.1/) and the SP (if any) was not included in gene synthesis

^proteins for array inclusion selected from bioinformatic analysis of second-generation *S. mansoni* array or proteomic analysis of *S. haematobium* T, ES, EES, SEA or EV.

T = adult tegument, AES = adult excretory/secretory products, EES = egg excretory/secretory products, SEA = soluble egg antigen, EV = adult extracellular vesicles.

Table S2. Fold change of IgG responses between infected and non-infected (S. haematobium-endemic) populations resulting from serum sample probing of *S. haematobium* protein arrays.

Antigen (WBPS14* accession)	P value	FDR	AUC	AUC Lower CI	AUC Upper CI	Mean infected	Mean non infected	Fold Change	Positive infected	Positive non infected	Positive infected (%)	Positive non infected (%)
MS3_10186	3.20E-22	2.50E-20	0.88	0.83	0.92	12.79	10.11	14.58509332	232	14	95.47325103	48.27586207
MS3_10385	3.20E-20	1.60E-17	0.88	0.83	0.92	12.08	8.22	47.46535481	197	1	81.06995885	3.448275862
MS3_02553	1.10E-17	3.80E-15	0.88	0.82	0.94	12.01	9.16	17.28778203	187	3	76.95473251	10.34482759
MS3_09207	4.20E-17	1.00E-14	0.78	0.71	0.84	8.84	7.17	5.31217083	74	0	30.4526749	0
MS3_09198	2.90E-16	5.80E-14	0.79	0.73	0.85	11.95	10.38	4.806648198	233	24	95.88477366	82.75862069
MS3_07972	7.10E-16	1.20E-13	0.86	0.8	0.92	9.98	7.39	13.32977666	136	1	55.96707819	3.448275862
MS3_01370	3.10E-15	3.80E-13	0.78	0.71	0.84	9.06	7.55	4.526731986	79	0	32.51028807	0
MS3_07231	3.10E-15	3.80E-13	0.79	0.73	0.86	8.53	9.61	0.339595514	29	7	11.93415638	24.13793103
MS3_05530	8.10E-14	9.00E-12	0.81	0.75	0.88	8.74	9.64	0.406569651	20	8	8.230452675	27.5862069
MS3_05950	1.00E-13	1.00E-11	0.76	0.7	0.82	10.96	9.53	4.178699213	169	4	69.5473251	13.79310345
MS3_04157	2.60E-13	2.40E-11	0.8	0.73	0.87	8.01	9.25	0.289384189	10	3	4.115226337	10.34482759
MS3_06828	1.30E-12	1.00E-10	0.84	0.77	0.91	8.19	6.54	5.206990291	28	0	11.52263374	0
MS3_01658	5.50E-11	4.20E-09	0.83	0.76	0.9	7.72	6.46	3.525429425	10	0	4.115226337	0
MS3_06368	6.90E-11	4.70E-09	0.86	0.78	0.93	7.91	6.44	4.349245639	13	0	5.349794239	0
MS3_08399	7.10E-11	4.70E-09	0.76	0.69	0.83	8.7	9.64	0.390627826	37	9	15.22633745	31.03448276
MS3_07892	1.50E-10	9.50E-09	0.78	0.7	0.85	7.59	6.65	2.559985051	4	0	1.646090535	0
MS3_00779	4.40E-10	0.000000026	0.78	0.71	0.85	8.67	9.46	0.453844785	18	5	7.407407407	17.24137931
MS3_01466	6.40E-10	0.000000035	0.69	0.62	0.75	10.9	9.59	3.706173728	161	8	66.25514403	27.5862069
MS3_00180	8.40E-10	0.000000044	0.77	0.69	0.85	9.33	7.96	3.935351144	74	0	30.4526749	0
MS3_08105	1.10E-09	0.000000057	0.76	0.69	0.84	8.72	9.65	0.394553701	35	8	14.40329218	27.5862069
MS3_06193	1.80E-09	0.000000085	0.71	0.64	0.79	10.72	8.57	8.584858702	129	2	53.08641975	6.896551724
MS3_09175	3.40E-09	0.00000015	0.75	0.67	0.82	7.89	7.1	2.203397617	10	0	4.115226337	0
MS3_09286	5.70E-09	0.00000025	0.71	0.63	0.8	8.9	9.75	0.427414925	51	10	20.98765432	34.48275862
MS3_08937	0.000000006	0.00000025	0.68	0.61	0.76	9.08	9.71	0.532591796	54	8	22.22222222	27.5862069
MS3_09779	7.60E-09	0.0000003	0.84	0.76	0.93	9.05	6.87	8.846315677	80	2	32.9218107	6.896551724
MS3_09903	8.50E-09	0.00000033	0.72	0.64	0.8	8.54	9.33	0.453844782	12	3	4.938271605	10.34482759
MS3_09828	0.000000009	0.00000033	0.76	0.68	0.84	8.37	7.21	3.189934848	33	0	13.58024691	0
MS3_10252	0.000000012	0.00000043	0.77	0.69	0.85	9.03	7.92	3.034358752	51	0	20.98765432	0
MS3_04774	0.000000013	0.00000044	0.75	0.67	0.83	7.88	7.03	2.339648349	6	0	2.469135802	0
MS3_03127	0.000000022	0.00000072	0.84	0.75	0.93	8.24	6.99	3.490345675	15	0	6.172839506	0
MS3_09780	0.000000026	0.00000083	0.73	0.65	0.81	9	9.77	0.463013063	46	11	18.93004115	37.93103448

MS3_08826	0.000000033	0.000001	0.74	0.66	0.81	8.09	7.24	2.339647836	10	0	4.115226337	0
MS3_08087	0.000000039	0.0000012	0.81	0.72	0.89	8.7	7.43	3.560853717	29	0	11.93415638	0
MS3_06532	0.000000049	0.0000014	0.76	0.68	0.84	10.19	9.05	3.126768404	127	4	52.26337449	13.79310345
MS3_05600	0.000000086	0.0000024	0.81	0.72	0.9	7.46	6.55	2.484326791	4	0	1.646090535	0
MS3_01478	0.00000011	0.0000028	0.69	0.61	0.76	9.02	9.54	0.594520542	37	4	15.22633745	13.79310345
MS3_02001	0.00000011	0.0000028	0.7	0.62	0.77	9.22	9.94	0.486752252	77	12	31.6872428	41.37931034
MS3_08530	0.00000011	0.0000028	0.71	0.63	0.79	8.88	9.63	0.472366546	46	7	18.93004115	24.13793103
MS3_09632	0.00000012	0.000003	0.68	0.59	0.77	7.41	6.6	2.247911323	18	0	7.407407407	0
MS3_09638	0.00000012	0.000003	0.76	0.68	0.84	7.88	7.02	2.363162244	4	0	1.646090535	0
MS3_00886	0.00000016	0.0000038	0.77	0.69	0.84	9.29	8.17	3.064854423	71	1	29.218107	3.448275862
MS3_04920	0.00000019	0.0000044	0.76	0.68	0.84	8.4	7.27	3.095657844	27	1	11.11111111	3.448275862
MS3_08925	0.00000021	0.0000048	0.68	0.6	0.76	8.98	9.62	0.527292418	45	9	18.51851852	31.03448276
MS3_03662	0.00000022	0.0000049	0.77	0.69	0.86	8.23	7.37	2.363161463	13	0	5.349794239	0
MS3_06798	0.00000022	0.0000049	0.76	0.67	0.85	7.29	6.56	2.075083802	6	0	2.469135802	0
MS3_08903	0.0000003	0.0000064	0.67	0.59	0.75	7.16	6.48	1.973881184	8	0	3.29218107	0
MS3_01095	0.00000033	0.000007	0.78	0.69	0.86	8.85	7.65	3.320117607	40	0	16.46090535	0
MS3_01422	0.00000038	0.0000078	0.69	0.59	0.78	7.65	6.56	2.974279361	32	0	13.16872428	0
MS3_07406	0.00000041	0.0000083	0.64	0.56	0.72	7.23	6.59	1.896483464	7	0	2.880658436	0
MS3_02709	0.0000005	0.0000099	0.71	0.63	0.79	7.84	7.2	1.896481642	3	0	1.234567901	0
MS3_04617	0.00000053	0.00001	0.75	0.65	0.84	7.05	6.33	2.054438189	8	0	3.29218107	0
MS3_04267	0.00000054	0.00001	0.67	0.59	0.75	8.95	9.56	0.543350863	37	5	15.22633745	17.24137931
MS3_08094	0.0000006	0.000011	0.69	0.61	0.78	7.63	6.57	2.88637598	33	0	13.58024691	0
MS3_01899	0.00000063	0.000012	0.78	0.69	0.87	8.86	7.65	3.353485345	57	1	23.45679012	3.448275862
MS3_02802	0.00000065	0.000012	0.72	0.63	0.8	6.99	6.39	1.822122387	3	0	1.234567901	0
MS3_10956	0.00000067	0.000012	0.66	0.57	0.75	9.29	9.82	0.588604966	72	11	29.62962963	37.93103448
MS3_07390	0.00000068	0.000012	0.75	0.67	0.83	7.83	6.89	2.559983666	11	0	4.526748971	0
MS3_07411	0.00000086	0.000015	0.75	0.67	0.84	7.75	6.9	2.339648794	3	0	1.234567901	0
MS3_10288	0.00000095	0.000016	0.72	0.64	0.81	8.67	9.34	0.511708567	20	6	8.230452675	20.68965517
MS3_00004	0.00000097	0.000016	0.8	0.7	0.9	8.59	7.84	2.117000271	6	0	2.469135802	0
MS3_04526	0.0000013	0.000021	0.61	0.53	0.69	9.13	9.63	0.606530655	59	6	24.27983539	20.68965517
MS3_03424	0.0000017	0.000026	0.7	0.61	0.79	9.03	8.15	2.410899873	45	0	18.51851852	0
MS3_11103	0.0000019	0.00003	0.67	0.59	0.75	8.99	9.47	0.618783386	22	3	9.053497942	10.34482759
MS3_07045	0.000002	0.00003	0.72	0.63	0.82	8.6	7.6	2.718282417	37	0	15.22633745	0
MS3_11537	0.0000021	0.000031	0.73	0.65	0.81	8.82	9.42	0.548811628	21	6	8.641975309	20.68965517
MS3_04981	0.0000021	0.000031	0.71	0.63	0.8	8.98	9.57	0.554327279	26	7	10.69958848	24.13793103
MS3_03789	0.0000026	0.000039	0.63	0.54	0.71	7.68	6.86	2.270501851	32	0	13.16872428	0
MS3_04932	0.0000028	0.000041	0.69	0.61	0.78	8.91	9.54	0.532591794	36	8	14.81481481	27.5862069

MS3_02674	0.0000035	0.000051	0.73	0.64	0.81	8.36	7.45	2.484323237	35	1	14.40329218	3.448275862
MS3_10141	0.0000036	0.000052	0.72	0.63	0.81	7.91	7.2	2.033992118	10	0	4.115226337	0
MS3_08008	0.0000039	0.000054	0.65	0.57	0.74	9.35	9.84	0.612626391	78	12	32.09876543	41.37931034
MS3_02407	0.0000046	0.000064	0.67	0.59	0.76	8.52	9.26	0.477113901	15	1	6.172839506	3.448275862
MS3_03096	0.000005	0.000068	0.67	0.58	0.75	9.17	9.79	0.537944433	66	10	27.16049383	34.48275862
MS3_07994	0.0000057	0.000077	0.69	0.61	0.77	9.12	9.73	0.543350864	60	10	24.69135802	34.48275862
MS3_06167	0.0000093	0.00012	0.74	0.65	0.82	7.66	8.77	0.329558896	16	3	6.58436214	10.34482759
MS3_10816	0.000012	0.00015	0.68	0.59	0.76	9.4	9.89	0.612626392	81	10	33.33333333	34.48275862
MS3_11432	0.000012	0.00015	0.69	0.6	0.79	8.86	9.54	0.506616985	36	9	14.81481481	31.03448276
MS3_05837	0.000013	0.00016	0.7	0.62	0.78	8.97	9.46	0.612626388	29	4	11.93415638	13.79310345
MS3_09073	0.000013	0.00016	0.69	0.6	0.77	7.42	6.84	1.786039835	1	0	0.411522634	0
MS3_06608	0.000014	0.00017	0.75	0.66	0.85	8.53	7.39	3.126769435	21	0	8.641975309	0
MS3_09970	0.000015	0.00018	0.77	0.67	0.87	8.66	7.37	3.632787888	50	2	20.57613169	6.896551724
MS3_01016	0.000016	0.00019	0.71	0.62	0.79	8.52	9.27	0.472366538	28	3	11.52263374	10.34482759
MS3_06719	0.000016	0.00019	0.78	0.67	0.89	8.59	7.62	2.637945003	15	1	6.172839506	3.448275862
MS3_01337	0.000017	0.00019	0.75	0.67	0.84	8.83	7.77	2.886371442	27	0	11.11111111	0
MS3_07612	0.000017	0.00019	0.74	0.64	0.83	8.61	9.28	0.511708565	13	4	5.349794239	13.79310345
MS3_08808	0.000018	0.0002	0.67	0.58	0.76	8.75	9.4	0.522045767	30	7	12.34567901	24.13793103
MS3_01425	0.000022	0.00025	0.78	0.67	0.88	8.19	6.89	3.669300187	24	1	9.87654321	3.448275862
MS3_09692	0.000023	0.00026	0.73	0.63	0.83	7.46	6.83	1.877612151	2	0	0.823045267	0
MS3_05718	0.000029	0.00032	0.65	0.57	0.74	8.81	9.37	0.571209055	23	3	9.465020576	10.34482759
MS3_11411	0.00003	0.00033	0.74	0.67	0.81	9.95	8.93	2.773194806	124	1	51.02880658	3.448275862
MS3_04499	0.000031	0.00033	0.69	0.61	0.77	7.94	8.67	0.481908943	10	1	4.115226337	3.448275862
MS3_05170	0.000031	0.00033	0.68	0.59	0.77	9.24	9.79	0.576949807	68	11	27.98353909	37.93103448
MS3_04193	0.000032	0.00034	0.7	0.61	0.79	8.91	9.38	0.625002261	16	4	6.58436214	13.79310345
MS3_05000	0.000034	0.00036	0.69	0.59	0.79	7.26	6.69	1.768268911	6	0	2.469135802	0
MS3_04225	0.000039	0.0004	0.61	0.53	0.69	8.81	9.32	0.60049557	29	3	11.93415638	10.34482759
MS3_05034	0.00004	0.00041	0.66	0.57	0.75	9.15	9.72	0.565525434	60	10	24.69135802	34.48275862
MS3_05213	0.000041	0.00041	0.69	0.61	0.78	8.34	9.29	0.386741005	34	4	13.99176955	13.79310345
MS3_10305	0.000041	0.00041	0.71	0.62	0.8	8.65	9.15	0.606530648	6	0	2.469135802	0
MS3_07304	0.000043	0.00042	0.73	0.64	0.82	8.57	7.9	1.954237519	10	0	4.115226337	0
MS3_02999	0.000044	0.00043	0.61	0.53	0.7	8.94	9.42	0.618783385	39	4	16.04938272	13.79310345
MS3_06732	0.000045	0.00044	0.67	0.58	0.75	8.9	9.44	0.582748245	35	6	14.40329218	20.68965517
MS3_07823	0.000046	0.00044	0.72	0.62	0.82	8.52	7.67	2.339647268	29	1	11.93415638	3.448275862
MS3_05011	0.000048	0.00045	0.65	0.55	0.74	9.01	9.55	0.582748247	41	7	16.87242798	24.13793103
MS3_08954	0.000053	0.0005	0.71	0.63	0.8	7.99	8.68	0.501576026	4	1	1.646090535	3.448275862
MS3_07685	0.000055	0.00051	0.68	0.58	0.77	8.66	9.31	0.522045765	20	6	8.230452675	20.68965517

MS3_09958	0.000057	0.00053	0.65	0.57	0.73	8.93	9.43	0.606530653	43	3	17.69547325	10.34482759
MS3_03295	0.000062	0.00057	0.66	0.57	0.75	9.39	9.95	0.571209061	98	16	40.32921811	55.17241379
MS3_09276	0.000069	0.00061	0.68	0.59	0.77	8.61	9.09	0.618783379	8	1	3.29218107	3.448275862
MS3_07757	0.000069	0.00061	0.68	0.59	0.77	7.96	7.44	1.682028025	7	0	2.880658436	0
MS3_09521	0.000069	0.00061	0.75	0.65	0.86	8.45	7.62	2.293319187	24	1	9.87654321	3.448275862
MS3_10421	0.000069	0.00061	0.69	0.6	0.77	9	9.39	0.677056869	17	2	6.995884774	6.896551724
MS3_07763	0.000071	0.00062	0.69	0.6	0.78	8.05	7.43	1.858928507	6	0	2.469135802	0
MS3_04767	0.000073	0.00063	0.69	0.61	0.78	8.79	9.2	0.663650242	8	1	3.29218107	3.448275862
MS3_06125	0.00008	0.00069	0.71	0.61	0.8	8.85	7.86	2.691234818	59	2	24.27983539	6.896551724
MS3_05677	0.000085	0.00073	0.66	0.57	0.74	8.79	9.44	0.522045768	30	4	12.34567901	13.79310345
MS3_03301	0.000089	0.00075	0.64	0.56	0.73	8.98	9.51	0.588604964	46	5	18.93004115	17.24137931
MS3_09700	0.000089	0.00075	0.66	0.58	0.75	7.99	7.42	1.768267483	12	0	4.938271605	0
MS3_07178	0.000096	0.0008	0.75	0.64	0.85	8.44	6.9	4.664594791	65	2	26.74897119	6.896551724
MS3_09826	0.000099	0.00082	0.7	0.61	0.8	8.62	9.2	0.559898354	12	4	4.938271605	13.79310345
MS3_05595	0.0001	0.00082	0.7	0.61	0.79	7.28	6.75	1.698933831	1	0	0.411522634	0
MS3_10485	0.0001	0.00083	0.67	0.58	0.76	8.54	7.71	2.293319114	31	0	12.75720165	0
MS3_08723	0.00011	0.0009	0.72	0.62	0.82	8.27	7.35	2.509291262	27	1	11.11111111	3.448275862
MS3_09253	0.00011	0.00088	0.61	0.52	0.7	6.75	6.2	1.73325778	6	0	2.469135802	0
MS3_04279	0.00012	0.00093	0.61	0.53	0.7	8.12	7.47	1.915541282	30	0	12.34567901	0
MS3_05040	0.00012	0.00096	0.73	0.63	0.84	8.96	8.05	2.484322745	46	2	18.93004115	6.896551724
MS3_06009	0.00012	0.00092	0.72	0.63	0.81	8.22	7.14	2.944681188	47	1	19.34156379	3.448275862
MS3_08498	0.00012	0.00096	0.76	0.65	0.88	8.84	7.99	2.339647071	35	4	14.40329218	13.79310345
MS3_10772	0.00012	0.00093	0.74	0.64	0.85	7.65	6.98	1.954238569	4	0	1.646090535	0
MS3_02428	0.00013	0.00098	0.69	0.6	0.77	8.6	9.11	0.600495566	12	4	4.938271605	13.79310345
MS3_05391	0.00013	0.00098	0.71	0.62	0.8	8.24	7.7	1.716007095	2	0	0.823045267	0
MS3_07465	0.00013	0.00096	0.73	0.63	0.84	8.79	7.93	2.363160945	42	2	17.28395062	6.896551724
No hits	0.00013	0.00098	0.74	0.64	0.84	7.75	6.97	2.181473787	8	1	3.29218107	3.448275862
MS3_10002	0.00014	0.001	0.62	0.53	0.7	8.98	9.46	0.618783386	43	3	17.69547325	10.34482759
MS3_10184	0.00014	0.0011	0.66	0.57	0.76	7.99	7.3	1.993716214	21	0	8.641975309	0
MS3_03509	0.00015	0.0011	0.72	0.62	0.82	11.29	10.18	3.034358398	211	15	86.83127572	51.72413793
MS3_00880	0.00017	0.0012	0.66	0.57	0.76	8.53	9.13	0.548811621	16	3	6.58436214	10.34482759
MS3_03419	0.00017	0.0012	0.64	0.55	0.73	9.51	9.93	0.657046818	90	14	37.03703704	48.27586207
MS3_10138	0.00017	0.0012	0.72	0.62	0.82	10.04	8.97	2.915379542	121	5	49.79423868	17.24137931
MS3_01262	0.00018	0.0012	0.71	0.62	0.8	8.89	8.18	2.03399138	44	1	18.10699588	3.448275862
MS3_06539	0.00018	0.0012	0.68	0.58	0.78	7	6.4	1.822122316	6	0	2.469135802	0
MS3_06680	0.00018	0.0012	0.77	0.68	0.87	6.74	6.14	1.822124713	1	0	0.411522634	0
MS3_07363	0.00018	0.0013	0.64	0.55	0.73	8.54	9.09	0.576949796	18	1	7.407407407	3.448275862

MS3_04449	0.00021	0.0015	0.6	0.51	0.7	9.52	9.94	0.657046818	112	14	46.09053498	48.27586207
MS3_10345	0.00021	0.0015	0.57	0.49	0.66	9.58	9.94	0.697676324	123	14	50.61728395	48.27586207
MS3_00223	0.00024	0.0017	0.63	0.54	0.73	8.84	9.35	0.600495571	22	4	9.053497942	13.79310345
MS3_00996	0.00025	0.0017	0.64	0.56	0.73	10.34	9.78	1.750672504	130	8	53.49794239	27.5862069
MS3_01153	0.00025	0.0017	0.67	0.58	0.76	8.24	7.51	2.075081085	22	0	9.053497942	0
MS3_05639	0.00026	0.0017	0.69	0.59	0.79	8.58	9	0.657046807	3	1	1.234567901	3.448275862
MS3_08019	0.00026	0.0017	0.62	0.54	0.71	9.42	9.8	0.683861407	85	11	34.97942387	37.93103448
MS3_08161	0.00026	0.0017	0.66	0.57	0.75	8.89	9.45	0.571209057	38	6	15.63786008	20.68965517
MS3_10820	0.00028	0.0018	0.66	0.56	0.75	7.27	6.77	1.648722643	4	0	1.646090535	0
MS3_02343	0.00029	0.0019	0.68	0.59	0.78	8.06	7.51	1.733253365	8	0	3.29218107	0
MS3_03047	0.00029	0.0019	0.64	0.56	0.73	9.02	9.52	0.606530654	46	6	18.93004115	20.68965517
MS3_05586	0.00029	0.0019	0.68	0.59	0.77	8.39	7.84	1.733253197	15	0	6.172839506	0
MS3_03453	0.0003	0.0019	0.74	0.63	0.85	8.47	7.6	2.386911346	24	3	9.87654321	10.34482759
MS3_04827	0.0003	0.0019	0.71	0.61	0.81	8.7	8.18	1.682027735	5	0	2.057613169	0
MS3_02899	0.00031	0.0019	0.73	0.62	0.83	8.63	7.99	1.896481036	7	0	2.880658436	0
MS3_10590	0.00031	0.002	0.66	0.57	0.76	8.85	9.36	0.600495571	24	5	9.87654321	17.24137931
MS3_05496	0.00032	0.002	0.73	0.62	0.84	7.75	7.09	1.934793319	7	0	2.880658436	0
MS3_09810	0.00034	0.0021	0.64	0.56	0.72	10.33	9.73	1.822118805	148	11	60.90534979	37.93103448
MS3_01650	0.00037	0.0023	0.62	0.53	0.7	9.08	9.56	0.618783387	63	6	25.92592593	20.68965517
MS3_10221	0.00037	0.0023	0.62	0.54	0.7	8.09	7.69	1.491824869	9	0	3.703703704	0
MS3_05999	0.0004	0.0024	0.67	0.58	0.76	8.99	9.48	0.612626388	38	6	15.63786008	20.68965517
MS3_05387	0.00042	0.0025	0.68	0.59	0.78	8.21	7.62	1.803988716	9	0	3.703703704	0
MS3_10935	0.00043	0.0026	0.71	0.6	0.81	8.13	7.58	1.733253319	0	0	0	0
MS3_10591	0.00046	0.0027	0.64	0.55	0.73	6.81	6.41	1.491826921	0	0	0	0
MS3_07294	0.00048	0.0028	0.62	0.53	0.71	9.21	9.65	0.644036417	71	10	29.218107	34.48275862
MS3_00286	0.00055	0.0032	0.64	0.55	0.73	8.67	9.32	0.522045766	52	7	21.39917695	24.13793103
MS3_00604	0.00056	0.0033	0.63	0.54	0.73	9.2	9.71	0.600495575	67	9	27.57201646	31.03448276
MS3_01852	0.0006	0.0035	0.69	0.6	0.79	7.2	6.66	1.716008722	0	0	0	0
MS3_04375	0.00061	0.0035	0.67	0.57	0.77	7.87	7.32	1.733253525	7	0	2.880658436	0
MS3_08158	0.00061	0.0035	0.7	0.59	0.8	8.64	9.12	0.61878338	7	4	2.880658436	13.79310345
MS3_07702	0.00062	0.0036	0.69	0.59	0.79	10.88	9.83	2.857651125	179	10	73.66255144	34.48275862
MS3_06507	0.00063	0.0036	0.66	0.56	0.76	8.75	9.26	0.600495569	20	5	8.230452675	17.24137931
MS3_00625	0.00069	0.0039	0.74	0.63	0.86	7.83	7.05	2.181473562	5	0	2.057613169	0
MS3_07473	0.00072	0.0041	0.66	0.58	0.75	11.27	10.66	1.840431399	234	25	96.2962963	86.20689655
MS3_07569	0.00074	0.0041	0.7	0.61	0.79	9.69	8.9	2.203396459	96	2	39.50617284	6.896551724
MS3_01686	0.00075	0.0042	0.65	0.56	0.74	8.55	8.04	1.665291306	24	0	9.87654321	0
MS3_07795	0.00077	0.0042	0.65	0.56	0.74	7.41	6.97	1.552708021	2	0	0.823045267	0

MS3_07905	0.00077	0.0042	0.67	0.58	0.77	7.84	7.28	1.750673061	2	0	0.823045267	0
MS3_05539	0.00078	0.0042	0.72	0.6	0.83	8.44	7.67	2.159766623	8	1	3.29218107	3.448275862
MS3_03641	0.00081	0.0044	0.71	0.61	0.81	9.56	8.58	2.664456323	118	5	48.55967078	17.24137931
MS3_03776	0.00083	0.0045	0.77	0.67	0.88	8.75	7.77	2.66445665	35	2	14.40329218	6.896551724
MS3_02289	0.00084	0.0045	0.68	0.58	0.78	8.45	8.88	0.650509078	4	0	1.646090535	0
MS3_02690	0.00084	0.0045	0.56	0.47	0.66	6.79	6.29	1.648724856	10	0	4.115226337	0
MS3_02855	0.00085	0.0045	0.68	0.58	0.78	8.42	8.93	0.60049556	8	1	3.29218107	3.448275862
MS3_06918	0.00086	0.0046	0.62	0.53	0.71	9.28	9.65	0.690734327	66	9	27.16049383	31.03448276
No hits	0.0009	0.0047	0.59	0.5	0.68	9.38	9.77	0.677056872	95	12	39.09465021	41.37931034
MS3_02027	0.00091	0.0047	0.63	0.54	0.73	9.63	10.07	0.644036419	116	16	47.73662551	55.17241379
MS3_05050	0.00093	0.0048	0.72	0.63	0.82	8.44	9.09	0.522045759	11	2	4.526748971	6.896551724
MS3_02425	0.00094	0.0048	0.68	0.58	0.77	9.08	9.88	0.449328959	49	8	20.16460905	27.5862069
MS3_03977	0.00094	0.0048	0.63	0.54	0.72	9.18	9.63	0.637628148	69	8	28.39506173	27.5862069
MS3_03992	0.00094	0.0048	0.71	0.6	0.81	8.76	8.07	1.993715679	38	3	15.63786008	10.34482759
MS3_04311	0.00095	0.0048	0.67	0.57	0.77	8.49	7.85	1.896481087	20	0	8.230452675	0
No hits	0.00095	0.0048	0.66	0.56	0.75	8.74	9.27	0.58860496	27	3	11.11111111	10.34482759
MS3_01261	0.00096	0.0048	0.6	0.52	0.68	9.23	9.66	0.650509091	83	9	34.1563786	31.03448276
MS3_06979	0.00096	0.0048	0.7	0.59	0.81	7.8	7.19	1.840432136	1	0	0.411522634	0
MS3_01348	0.00097	0.0048	0.63	0.55	0.71	8.07	7.74	1.390968256	2	0	0.823045267	0
MS3_02681	0.00097	0.0048	0.65	0.56	0.73	8.03	8.43	0.670320007	3	0	1.234567901	0
MS3_01653	0.001	0.0051	0.67	0.58	0.77	8.88	9.36	0.618783384	17	4	6.995884774	13.79310345
MS3_08607	0.0011	0.0053	0.67	0.58	0.76	8.63	9.08	0.63762814	12	1	4.938271605	3.448275862
MS3_01710	0.0012	0.006	0.66	0.57	0.75	8.27	7.88	1.476980908	2	0	0.823045267	0
MS3_05516	0.0012	0.0057	0.61	0.52	0.7	9.09	9.54	0.637628147	59	7	24.27983539	24.13793103
MS3_06022	0.0012	0.0059	0.69	0.58	0.8	8.78	7.88	2.459603405	52	3	21.39917695	10.34482759
No hits	0.0012	0.006	0.66	0.56	0.77	7.53	7.09	1.55270785	1	0	0.411522634	0
MS3_01761	0.0013	0.0062	0.7	0.59	0.8	8.65	9.12	0.625002257	9	1	3.703703704	3.448275862
MS3_05945	0.0013	0.0061	0.68	0.58	0.77	8.52	7.92	1.822118969	24	1	9.87654321	3.448275862
MS3_02787	0.0014	0.0066	0.77	0.64	0.9	9.31	8.15	3.189933516	68	5	27.98353909	17.24137931
MS3_08059	0.0014	0.0066	0.68	0.58	0.79	7.25	6.81	1.552708323	1	0	0.411522634	0
MS3_09353	0.0015	0.0072	0.67	0.58	0.76	8.74	8.28	1.584074046	11	0	4.526748971	0
MS3_06126	0.0015	0.0072	0.68	0.58	0.78	8.74	8.27	1.599994257	7	0	2.880658436	0
MS3_10083	0.0015	0.0068	0.7	0.59	0.8	9.12	8.36	2.138276312	67	4	27.57201646	13.79310345
MS3_01365	0.0016	0.0073	0.74	0.63	0.85	10.13	9.16	2.637944484	132	6	54.32098765	20.68965517
MS3_05465	0.0016	0.0073	0.69	0.59	0.8	8.68	9.23	0.576949799	14	5	5.761316872	17.24137931
MS3_08398	0.0016	0.0075	0.63	0.54	0.73	8.85	9.21	0.697676319	14	3	5.761316872	10.34482759
MS3_00805	0.0017	0.0077	0.66	0.56	0.76	6.77	6.29	1.616077833	5	0	2.057613169	0

MS3_00900	0.0017	0.0077	0.64	0.53	0.74	8.98	9.49	0.600495573	39	8	16.04938272	27.5862069
MS3_01302	0.0017	0.0077	0.68	0.58	0.79	7.69	7.06	1.877611571	4	0	1.646090535	0
MS3_02157	0.0017	0.0077	0.71	0.59	0.82	9.05	8.38	1.954237397	43	3	17.69547325	10.34482759
No hits	0.0017	0.0078	0.65	0.56	0.75	7.76	7.26	1.648721786	2	0	0.823045267	0
MS3_01276	0.0018	0.0079	0.65	0.57	0.73	8.76	8.39	1.447734654	17	0	6.995884774	0
MS3_02856	0.0018	0.0079	0.58	0.5	0.67	9.18	9.59	0.663650246	67	7	27.57201646	24.13793103
MS3_05219	0.0018	0.0081	0.68	0.58	0.77	8.79	8.4	1.476980834	6	0	2.469135802	0
MS3_06898	0.0018	0.0079	0.67	0.57	0.78	8.51	7.99	1.682027775	12	0	4.938271605	0
MS3_08262	0.0018	0.0079	0.65	0.57	0.74	8.22	8.72	0.606530632	10	0	4.115226337	0
MS3_07944	0.0019	0.0082	0.67	0.57	0.77	9.09	8.47	1.8589281	58	3	23.86831276	10.34482759
MS3_07968	0.0019	0.0082	0.76	0.65	0.88	7.7	6.72	2.664459574	20	3	8.230452675	10.34482759
MS3_00048	0.0021	0.0089	0.59	0.51	0.68	9.09	8.62	1.599994225	43	0	17.69547325	0
MS3_00891	0.0021	0.009	0.73	0.62	0.85	7.67	7.14	1.698933006	2	0	0.823045267	0
MS3_03576	0.0024	0.01	0.65	0.56	0.74	8.42	7.96	1.584074101	9	0	3.703703704	0
MS3_05280	0.0024	0.01	0.64	0.54	0.74	9.15	9.51	0.697676322	40	7	16.46090535	24.13793103
MS3_05836	0.0024	0.01	0.62	0.53	0.72	7.27	6.9	1.447735383	2	0	0.823045267	0
MS3_00560	0.0025	0.011	0.7	0.59	0.82	8.1	7.43	1.954237828	10	0	4.115226337	0
MS3_01643	0.0025	0.01	0.64	0.54	0.73	8.62	8.2	1.521961621	16	0	6.58436214	0
MS3_07590	0.0025	0.01	0.64	0.56	0.73	9.01	9.57	0.571209058	55	5	22.63374486	17.24137931
MS3_09290	0.0025	0.011	0.64	0.53	0.74	7.85	7.33	1.682028117	9	0	3.703703704	0
MS3_09684	0.0025	0.01	0.58	0.48	0.69	8.16	7.61	1.733253302	25	0	10.28806584	0
MS3_06149	0.0027	0.011	0.63	0.54	0.72	9.19	9.62	0.650509091	65	10	26.74897119	34.48275862
MS3_02734	0.0027	0.011	0.65	0.56	0.75	7.88	7.44	1.552707532	2	0	0.823045267	0
MS3_04646	0.0027	0.011	0.71	0.59	0.83	9.94	9.09	2.339646876	134	7	55.14403292	24.13793103
MS3_01902	0.0028	0.011	0.65	0.55	0.74	8.59	8.96	0.690734318	4	0	1.646090535	0
MS3_11429	0.0028	0.011	0.65	0.57	0.74	8.39	8.82	0.650509075	8	1	3.29218107	3.448275862
MS3_00316	0.0029	0.012	0.64	0.55	0.73	7.42	7.09	1.390968595	1	0	0.411522634	0
MS3_03101	0.0029	0.012	0.64	0.54	0.74	9.14	9.64	0.606530655	55	10	22.63374486	34.48275862
MS3_09089	0.0029	0.012	0.7	0.59	0.81	7.44	6.9	1.716008013	2	0	0.823045267	0
MS3_05216	0.003	0.012	0.73	0.63	0.82	8.77	9.41	0.527292415	32	8	13.16872428	27.5862069
MS3_08975	0.003	0.012	0.67	0.57	0.77	8.46	7.5	2.611697155	59	2	24.27983539	6.896551724
MS3_10193	0.003	0.012	0.68	0.57	0.78	7.93	7.39	1.716007294	10	0	4.115226337	0
MS3_00196	0.0031	0.012	0.69	0.58	0.8	8.72	8.13	1.803988524	38	2	15.63786008	6.896551724
MS3_09662	0.0031	0.012	0.61	0.52	0.71	7.32	6.76	1.750674085	17	0	6.995884774	0
MS3_02234	0.0032	0.013	0.67	0.57	0.78	8.4	7.86	1.716007031	12	0	4.938271605	0
MS3_08160	0.0032	0.013	0.65	0.56	0.74	9.05	9.52	0.625002263	55	9	22.63374486	31.03448276
MS3_08737	0.0032	0.012	0.61	0.52	0.71	8.88	8.44	1.552707261	31	0	12.75720165	0

MS3_10729	0.0032	0.013	0.65	0.56	0.74	8.33	8.67	0.711770302	3	0	1.234567901	0
MS3_01516	0.0033	0.013	0.67	0.57	0.78	8.8	8.18	1.858928146	30	1	12.34567901	3.448275862
MS3_06877	0.0033	0.013	0.62	0.53	0.72	9.36	9.91	0.576949808	86	14	35.3909465	48.27586207
MS3_02141	0.0035	0.013	0.69	0.59	0.78	8.58	8.94	0.697676313	2	0	0.823045267	0
MS3_06538	0.0035	0.013	0.68	0.57	0.79	8.29	8.77	0.618783368	6	2	2.469135802	6.896551724
MS3_05953	0.0037	0.014	0.65	0.56	0.74	8.91	8.58	1.390968152	15	0	6.172839506	0
MS3_07010	0.0037	0.014	0.63	0.54	0.72	8.9	9.45	0.576949803	62	8	25.51440329	27.5862069
MS3_08776	0.0037	0.014	0.67	0.56	0.78	8.68	9.04	0.697676316	5	1	2.057613169	3.448275862
MS3_01611	0.004	0.015	0.68	0.58	0.78	8.26	8.75	0.612626369	9	3	3.703703704	10.34482759
MS3_01938	0.004	0.015	0.65	0.55	0.76	8.95	9.44	0.612626388	37	9	15.22633745	31.03448276
MS3_03979	0.004	0.015	0.65	0.54	0.75	8.11	7.62	1.632316465	13	0	5.349794239	0
MS3_06928	0.004	0.015	0.58	0.49	0.66	9.47	9.75	0.75578374	87	10	35.80246914	34.48275862
MS3_11250	0.004	0.015	0.6	0.51	0.7	9.14	9.51	0.690734326	51	7	20.98765432	24.13793103
MS3_03853	0.0042	0.016	0.64	0.54	0.73	7.18	6.82	1.433330291	0	0	0	0
MS3_08953	0.0044	0.016	0.65	0.54	0.75	8.27	7.6	1.954237682	33	1	13.58024691	3.448275862
MS3_09691	0.0044	0.016	0.62	0.51	0.72	9.84	10.23	0.677056873	156	22	64.19753086	75.86206897
MS3_06211	0.0045	0.016	0.63	0.54	0.72	8.9	9.26	0.697676319	25	2	10.28806584	6.896551724
MS3_04609	0.0046	0.017	0.69	0.57	0.8	8.43	7.91	1.682027796	5	1	2.057613169	3.448275862
MS3_07637	0.0047	0.017	0.63	0.53	0.72	7.58	7.27	1.363425419	1	0	0.411522634	0
MS3_03695	0.0048	0.017	0.67	0.56	0.78	6.23	6.95	0.486750815	1	0	0.411522634	0
MS3_00498	0.0049	0.018	0.65	0.54	0.75	9.63	9.07	1.750672516	88	5	36.21399177	17.24137931
MS3_03417	0.0051	0.018	0.67	0.55	0.79	9.03	8.56	1.599994229	24	2	9.87654321	6.896551724
MS3_02685	0.0052	0.019	0.55	0.46	0.64	9.46	9.79	0.718923731	106	11	43.62139918	37.93103448
MS3_06559	0.0052	0.018	0.67	0.55	0.79	8.15	7.62	1.698932576	0	0	0	0
MS3_08413	0.0052	0.018	0.63	0.54	0.72	8.49	8.87	0.683861394	10	0	4.115226337	0
MS3_08823	0.0054	0.019	0.64	0.54	0.74	8.46	8.02	1.552707317	18	1	7.407407407	3.448275862
MS3_05676	0.0055	0.019	0.66	0.56	0.77	8.77	8.32	1.568312241	7	0	2.880658436	0
MS3_07374	0.0055	0.019	0.61	0.51	0.72	9.06	9.54	0.618783387	51	10	20.98765432	34.48275862
MS3_08144	0.0055	0.019	0.64	0.55	0.72	7.81	7.29	1.682028156	8	1	3.29218107	3.448275862
MS3_10510	0.0055	0.019	0.66	0.56	0.76	8.86	9.51	0.522045769	61	9	25.10288066	31.03448276
MS3_10753	0.0055	0.019	0.62	0.52	0.72	9.16	9.51	0.704688086	44	6	18.10699588	20.68965517
MS3_09735	0.0056	0.019	0.62	0.52	0.71	9.18	9.56	0.683861405	53	6	21.81069959	20.68965517
MS3_03350	0.0057	0.019	0.68	0.57	0.79	8.52	7.73	2.203396764	43	3	17.69547325	10.34482759
MS3_07213	0.0057	0.02	0.7	0.59	0.81	8.32	7.38	2.559982262	47	2	19.34156379	6.896551724
MS3_07816	0.0057	0.02	0.66	0.57	0.75	7.46	8.15	0.501575945	18	2	7.407407407	6.896551724
MS3_02752	0.0059	0.02	0.58	0.49	0.68	9.22	9.6	0.683861406	64	6	26.33744856	20.68965517
MS3_00934	0.006	0.02	0.62	0.52	0.72	7.68	7.34	1.404947883	0	0	0	0

MS3_03618	0.006	0.02	0.63	0.53	0.72	7.61	7.16	1.568312747	1	0	0.411522634	0
MS3_02048	0.0062	0.021	0.65	0.55	0.76	7.74	8.19	0.63762808	1	0	0.411522634	0
MS3_03938	0.0062	0.021	0.63	0.52	0.74	7.24	6.78	1.584075215	5	0	2.057613169	0
MS3_09160	0.0062	0.021	0.62	0.53	0.71	7.87	7.5	1.447734846	5	0	2.057613169	0
MS3_09371	0.0065	0.022	0.64	0.54	0.74	8.58	8.07	1.665291299	30	1	12.34567901	3.448275862
MS3_07824	0.0066	0.022	0.67	0.57	0.78	9.58	9	1.786038449	79	4	32.51028807	13.79310345
MS3_05203	0.0067	0.022	0.66	0.56	0.76	8.24	8.64	0.67032002	2	1	0.823045267	3.448275862
MS3_06069	0.0067	0.022	0.69	0.58	0.79	8.95	9.57	0.537944431	41	8	16.87242798	27.5862069
MS3_06669	0.0067	0.022	0.56	0.47	0.65	9.1	9.4	0.740818217	37	4	15.22633745	13.79310345
MS3_10017	0.0068	0.022	0.67	0.55	0.79	8.24	7.69	1.73325326	8	1	3.29218107	3.448275862
MS3_09119	0.0071	0.023	0.62	0.52	0.72	8.69	8.03	1.934792485	48	1	19.75308642	3.448275862
MS3_02160	0.0072	0.023	0.66	0.55	0.77	7.9	7.44	1.584074314	2	0	0.823045267	0
MS3_02688	0.0074	0.024	0.63	0.54	0.73	10.73	10.3	1.537257525	206	17	84.77366255	58.62068966
MS3_04688	0.0074	0.024	0.42	0.32	0.52	9.28	8.67	1.840431437	70	2	28.80658436	6.896551724
MS3_05150	0.0075	0.024	0.66	0.56	0.76	7.87	7.39	1.616074782	5	0	2.057613169	0
MS3_01627	0.0076	0.025	0.45	0.35	0.55	9.61	9.96	0.704688088	118	11	48.55967078	37.93103448
MS3_10489	0.0076	0.024	0.64	0.56	0.73	8.05	8.45	0.670320008	6	1	2.469135802	3.448275862
MS3_09644	0.0078	0.025	0.67	0.56	0.78	8.22	7.63	1.80398871	25	1	10.28806584	3.448275862
MS3_04598	0.0083	0.027	0.67	0.55	0.78	8.71	8.13	1.786038537	29	4	11.93415638	13.79310345
MS3_08805	0.0083	0.027	0.64	0.54	0.74	8.71	9.03	0.726149028	5	3	2.057613169	10.34482759
MS3_01339	0.0084	0.027	0.64	0.54	0.75	8.66	9.11	0.63762814	16	4	6.58436214	13.79310345
MS3_03269	0.0085	0.027	0.64	0.54	0.74	9.27	9.73	0.631283642	64	10	26.33744856	34.48275862
MS3_05016	0.0085	0.027	0.68	0.57	0.8	8.47	7.94	1.69893245	4	1	1.646090535	3.448275862
MS3_09086	0.0086	0.027	0.62	0.52	0.72	7.66	7.31	1.419067868	0	0	0	0
MS3_02545	0.0087	0.027	0.67	0.55	0.78	8.97	8.42	1.733253074	38	2	15.63786008	6.896551724
MS3_11139	0.009	0.028	0.55	0.47	0.64	9.55	9.79	0.78662786	104	10	42.79835391	34.48275862
MS3_07337	0.0092	0.029	0.65	0.55	0.76	7.39	6.86	1.69893353	9	0	3.703703704	0
MS3_07158	0.0095	0.029	0.64	0.54	0.74	8.39	7.99	1.491824792	6	0	2.469135802	0
MS3_01141	0.0099	0.031	0.64	0.54	0.75	8.19	7.6	1.803988728	12	0	4.938271605	0
MS3_01922	0.01	0.032	0.6	0.51	0.69	8.84	9.2	0.697676319	22	2	9.053497942	6.896551724
MS3_07606	0.01	0.031	0.57	0.47	0.68	9.59	9.9	0.733446955	109	13	44.85596708	44.82758621
MS3_01777	0.011	0.035	0.66	0.57	0.76	8.7	9.03	0.718923724	9	0	3.703703704	0
MS3_01857	0.011	0.033	0.64	0.55	0.73	10.39	9.68	2.033991265	170	14	69.95884774	48.27586207
MS3_02393	0.011	0.033	0.63	0.53	0.72	8.48	8.1	1.462284661	14	0	5.761316872	0
MS3_03193	0.011	0.034	0.64	0.53	0.76	8.55	8.91	0.697676313	7	2	2.880658436	6.896551724
MS3_07372	0.011	0.033	0.63	0.54	0.72	9.11	9.77	0.51685133	82	10	33.74485597	34.48275862
MS3_09536	0.011	0.033	0.56	0.47	0.65	7	6.74	1.296930822	3	0	1.234567901	0

MS3_01597	0.012	0.037	0.63	0.52	0.75	7.26	6.89	1.447735399	3	0	1.234567901	0
MS3_07531	0.012	0.037	0.67	0.58	0.77	8.86	9.41	0.576949803	42	8	17.28395062	27.5862069
MS3_01049	0.013	0.039	0.65	0.54	0.77	9.32	8.45	2.386910944	95	6	39.09465021	20.68965517
MS3_01193	0.013	0.04	0.55	0.45	0.65	8.62	8.13	1.632316308	41	0	16.87242798	0
MS3_01668	0.013	0.038	0.67	0.56	0.78	9.4	8.7	2.01375275	67	3	27.57201646	10.34482759
MS3_02086	0.013	0.039	0.46	0.36	0.55	9.58	9.88	0.740818219	113	13	46.50205761	44.82758621
MS3_07345	0.013	0.039	0.55	0.46	0.64	8.85	9.17	0.72614903	30	1	12.34567901	3.448275862
MS3_08689	0.013	0.038	0.67	0.56	0.78	9.14	8.65	1.632316251	29	2	11.93415638	6.896551724
MS3_08943	0.013	0.038	0.65	0.55	0.76	8.42	8.78	0.697676309	2	0	0.823045267	0
MS3_00862	0.014	0.041	0.59	0.49	0.69	9	9.41	0.663650244	59	7	24.27983539	24.13793103
MS3_02044	0.014	0.041	0.7	0.58	0.82	8.92	8.24	1.973877834	49	3	20.16460905	10.34482759
MS3_06403	0.014	0.041	0.59	0.5	0.68	7.24	6.74	1.648722728	16	1	6.58436214	3.448275862
MS3_06834	0.014	0.041	0.63	0.52	0.74	7.31	6.9	1.506818641	1	0	0.411522634	0
MS3_09683	0.014	0.041	0.64	0.55	0.73	8.7	9.27	0.565525428	31	4	12.75720165	13.79310345
MS3_01983	0.015	0.043	0.64	0.53	0.74	8.87	9.22	0.704688083	23	4	9.465020576	13.79310345
MS3_04286	0.015	0.043	0.66	0.55	0.77	7.77	7.24	1.69893288	8	1	3.29218107	3.448275862
MS3_06243	0.015	0.043	0.64	0.53	0.75	7.86	7.49	1.447734851	4	0	1.646090535	0
MS3_08717	0.015	0.042	0.63	0.52	0.74	8.83	9.16	0.718923726	9	2	3.703703704	6.896551724
MS3_09070	0.015	0.043	0.65	0.53	0.78	6.36	6.99	0.53259066	2	1	0.823045267	3.448275862
No hits	0.015	0.042	0.61	0.52	0.71	8.33	8.86	0.588604947	25	2	10.28806584	6.896551724
MS3_01775	0.016	0.044	0.61	0.52	0.71	8.32	7.95	1.447734709	7	0	2.880658436	0
MS3_02176	0.016	0.044	0.67	0.54	0.79	8.86	9.25	0.677056867	12	5	4.938271605	17.24137931
MS3_02747	0.016	0.046	0.61	0.51	0.72	8.38	8.9	0.594520528	17	4	6.995884774	13.79310345
MS3_03603	0.016	0.045	0.63	0.52	0.73	8.47	8.79	0.726149022	4	0	1.646090535	0
MS3_06112	0.016	0.044	0.61	0.51	0.72	8.77	9.15	0.6838614	25	6	10.28806584	20.68965517
MS3_07594	0.016	0.044	0.63	0.53	0.74	7.81	7.44	1.447734876	1	0	0.411522634	0
MS3_08996	0.016	0.044	0.61	0.51	0.71	9.46	9.84	0.683861407	98	15	40.32921811	51.72413793
MS3_09865	0.016	0.044	0.7	0.6	0.81	9.65	9.27	1.462284596	69	3	28.39506173	10.34482759
MS3_00719	0.017	0.047	0.63	0.53	0.73	8.53	8.12	1.50681786	19	0	7.818930041	0
MS3_01445	0.017	0.047	0.55	0.45	0.65	7.1	6.72	1.462285723	12	0	4.938271605	0
MS3_02928	0.017	0.046	0.66	0.55	0.78	8.77	8.3	1.599994253	13	2	5.349794239	6.896551724
MS3_04178	0.017	0.046	0.65	0.54	0.76	7.38	6.91	1.599995164	9	1	3.703703704	3.448275862
MS3_05730	0.018	0.049	0.65	0.54	0.75	11.33	10.66	1.954237321	230	21	94.65020576	72.4137931
MS3_07126	0.018	0.049	0.62	0.53	0.72	8.06	8.35	0.748263535	3	0	1.234567901	0
MS3_08533	0.018	0.049	0.64	0.52	0.75	8.25	8.62	0.690734306	3	1	1.234567901	3.448275862
MS3_09274	0.018	0.049	0.54	0.45	0.63	9.09	9.38	0.748263563	56	4	23.04526749	13.79310345
MS3_10671	0.018	0.049	0.64	0.53	0.75	7.92	8.74	0.440431608	26	4	10.69958848	13.79310345

MS3_02944	0.019	0.051	0.63	0.53	0.73	8.74	9.03	0.748263559	5	1	2.057613169	3.448275862
MS3_10440	0.019	0.051	0.63	0.53	0.73	8.57	8.17	1.491824763	19	0	7.818930041	0
MS3_04158	0.02	0.054	0.59	0.49	0.69	8.78	8.37	1.50681783	30	0	12.34567901	0
MS3_05350	0.02	0.053	0.62	0.52	0.72	7.97	7.58	1.476981002	5	0	2.057613169	0
MS3_08891	0.02	0.053	0.6	0.49	0.71	7.43	7.11	1.377128199	2	0	0.823045267	0
MS3_09952	0.02	0.055	0.64	0.53	0.75	8.43	8.81	0.683861392	4	0	1.646090535	0
MS3_02356	0.021	0.055	0.63	0.53	0.74	8.76	9.08	0.726149029	15	2	6.172839506	6.896551724
MS3_03270	0.021	0.055	0.65	0.52	0.77	8.77	8.29	1.616074465	12	1	4.938271605	3.448275862
MS3_04025	0.021	0.055	0.63	0.52	0.74	8.31	8.64	0.718923712	1	0	0.411522634	0
MS3_06668	0.021	0.055	0.63	0.52	0.73	8.38	8.78	0.670320027	4	2	1.646090535	6.896551724
MS3_01001	0.023	0.061	0.62	0.53	0.71	7.97	8.22	0.778800746	0	0	0	0
MS3_05614	0.023	0.059	0.63	0.53	0.72	9.08	8.83	1.284025427	16	0	6.58436214	0
MS3_01905	0.024	0.062	0.64	0.53	0.75	8.44	8.78	0.711770306	7	1	2.880658436	3.448275862
MS3_04276	0.024	0.063	0.62	0.5	0.74	8.03	7.52	1.665291508	15	1	6.172839506	3.448275862
MS3_05646	0.024	0.064	0.61	0.51	0.71	7.93	7.6	1.390968297	4	0	1.646090535	0
MS3_02807	0.025	0.065	0.58	0.48	0.67	9.05	9.47	0.657046815	67	6	27.57201646	20.68965517
MS3_03775	0.025	0.065	0.59	0.5	0.68	9.26	9.56	0.740818218	58	7	23.86831276	24.13793103
MS3_04896	0.025	0.065	0.68	0.55	0.8	8.84	9.21	0.690734323	14	6	5.761316872	20.68965517
MS3_05370	0.025	0.064	0.57	0.48	0.66	7.79	7.48	1.363425315	6	0	2.469135802	0
MS3_11376	0.025	0.064	0.64	0.53	0.76	8.7	9.1	0.670320036	10	2	4.115226337	6.896551724
MS3_01771	0.026	0.066	0.66	0.54	0.77	8.91	9.29	0.683861403	24	7	9.87654321	24.13793103
MS3_02275	0.026	0.066	0.56	0.47	0.65	9.24	9.52	0.755783738	65	6	26.74897119	20.68965517
MS3_08366	0.026	0.066	0.61	0.51	0.71	8.21	7.9	1.363425201	6	0	2.469135802	0
MS3_09942	0.026	0.067	0.56	0.46	0.66	9.45	9.71	0.771051584	84	9	34.56790123	31.03448276
MS3_02346	0.027	0.068	0.59	0.49	0.68	7.73	7.42	1.36342534	4	0	1.646090535	0
MS3_03824	0.027	0.068	0.6	0.5	0.71	7.9	7.51	1.476981034	10	0	4.115226337	0
MS3_04261	0.027	0.068	0.6	0.49	0.71	7.71	7.33	1.462284924	9	0	3.703703704	0
MS3_06214	0.027	0.069	0.64	0.53	0.75	8.35	7.96	1.476980891	9	0	3.703703704	0
MS3_08000	0.027	0.068	0.59	0.5	0.67	8.33	8.06	1.309964505	6	0	2.469135802	0
MS3_10036	0.027	0.068	0.64	0.54	0.74	8.41	7.96	1.568312299	25	2	10.28806584	6.896551724
MS3_03655	0.028	0.07	0.62	0.53	0.71	9.1	8.74	1.433329433	69	2	28.39506173	6.896551724
MS3_05739	0.028	0.07	0.62	0.51	0.72	6.64	6.4	1.271250488	0	0	0	0
MS3_00569	0.029	0.072	0.63	0.51	0.74	8.98	8.53	1.568312222	47	2	19.34156379	6.896551724
MS3_10493	0.029	0.072	0.62	0.52	0.72	8.97	9.41	0.644036415	41	5	16.87242798	17.24137931
MS3_11247	0.029	0.073	0.62	0.52	0.73	8.55	8.94	0.677056861	6	2	2.469135802	6.896551724
MS3_02314	0.03	0.074	0.57	0.48	0.66	9.48	9.74	0.771051584	93	12	38.27160494	41.37931034
MS3_01114	0.03	0.075	0.59	0.49	0.68	7.33	7.05	1.323130239	3	0	1.234567901	0

MS3_06746	0.03	0.075	0.57	0.48	0.67	9.54	9.86	0.726149035	106	13	43.62139918	44.82758621
MS3_00670	0.031	0.075	0.62	0.51	0.74	8.79	8.38	1.506817829	12	1	4.938271605	3.448275862
MS3_03420	0.031	0.075	0.63	0.52	0.73	9.25	8.85	1.491824715	57	3	23.45679012	10.34482759
MS3_08169	0.031	0.075	0.66	0.55	0.76	8.58	9.05	0.625002255	18	2	7.407407407	6.896551724
MS3_10736	0.031	0.076	0.6	0.51	0.69	8.5	8.18	1.377127815	17	0	6.995884774	0
MS3_04437	0.032	0.078	0.61	0.51	0.7	8.59	8.84	0.778800772	5	0	2.057613169	0
MS3_10475	0.032	0.077	0.62	0.53	0.71	8.72	8.45	1.309964476	14	0	5.761316872	0
MS3_00440	0.033	0.079	0.62	0.51	0.73	7.51	7.16	1.41906798	0	0	0	0
MS3_08811	0.033	0.079	0.63	0.53	0.74	8.49	8.16	1.390968183	5	1	2.057613169	3.448275862
MS3_10022	0.033	0.079	0.62	0.52	0.73	7.8	7.52	1.323129979	0	0	0	0
MS3_01245	0.034	0.082	0.61	0.51	0.71	8.23	7.95	1.323129883	4	0	1.646090535	0
MS3_07422	0.034	0.081	0.65	0.52	0.77	8.5	8.91	0.663650235	9	4	3.703703704	13.79310345
MS3_06296	0.035	0.084	0.65	0.55	0.76	8.58	9.05	0.625002255	21	3	8.641975309	10.34482759
MS3_07370	0.035	0.084	0.6	0.5	0.7	8.34	8.6	0.771051568	3	0	1.234567901	0
MS3_03814	0.036	0.086	0.65	0.55	0.75	8.89	9.39	0.606530652	36	6	14.81481481	20.68965517
MS3_04262	0.036	0.086	0.62	0.51	0.73	8.52	8.16	1.433329475	5	0	2.057613169	0
MS3_06276	0.036	0.085	0.62	0.51	0.73	8.95	9.24	0.748263562	21	5	8.641975309	17.24137931
MS3_07105	0.036	0.086	0.59	0.5	0.69	8.39	8.04	1.419067623	20	2	8.230452675	6.896551724
MS3_07419	0.036	0.086	0.62	0.52	0.72	8.85	8.47	1.462284624	37	2	15.22633745	6.896551724
MS3_00452	0.037	0.086	0.61	0.51	0.71	8.36	8.1	1.296930135	2	0	0.823045267	0
MS3_01870	0.037	0.086	0.6	0.5	0.7	7.7	7.35	1.419067844	4	0	1.646090535	0
MS3_05252	0.037	0.086	0.63	0.52	0.73	8.06	8.38	0.726149003	0	0	0	0
MS3_08726	0.037	0.086	0.57	0.46	0.68	8.03	7.68	1.419067701	11	0	4.526748971	0
MS3_09427	0.037	0.086	0.58	0.48	0.69	7.93	7.66	1.309964572	8	0	3.29218107	0
MS3_00151	0.038	0.088	0.63	0.52	0.73	7.99	7.68	1.363425249	2	0	0.823045267	0
MS3_04227	0.038	0.089	0.64	0.53	0.75	8.75	9.07	0.726149028	17	1	6.995884774	3.448275862
MS3_05734	0.038	0.088	0.62	0.49	0.75	8.07	7.61	1.584074219	2	0	0.823045267	0
MS3_00412	0.039	0.09	0.61	0.51	0.7	8.67	8.9	0.794533594	8	1	3.29218107	3.448275862
MS3_10028	0.039	0.089	0.59	0.49	0.7	8.23	7.93	1.349858886	10	0	4.115226337	0
MS3_02653	0.04	0.091	0.62	0.5	0.73	8.12	8.51	0.677056842	5	2	2.057613169	6.896551724
MS3_03304	0.04	0.091	0.62	0.52	0.72	8.6	8.85	0.778800773	4	0	1.646090535	0
MS3_03768	0.04	0.091	0.63	0.52	0.73	7.42	7.87	0.637628016	7	1	2.880658436	3.448275862
MS3_06299	0.04	0.091	0.6	0.5	0.7	7.6	7.33	1.309964686	1	0	0.411522634	0
MS3_07509	0.04	0.091	0.63	0.52	0.74	8.32	8.62	0.740818201	4	1	1.646090535	3.448275862
MS3_10785	0.041	0.093	0.58	0.48	0.68	6.79	6.56	1.25860094	0	0	0	0
MS3_02474	0.042	0.095	0.63	0.51	0.75	8.65	8.92	0.763379485	4	1	1.646090535	3.448275862
MS3_04887	0.042	0.095	0.65	0.53	0.76	8.22	7.68	1.716007104	27	2	11.11111111	6.896551724

MS3_08692	0.042	0.096	0.61	0.5	0.71	8.96	9.41	0.637628145	55	9	22.63374486	31.03448276
MS3_00447	0.043	0.096	0.61	0.49	0.73	8.93	9.21	0.755783736	20	3	8.230452675	10.34482759
MS3_05352	0.043	0.096	0.59	0.48	0.69	8.61	9.02	0.663650238	33	6	13.58024691	20.68965517
MS3_08472	0.043	0.096	0.56	0.46	0.66	9.33	9.62	0.748263565	88	10	36.21399177	34.48275862
MS3_04342	0.044	0.098	0.56	0.47	0.65	8.77	9.11	0.711770314	35	2	14.40329218	6.896551724
MS3_06832	0.044	0.099	0.61	0.5	0.72	8.16	7.82	1.404947702	7	0	2.880658436	0
MS3_10177	0.044	0.097	0.6	0.5	0.71	8.19	7.92	1.309964523	2	0	0.823045267	0
MS3_11059	0.045	0.099	0.7	0.59	0.8	9.28	9.76	0.618783388	82	18	33.74485597	62.06896552
MS3_03400	0.047	0.1	0.58	0.49	0.68	8.71	8.89	0.835270205	3	0	1.234567901	0
MS3_06500	0.047	0.1	0.63	0.52	0.73	8.18	7.9	1.32312989	2	0	0.823045267	0
MS3_07481	0.047	0.1	0.57	0.47	0.66	9.9	9.29	1.84043141	122	10	50.20576132	34.48275862
MS3_01483	0.048	0.11	0.6	0.51	0.69	8.59	8.84	0.778800772	6	0	2.469135802	0
MS3_06380	0.048	0.1	0.65	0.53	0.76	8.65	8.23	1.521961617	18	1	7.407407407	3.448275862
MS3_08945	0.049	0.11	0.65	0.55	0.74	9.05	9.5	0.637628146	64	10	26.33744856	34.48275862
MS3_09510	0.049	0.11	0.57	0.47	0.66	8.79	9.12	0.718923725	29	3	11.93415638	10.34482759
MS3_01833	0.05	0.11	0.57	0.48	0.65	9.13	9.41	0.755783738	51	1	20.98765432	3.448275862
MS3_01871	0.05	0.11	0.62	0.49	0.74	8.43	8.05	1.462284669	9	0	3.703703704	0
MS3_07600	0.05	0.11	0.6	0.5	0.7	8.36	8.63	0.763379477	1	1	0.411522634	3.448275862
MS3_06748	0.051	0.11	0.67	0.58	0.77	9.19	9.77	0.559898363	57	10	23.45679012	34.48275862
MS3_06914	0.051	0.11	0.6	0.49	0.7	6.85	6.61	1.271250029	0	0	0	0
MS3_03427	0.052	0.11	0.64	0.53	0.75	8.43	8.84	0.663650232	5	0	2.057613169	0
MS3_01053	0.053	0.11	0.59	0.49	0.68	7.73	7.44	1.336427691	1	0	0.411522634	0
MS3_00812	0.054	0.12	0.58	0.48	0.68	9.34	9.6	0.771051583	74	9	30.4526749	31.03448276
MS3_02256	0.054	0.12	0.64	0.52	0.76	8.73	9.05	0.726149028	9	3	3.703703704	10.34482759
MS3_09229	0.055	0.12	0.6	0.49	0.71	9.12	8.81	1.363425128	37	1	15.22633745	3.448275862
MS3_09415	0.055	0.12	0.67	0.57	0.78	8.22	7.84	1.46228471	7	1	2.880658436	3.448275862
MS3_06327	0.057	0.12	0.59	0.48	0.7	6.86	6.59	1.309965483	1	0	0.411522634	0
MS3_08593	0.059	0.13	0.62	0.51	0.72	6.83	7.43	0.548811188	5	2	2.057613169	6.896551724
MS3_09426	0.059	0.13	0.61	0.5	0.72	6.72	7.08	0.697675805	1	0	0.411522634	0
MS3_06950	0.061	0.13	0.66	0.54	0.78	8.1	7.74	1.433329554	5	1	2.057613169	3.448275862
MS3_00076	0.062	0.13	0.6	0.5	0.7	8.43	8.66	0.794533589	2	0	0.823045267	0
MS3_06736	0.062	0.13	0.62	0.5	0.74	8.65	8.94	0.748263557	4	1	1.646090535	3.448275862
MS3_07686	0.064	0.13	0.61	0.51	0.7	9.55	9.85	0.740818219	106	13	43.62139918	44.82758621
MS3_00676	0.066	0.14	0.59	0.48	0.69	7.55	7.28	1.30996471	2	0	0.823045267	0
MS3_08220	0.066	0.14	0.58	0.48	0.69	10.19	10.61	0.657046819	186	22	76.54320988	75.86206897
MS3_11045	0.066	0.14	0.6	0.49	0.71	6.96	7.4	0.644036082	2	1	0.823045267	3.448275862
MS3_10148	0.067	0.14	0.6	0.49	0.7	8.55	8.81	0.771051574	8	0	3.29218107	0

MS3_01333	0.067	0.14	0.64	0.52	0.76	6.8	6.49	1.363426567	1	0	0.411522634	0
MS3_09744	0.067	0.14	0.62	0.52	0.72	10.24	9.53	2.033991267	174	16	71.60493827	55.17241379
MS3_01749	0.069	0.14	0.58	0.46	0.7	10.65	10.06	1.803988418	192	19	79.01234568	65.51724138
MS3_05077	0.07	0.14	0.56	0.45	0.68	9.33	8.9	1.53725754	58	5	23.86831276	17.24137931
MS3_05715	0.071	0.15	0.61	0.49	0.72	8.39	8	1.476980884	16	1	6.58436214	3.448275862
MS3_09296	0.071	0.15	0.61	0.5	0.72	9.33	9.66	0.718923731	65	12	26.74897119	41.37931034
MS3_00147	0.072	0.15	0.58	0.49	0.67	8.31	8.52	0.810584229	4	0	1.646090535	0
MS3_00148	0.072	0.15	0.57	0.47	0.67	10.04	10.31	0.763379494	160	18	65.8436214	62.06896552
MS3_04550	0.072	0.15	0.56	0.46	0.66	7.59	7.4	1.20924974	1	0	0.411522634	0
MS3_09287	0.072	0.15	0.59	0.48	0.69	9.08	8.79	1.336427502	40	2	16.46090535	6.896551724
MS3_08926	0.073	0.15	0.64	0.54	0.74	8.92	9.3	0.683861403	47	5	19.34156379	17.24137931
MS3_01289	0.074	0.15	0.56	0.45	0.67	9.62	9.82	0.818730752	103	13	42.38683128	44.82758621
MS3_08625	0.076	0.15	0.61	0.5	0.72	7.41	7.11	1.349859214	1	0	0.411522634	0
MS3_10292	0.076	0.15	0.61	0.5	0.73	8.32	8.63	0.733446936	7	2	2.880658436	6.896551724
MS3_01014	0.077	0.15	0.61	0.5	0.71	7.33	7.77	0.644036259	6	1	2.469135802	3.448275862
MS3_08178	0.077	0.16	0.58	0.47	0.68	7.82	7.6	1.246076842	5	0	2.057613169	0
MS3_06075	0.078	0.16	0.58	0.48	0.69	8.59	8.81	0.802518788	4	1	1.646090535	3.448275862
MS3_03461	0.079	0.16	0.65	0.53	0.77	8.63	9.12	0.612626382	18	6	7.407407407	20.68965517
MS3_08509	0.079	0.16	0.62	0.51	0.73	6.49	6.86	0.690733498	2	0	0.823045267	0
MS3_03054	0.084	0.17	0.6	0.48	0.71	8.82	8.52	1.349858832	13	0	5.349794239	0
MS3_03385	0.085	0.17	0.61	0.5	0.72	8.22	8.47	0.778800761	5	0	2.057613169	0
MS3_06080	0.085	0.17	0.58	0.47	0.7	8.58	8.28	1.349858847	12	0	4.938271605	0
MS3_08024	0.085	0.17	0.6	0.49	0.7	8.39	8.04	1.419067623	21	2	8.641975309	6.896551724
MS3_08907	0.086	0.17	0.57	0.46	0.67	7.13	6.92	1.233678473	1	0	0.411522634	0
MS3_02494	0.087	0.17	0.57	0.46	0.67	7.55	7.32	1.258600213	6	0	2.469135802	0
MS3_10209	0.087	0.17	0.64	0.55	0.74	9.14	9.52	0.683861405	68	9	27.98353909	31.03448276
MS3_00143	0.088	0.17	0.63	0.51	0.74	8.63	8.91	0.755783731	5	2	2.057613169	6.896551724
MS3_00703	0.089	0.17	0.57	0.47	0.67	7.67	7.42	1.284025598	2	0	0.823045267	0
MS3_07467	0.09	0.18	0.5	0.41	0.59	9.5	9.72	0.802518796	115	11	47.32510288	37.93103448
MS3_04063	0.091	0.18	0.59	0.47	0.71	8.51	9.08	0.565525423	34	7	13.99176955	24.13793103
MS3_07403	0.092	0.18	0.48	0.39	0.57	6.34	6.19	1.161835508	0	0	0	0
MS3_00257	0.093	0.18	0.6	0.49	0.7	8.25	8.59	0.711770299	2	1	0.823045267	3.448275862
MS3_03534	0.094	0.18	0.59	0.47	0.71	8.86	8.58	1.323129832	17	2	6.995884774	6.896551724
MS3_05748	0.094	0.18	0.6	0.49	0.71	8.74	8.98	0.786627853	14	1	5.761316872	3.448275862
MS3_02637	0.096	0.19	0.61	0.5	0.71	9.06	9.43	0.690734326	64	9	26.33744856	31.03448276
MS3_02838	0.097	0.19	0.58	0.47	0.69	8.84	9.09	0.778800777	20	3	8.230452675	10.34482759
MS3_04800	0.097	0.19	0.59	0.49	0.69	8.49	8.86	0.690734315	21	1	8.641975309	3.448275862

MS3_05337	0.097	0.19	0.59	0.47	0.71	8.36	8.02	1.404947666	13	1	5.349794239	3.448275862
MS3_10803	0.097	0.19	0.58	0.48	0.67	9.7	9.94	0.78662786	113	14	46.50205761	48.27586207
MS3_07737	0.098	0.19	0.51	0.42	0.61	9.68	9.95	0.763379493	135	14	55.55555556	48.27586207
MS3_02155	0.098	0.19	0.59	0.5	0.67	7.93	8.11	0.835270179	4	0	1.646090535	0
MS3_03625	0.098	0.19	0.59	0.48	0.71	8.14	8.42	0.755783714	1	1	0.411522634	3.448275862
MS3_04778	0.098	0.19	0.59	0.49	0.69	8.46	8.81	0.704688074	14	2	5.761316872	6.896551724
MS3_07273	0.098	0.19	0.56	0.46	0.66	8.67	8.37	1.34985884	22	1	9.053497942	3.448275862
MS3_09231	0.099	0.19	0.62	0.5	0.73	8.51	8.77	0.771051573	8	0	3.29218107	0
MS3_10187	0.099	0.19	0.6	0.51	0.68	9.85	9.5	1.419067553	139	10	57.20164609	34.48275862
MS3_00287	0.1	0.19	0.56	0.47	0.66	8.09	7.88	1.23367812	4	0	1.646090535	0
MS3_04307	0.1	0.19	0.5	0.42	0.58	9.82	9.51	1.363425118	99	6	40.74074074	20.68965517
MS3_06745	0.1	0.19	0.6	0.51	0.69	8.91	9.11	0.818730748	30	2	12.34567901	6.896551724
MS3_08999	0.1	0.2	0.57	0.46	0.67	8.98	8.71	1.309964466	32	2	13.16872428	6.896551724
MS3_10713	0.1	0.19	0.55	0.48	0.63	9.92	9.71	1.233678062	117	6	48.14814815	20.68965517
MS3_11509	0.1	0.19	0.6	0.49	0.71	8.58	8.83	0.778800772	7	1	2.880658436	3.448275862
MS3_00881	0.11	0.21	0.59	0.49	0.7	8.51	8.84	0.718923719	15	3	6.172839506	10.34482759
MS3_01328	0.11	0.21	0.54	0.43	0.64	9.73	9.94	0.810584245	137	16	56.37860082	55.17241379
MS3_01527	0.11	0.2	0.57	0.47	0.67	8.82	9.08	0.771051579	20	1	8.230452675	3.448275862
MS3_01764	0.11	0.2	0.54	0.44	0.63	10.18	10.57	0.677056874	170	20	69.95884774	68.96551724
MS3_04179	0.11	0.2	0.59	0.49	0.68	8.85	8.7	1.161834251	6	0	2.469135802	0
MS3_08663	0.11	0.21	0.54	0.44	0.65	8.63	8.38	1.284025443	21	0	8.641975309	0
MS3_09396	0.11	0.2	0.62	0.5	0.74	8.49	8.78	0.748263554	4	2	1.646090535	6.896551724
MS3_00785	0.12	0.22	0.55	0.46	0.65	9.43	9.66	0.794533601	88	11	36.21399177	37.93103448
MS3_01160	0.12	0.22	0.57	0.46	0.69	8.27	7.96	1.363425191	22	0	9.053497942	0
MS3_01937	0.12	0.21	0.6	0.48	0.73	8.64	8.94	0.74081821	15	3	6.172839506	10.34482759
MS3_04453	0.12	0.22	0.57	0.48	0.66	8.57	8.35	1.246076755	22	0	9.053497942	0
MS3_04564	0.12	0.22	0.63	0.5	0.76	7.01	6.72	1.336428344	1	0	0.411522634	0
MS3_05024	0.12	0.21	0.62	0.5	0.73	8.2	7.86	1.404947694	7	1	2.880658436	3.448275862
MS3_05038	0.12	0.22	0.64	0.53	0.75	9.05	9.39	0.711770318	48	9	19.75308642	31.03448276
MS3_06449	0.12	0.22	0.57	0.47	0.67	8.44	8.22	1.246076763	10	0	4.115226337	0
MS3_08613	0.12	0.22	0.61	0.49	0.73	8.97	9.22	0.778800778	23	4	9.465020576	13.79310345
MS3_10459	0.12	0.22	0.54	0.44	0.63	8.64	8.42	1.246076752	25	0	10.28806584	0
MS3_10943	0.12	0.22	0.52	0.43	0.62	7.97	7.74	1.258600098	8	0	3.29218107	0
MS3_01274	0.13	0.23	0.58	0.47	0.69	8.29	8.07	1.246076774	1	0	0.411522634	0
MS3_06424	0.13	0.24	0.62	0.48	0.75	8.82	9.09	0.763379487	12	4	4.938271605	13.79310345
MS3_06482	0.13	0.23	0.67	0.56	0.78	9.05	9.38	0.718923729	31	9	12.75720165	31.03448276
MS3_07854	0.13	0.24	0.59	0.48	0.7	7.98	8.32	0.711770282	1	1	0.411522634	3.448275862

MS3_09619	0.13	0.23	0.48	0.39	0.57	9.17	9.44	0.763379491	69	6	28.39506173	20.68965517
MS3_10499	0.13	0.23	0.57	0.46	0.67	8.7	8.86	0.852143782	2	0	0.823045267	0
MS3_10687	0.13	0.23	0.59	0.48	0.7	8.73	9.02	0.748263559	14	2	5.761316872	6.896551724
MS3_00494	0.14	0.24	0.68	0.57	0.79	7.26	6.9	1.433330162	1	1	0.411522634	3.448275862
MS3_00769	0.14	0.24	0.59	0.48	0.7	8.17	8.41	0.786627837	3	1	1.234567901	3.448275862
MS3_00939	0.14	0.25	0.55	0.45	0.66	7.33	7.15	1.197217586	0	0	0	0
MS3_06583	0.14	0.25	0.53	0.43	0.63	9.15	9.35	0.81873075	49	4	20.16460905	13.79310345
MS3_07487	0.14	0.26	0.6	0.49	0.7	8.25	8.45	0.818730735	4	0	1.646090535	0
MS3_08004	0.14	0.24	0.62	0.52	0.72	9.03	9.35	0.726149032	52	7	21.39917695	24.13793103
No hits	0.14	0.25	0.58	0.47	0.7	8.14	7.85	1.336427577	6	0	2.469135802	0
MS3_08460	0.15	0.27	0.57	0.49	0.66	9.62	9.33	1.336427493	84	4	34.56790123	13.79310345
MS3_01934	0.15	0.27	0.58	0.48	0.67	7.02	6.8	1.246077281	1	0	0.411522634	0
MS3_02050	0.15	0.27	0.58	0.47	0.69	8.36	8.61	0.778800766	7	2	2.880658436	6.896551724
MS3_05322	0.15	0.27	0.61	0.49	0.72	8.3	8.51	0.810584229	0	0	0	0
MS3_08210	0.15	0.27	0.56	0.47	0.65	8.08	7.93	1.161834282	0	0	0	0
MS3_08455	0.15	0.26	0.59	0.47	0.7	8.49	8.15	1.404947648	34	3	13.99176955	10.34482759
MS3_03171	0.16	0.28	0.59	0.48	0.69	8.41	8.65	0.786627846	10	1	4.115226337	3.448275862
MS3_06707	0.16	0.29	0.59	0.46	0.72	8.23	8.53	0.740818197	4	2	1.646090535	6.896551724
MS3_08176	0.16	0.27	0.55	0.46	0.64	8.4	8.23	1.185304876	11	0	4.526748971	0
MS3_09457	0.16	0.28	0.59	0.48	0.7	8.31	8.03	1.323129872	19	2	7.818930041	6.896551724
MS3_02805	0.17	0.29	0.58	0.47	0.7	8.67	8.95	0.755783732	27	5	11.11111111	17.24137931
MS3_03569	0.17	0.29	0.58	0.47	0.68	8.15	8.38	0.794533578	6	0	2.469135802	0
MS3_03976	0.17	0.29	0.59	0.48	0.69	7.93	8.26	0.718923688	21	0	8.641975309	0
MS3_05602	0.17	0.29	0.59	0.48	0.7	7.86	8.09	0.794533559	0	0	0	0
MS3_06161	0.17	0.29	0.6	0.5	0.7	9.26	9.45	0.826959132	56	6	23.04526749	20.68965517
MS3_07156	0.17	0.29	0.54	0.43	0.65	6.93	6.72	1.233678676	4	0	1.646090535	0
MS3_07395	0.17	0.29	0.59	0.48	0.7	8.99	8.74	1.28402543	43	4	17.69547325	13.79310345
MS3_10721	0.17	0.3	0.56	0.45	0.66	8.9	8.68	1.246076743	28	2	11.52263374	6.896551724
MS3_04347	0.18	0.3	0.57	0.46	0.68	9.49	9.22	1.309964456	81	8	33.33333333	27.5862069
MS3_05960	0.18	0.3	0.49	0.4	0.57	10.11	9.89	1.246076732	137	15	56.37860082	51.72413793
MS3_07593	0.18	0.31	0.54	0.44	0.64	9.63	9.82	0.826959133	113	13	46.50205761	44.82758621
MS3_09000	0.18	0.31	0.56	0.45	0.66	9.35	9.12	1.258600015	71	5	29.218107	17.24137931
MS3_09626	0.18	0.31	0.57	0.46	0.68	8.63	8.42	1.233678081	5	0	2.057613169	0
MS3_10471	0.18	0.31	0.58	0.46	0.7	8.55	8.32	1.258600037	6	0	2.469135802	0
MS3_10847	0.19	0.32	0.62	0.53	0.71	9.01	9.28	0.76337949	49	6	20.16460905	20.68965517
MS3_02538	0.19	0.31	0.45	0.33	0.56	8.16	7.94	1.246076787	3	0	1.234567901	0
MS3_04269	0.19	0.31	0.58	0.45	0.71	8.94	9.15	0.810584241	19	5	7.818930041	17.24137931

MS3_06947	0.19	0.32	0.57	0.46	0.68	8.61	8.78	0.843664809	8	1	3.29218107	3.448275862
MS3_08391	0.19	0.31	0.57	0.46	0.68	8.31	8.55	0.786627843	14	2	5.761316872	6.896551724
MS3_10378	0.19	0.31	0.44	0.34	0.55	8.2	7.98	1.246076783	3	0	1.234567901	0
MS3_10619	0.19	0.31	0.59	0.47	0.7	8.6	8.93	0.718923722	37	7	15.22633745	24.13793103
MS3_01504	0.2	0.33	0.57	0.45	0.68	8.55	8.32	1.258600037	26	2	10.69958848	6.896551724
MS3_02162	0.2	0.33	0.57	0.46	0.68	8.88	9.07	0.826959129	19	2	7.818930041	6.896551724
MS3_02499	0.2	0.33	0.56	0.46	0.66	8.53	8.71	0.835270202	8	1	3.29218107	3.448275862
MS3_03381	0.2	0.34	0.58	0.47	0.7	8.23	8.45	0.802518778	3	0	1.234567901	0
MS3_05289	0.2	0.33	0.55	0.45	0.65	8.72	8.53	1.209249613	27	1	11.11111111	3.448275862
MS3_06430	0.2	0.33	0.58	0.47	0.68	8.2	8	1.221402803	2	0	0.823045267	0
MS3_08727	0.2	0.33	0.6	0.49	0.7	7.44	7.16	1.323130155	6	1	2.469135802	3.448275862
MS3_00178	0.21	0.34	0.56	0.46	0.66	8.27	8.12	1.161834269	3	0	1.234567901	0
MS3_05910	0.21	0.34	0.57	0.44	0.69	7.84	8.09	0.778800736	1	1	0.411522634	3.448275862
MS3_05976	0.21	0.34	0.57	0.45	0.68	7.18	7.38	0.818730596	0	0	0	0
MS3_07061	0.21	0.35	0.56	0.45	0.67	8.06	7.88	1.197217415	5	0	2.057613169	0
MS3_07799	0.21	0.34	0.56	0.45	0.67	8.63	8.79	0.852143782	3	0	1.234567901	0
MS3_09271	0.21	0.35	0.59	0.49	0.7	6.75	6.99	0.78662745	1	0	0.411522634	0
MS3_00047	0.22	0.35	0.58	0.48	0.68	9.29	9.55	0.771051583	80	9	32.9218107	31.03448276
MS3_01313	0.22	0.36	0.47	0.34	0.6	9.48	9.21	1.309964456	77	9	31.6872428	31.03448276
MS3_02087	0.22	0.35	0.63	0.54	0.73	8.89	9.05	0.852143785	20	0	8.230452675	0
MS3_02804	0.22	0.36	0.56	0.47	0.66	9.69	9.52	1.185304853	94	5	38.68312757	17.24137931
MS3_05226	0.22	0.36	0.52	0.43	0.62	8.47	8.29	1.197217386	10	0	4.115226337	0
MS3_09846	0.22	0.36	0.64	0.52	0.76	8.55	8.87	0.726149024	16	4	6.58436214	13.79310345
MS3_01558	0.23	0.36	0.57	0.46	0.68	6.87	7.07	0.818730462	1	0	0.411522634	0
MS3_01636	0.23	0.37	0.59	0.47	0.71	7.81	7.58	1.258600131	6	1	2.469135802	3.448275862
MS3_02758	0.23	0.36	0.57	0.48	0.67	8.7	8.88	0.835270204	20	1	8.230452675	3.448275862
MS3_03091	0.23	0.36	0.54	0.44	0.64	8.45	8.27	1.197217387	11	0	4.526748971	0
MS3_05911	0.23	0.37	0.6	0.5	0.71	9.13	9.38	0.778800779	53	9	21.81069959	31.03448276
MS3_06223	0.23	0.37	0.56	0.45	0.66	6.62	6.46	1.173511658	0	0	0	0
MS3_08361	0.23	0.37	0.48	0.39	0.57	8.81	9	0.826959128	22	0	9.053497942	0
MS3_09634	0.23	0.37	0.56	0.45	0.67	8.57	8.73	0.852143781	1	1	0.411522634	3.448275862
MS3_10225	0.23	0.37	0.54	0.44	0.65	9.76	9.93	0.843664816	143	17	58.84773663	58.62068966
MS3_00066	0.24	0.38	0.58	0.45	0.7	8.4	8.6	0.818730739	5	2	2.057613169	6.896551724
MS3_01542	0.24	0.38	0.55	0.45	0.66	10.03	10.2	0.843664816	171	20	70.37037037	68.96551724
MS3_03429	0.24	0.38	0.46	0.36	0.57	9.01	8.72	1.336427504	64	3	26.33744856	10.34482759
MS3_06101	0.24	0.37	0.57	0.46	0.68	8.71	8.88	0.84366481	11	3	4.526748971	10.34482759
MS3_06471	0.24	0.38	0.61	0.5	0.72	8.67	8.86	0.826959126	12	0	4.938271605	0

MS3_08450	0.24	0.38	0.58	0.48	0.68	8.96	8.68	1.323129829	39	1	16.04938272	3.448275862
MS3_09283	0.24	0.37	0.57	0.46	0.68	8.05	8.21	0.852143765	1	0	0.411522634	0
MS3_02641	0.25	0.39	0.55	0.44	0.66	8.51	8.34	1.185304871	6	0	2.469135802	0
MS3_05026	0.25	0.39	0.51	0.4	0.62	9.6	9.74	0.869358234	103	10	42.38683128	34.48275862
MS3_06283	0.25	0.4	0.59	0.47	0.71	8.54	8.75	0.810584235	9	2	3.703703704	6.896551724
MS3_10423	0.25	0.39	0.48	0.36	0.59	9.49	9.28	1.233678064	67	5	27.57201646	17.24137931
MS3_10492	0.25	0.39	0.55	0.44	0.65	9.16	9.32	0.852143786	45	6	18.51851852	20.68965517
MS3_00187	0.26	0.41	0.58	0.47	0.68	8.39	8.56	0.843664804	12	0	4.938271605	0
MS3_05425	0.26	0.41	0.64	0.54	0.74	8.85	9.06	0.81058424	11	3	4.526748971	10.34482759
MS3_08157	0.26	0.4	0.56	0.45	0.67	8.59	8.42	1.185304868	11	0	4.526748971	0
MS3_08929	0.26	0.4	0.47	0.36	0.57	8.43	8.24	1.209249624	16	0	6.58436214	0
MS3_09110	0.26	0.4	0.59	0.48	0.7	8.42	8.58	0.852143778	1	0	0.411522634	0
MS3_00183	0.27	0.42	0.59	0.49	0.69	9.16	9.4	0.786627858	55	7	22.63374486	24.13793103
MS3_04083	0.27	0.42	0.58	0.47	0.69	11.55	11.16	1.476980794	228	23	93.82716049	79.31034483
MS3_05351	0.27	0.42	0.54	0.43	0.64	6.36	6.2	1.173512195	1	0	0.411522634	0
MS3_09190	0.27	0.42	0.56	0.44	0.67	8.3	8.47	0.843664802	6	0	2.469135802	0
MS3_03443	0.28	0.43	0.53	0.43	0.64	8.09	7.92	1.185304896	13	0	5.349794239	0
MS3_00702	0.28	0.43	0.56	0.46	0.66	8.53	8.68	0.860707968	10	1	4.115226337	3.448275862
MS3_05754	0.28	0.43	0.56	0.45	0.67	8	7.85	1.161834288	0	0	0	0
MS3_09690	0.28	0.43	0.57	0.46	0.68	8.85	9.03	0.835270206	33	4	13.58024691	13.79310345
MS3_02136	0.29	0.44	0.65	0.53	0.76	9.13	9.4	0.763379491	62	15	25.51440329	51.72413793
MS3_04386	0.29	0.44	0.47	0.37	0.57	8.01	7.85	1.17351092	9	0	3.703703704	0
MS3_04962	0.29	0.44	0.61	0.48	0.73	9.04	8.78	1.296930099	37	5	15.22633745	17.24137931
MS3_05735	0.29	0.44	0.55	0.45	0.64	9.08	9.25	0.843664813	41	3	16.87242798	10.34482759
MS3_06462	0.29	0.44	0.52	0.43	0.6	9.59	9.76	0.843664815	106	10	43.62139918	34.48275862
MS3_06825	0.29	0.44	0.55	0.44	0.67	8.6	8.45	1.161834257	7	0	2.880658436	0
MS3_07002	0.29	0.44	0.56	0.45	0.66	8.6	8.74	0.869358228	8	0	3.29218107	0
MS3_09305	0.29	0.44	0.55	0.46	0.65	8.57	8.66	0.91393118	2	0	0.823045267	0
MS3_09993	0.29	0.44	0.45	0.33	0.57	8.46	8.29	1.185304873	7	0	2.880658436	0
MS3_00403	0.3	0.44	0.55	0.44	0.66	8.5	8.35	1.16183426	8	0	3.29218107	0
MS3_00844	0.3	0.45	0.53	0.42	0.63	7.65	7.48	1.18530496	6	0	2.469135802	0
MS3_00876	0.3	0.45	0.58	0.48	0.69	8.5	8.34	1.173510889	11	2	4.526748971	6.896551724
MS3_02486	0.3	0.45	0.55	0.44	0.66	7.79	7.66	1.138828441	1	0	0.411522634	0
MS3_05142	0.3	0.45	0.56	0.45	0.66	8.76	8.89	0.878095426	9	1	3.703703704	3.448275862
MS3_09682	0.3	0.44	0.5	0.4	0.59	9.41	9.6	0.826959132	106	9	43.62139918	31.03448276
MS3_02375	0.31	0.47	0.54	0.43	0.65	8.71	8.57	1.150273809	2	0	0.823045267	0
MS3_02489	0.31	0.46	0.54	0.45	0.63	8.22	8.09	1.138828408	8	1	3.29218107	3.448275862

MS3_03818	0.31	0.46	0.52	0.42	0.63	6.38	6.27	1.11627886	1	0	0.411522634	0
MS3_06431	0.31	0.46	0.56	0.45	0.67	8.32	8.47	0.860707963	5	1	2.057613169	3.448275862
MS3_07716	0.31	0.46	0.55	0.43	0.67	7.93	7.76	1.185304913	8	0	3.29218107	0
MS3_00450	0.32	0.47	0.55	0.45	0.65	8.37	8.26	1.116278085	0	0	0	0
MS3_04493	0.32	0.47	0.58	0.46	0.7	7.91	8.08	0.843664784	2	0	0.823045267	0
MS3_05495	0.32	0.47	0.55	0.42	0.68	8.81	8.61	1.221402772	12	3	4.938271605	10.34482759
MS3_09076	0.32	0.47	0.54	0.43	0.64	8.06	7.88	1.197217415	12	0	4.938271605	0
MS3_09124	0.32	0.47	0.58	0.47	0.68	6.66	6.83	0.843664417	0	0	0	0
MS3_01218	0.33	0.49	0.54	0.43	0.65	8.87	8.72	1.161834251	13	1	5.349794239	3.448275862
MS3_01353	0.33	0.48	0.56	0.45	0.66	7.92	8.06	0.869358207	5	0	2.057613169	0
MS3_02539	0.33	0.48	0.53	0.41	0.65	8.61	8.4	1.233678081	12	0	4.938271605	0
MS3_03084	0.33	0.48	0.58	0.46	0.69	9.89	10.19	0.74081822	127	16	52.26337449	55.17241379
MS3_03405	0.33	0.49	0.55	0.44	0.66	8.46	8.6	0.869358226	4	0	1.646090535	0
MS3_03802	0.33	0.48	0.58	0.47	0.68	9.02	9.23	0.810584242	50	7	20.57613169	24.13793103
MS3_03918	0.33	0.48	0.55	0.43	0.67	8.05	8.21	0.852143765	3	0	1.234567901	0
MS3_08636	0.33	0.48	0.48	0.38	0.58	7.75	7.63	1.127496908	1	0	0.411522634	0
MS3_04053	0.34	0.49	0.44	0.34	0.55	8.98	8.77	1.23367807	48	3	19.75308642	10.34482759
MS3_09273	0.34	0.49	0.56	0.46	0.67	7.8	7.61	1.209249692	6	1	2.469135802	3.448275862
MS3_10600	0.34	0.49	0.55	0.46	0.65	7.46	7.62	0.852143712	2	1	0.823045267	3.448275862
MS3_00383	0.35	0.5	0.55	0.44	0.66	9.24	9.45	0.810584243	58	6	23.86831276	20.68965517
MS3_01104	0.35	0.5	0.52	0.43	0.62	9.5	9.62	0.886920436	104	10	42.79835391	34.48275862
MS3_01286	0.35	0.5	0.56	0.44	0.68	6.63	6.48	1.161834951	0	0	0	0
MS3_01898	0.35	0.5	0.55	0.42	0.68	9.14	8.93	1.233678067	44	6	18.10699588	20.68965517
MS3_05555	0.35	0.5	0.57	0.46	0.67	6.57	6.72	0.860707538	1	0	0.411522634	0
MS3_09406	0.35	0.5	0.54	0.44	0.65	8.4	8.26	1.150273818	14	1	5.761316872	3.448275862
MS3_09620	0.35	0.51	0.56	0.45	0.68	8.27	8.43	0.852143774	2	0	0.823045267	0
MS3_10297	0.35	0.5	0.55	0.44	0.66	7.56	7.74	0.835270143	3	0	1.234567901	0
MS3_10486	0.35	0.5	0.57	0.46	0.68	9.94	10.11	0.843664816	170	22	69.95884774	75.86206897
MS3_10607	0.35	0.5	0.5	0.41	0.6	6.67	6.55	1.127497344	4	0	1.646090535	0
MS3_11526	0.35	0.5	0.59	0.5	0.69	9.22	9.41	0.826959131	62	7	25.51440329	24.13793103
MS3_00850	0.37	0.53	0.59	0.48	0.71	8.44	8.61	0.843664805	20	2	8.230452675	6.896551724
MS3_02954	0.37	0.53	0.56	0.44	0.67	8.54	8.36	1.197217383	15	1	6.172839506	3.448275862
MS3_03558	0.37	0.53	0.48	0.38	0.58	8.23	8.36	0.878095417	2	1	0.823045267	3.448275862
MS3_05959	0.38	0.54	0.55	0.44	0.65	9.26	9.06	1.221402764	42	3	17.28395062	10.34482759
MS3_09546	0.38	0.53	0.49	0.38	0.6	8.9	8.76	1.150273806	27	1	11.11111111	3.448275862
MS3_10898	0.38	0.53	0.61	0.5	0.72	9.57	9.77	0.818730752	115	15	47.32510288	51.72413793
MS3_11161	0.38	0.54	0.56	0.45	0.66	7.44	7.31	1.1388285	1	0	0.411522634	0

MS3_00508	0.39	0.54	0.48	0.36	0.59	9.05	8.76	1.336427503	69	7	28.39506173	24.13793103
MS3_03513	0.39	0.55	0.57	0.45	0.69	6.76	6.61	1.161834789	4	0	1.646090535	0
MS3_06704	0.39	0.54	0.54	0.42	0.65	8.83	8.69	1.150273807	6	1	2.469135802	3.448275862
MS3_10900	0.39	0.55	0.57	0.46	0.68	7	7.17	0.843664614	3	1	1.234567901	3.448275862
MS3_03372	0.4	0.55	0.56	0.45	0.68	8.99	9.18	0.82695913	39	5	16.04938272	17.24137931
MS3_03571	0.4	0.56	0.58	0.47	0.69	7.79	7.92	0.878095396	2	0	0.823045267	0
MS3_05952	0.4	0.55	0.51	0.41	0.61	9.14	8.96	1.197217369	38	1	15.63786008	3.448275862
MS3_06488	0.4	0.56	0.56	0.45	0.66	8.89	9.17	0.755783735	67	5	27.57201646	17.24137931
MS3_08415	0.4	0.56	0.49	0.39	0.58	7.8	7.71	1.09417432	3	0	1.234567901	0
MS3_09128	0.4	0.56	0.57	0.46	0.69	8.67	8.87	0.818730745	35	6	14.40329218	20.68965517
MS3_01030	0.41	0.57	0.55	0.44	0.66	8.73	8.91	0.835270205	24	1	9.87654321	3.448275862
MS3_03206	0.41	0.56	0.55	0.45	0.66	8.92	9.09	0.843664812	37	6	15.22633745	20.68965517
MS3_07918	0.41	0.57	0.54	0.44	0.65	8.69	8.85	0.852143782	33	2	13.58024691	6.896551724
MS3_09443	0.41	0.56	0.55	0.45	0.65	8.35	8.24	1.116278086	1	0	0.411522634	0
MS3_10513	0.41	0.57	0.48	0.39	0.58	8.62	8.7	0.923116342	2	0	0.823045267	0
MS3_11544	0.41	0.57	0.52	0.42	0.62	9.57	9.68	0.895834134	97	11	39.91769547	37.93103448
MS3_01693	0.42	0.58	0.55	0.45	0.65	7.66	7.79	0.878095386	0	0	0	0
MS3_06889	0.42	0.58	0.55	0.44	0.65	9.05	8.88	1.185304858	43	2	17.69547325	6.896551724
MS3_05908	0.43	0.59	0.53	0.42	0.64	8.78	8.66	1.127496859	20	1	8.230452675	3.448275862
MS3_10397	0.43	0.59	0.55	0.45	0.65	7.71	7.88	0.843664768	8	1	3.29218107	3.448275862
MS3_03973	0.44	0.6	0.56	0.44	0.67	7.34	7.46	0.886920357	0	0	0	0
MS3_04559	0.44	0.6	0.49	0.38	0.61	8.69	8.55	1.150273809	17	0	6.995884774	0
MS3_04820	0.44	0.6	0.51	0.42	0.61	9.66	9.47	1.2092496	102	7	41.97530864	24.13793103
MS3_06677	0.44	0.6	0.55	0.42	0.67	7.91	8.06	0.860707946	1	0	0.411522634	0
MS3_06789	0.44	0.6	0.54	0.43	0.65	8.61	8.72	0.895834129	7	0	2.880658436	0
MS3_11484	0.45	0.61	0.56	0.45	0.67	9.16	9.32	0.852143786	67	6	27.57201646	20.68965517
MS3_02368	0.45	0.61	0.54	0.43	0.64	8.03	8.13	0.904837401	3	0	1.234567901	0
MS3_02442	0.45	0.61	0.53	0.42	0.64	9.68	9.79	0.895834135	117	12	48.14814815	41.37931034
MS3_04268	0.45	0.61	0.54	0.43	0.66	7.21	7.12	1.094174402	0	0	0	0
MS3_04285	0.45	0.61	0.5	0.42	0.59	9.7	9.79	0.913931185	117	8	48.14814815	27.5862069
MS3_04781	0.45	0.61	0.53	0.42	0.64	8.79	8.91	0.886920432	17	3	6.995884774	10.34482759
MS3_05520	0.45	0.61	0.54	0.44	0.64	8.48	8.57	0.913931179	3	0	1.234567901	0
MS3_10998	0.45	0.61	0.56	0.45	0.66	9.29	9.43	0.869358234	79	10	32.51028807	34.48275862
MS3_03988	0.46	0.62	0.53	0.41	0.64	7.31	7.21	1.105171028	0	0	0	0
MS3_08480	0.46	0.61	0.56	0.45	0.66	10.35	10.12	1.258600011	194	21	79.83539095	72.4137931
MS3_09879	0.46	0.61	0.52	0.41	0.63	7.31	7.21	1.105171028	0	0	0	0
MS3_00808	0.47	0.63	0.54	0.44	0.64	9	9.1	0.904837416	26	2	10.69958848	6.896551724

MS3_01051	0.47	0.63	0.48	0.39	0.57	8.67	8.59	1.083287073	14	0	5.761316872	0
MS3_03119	0.47	0.62	0.54	0.42	0.65	7.89	8.01	0.88692041	2	0	0.823045267	0
MS3_08725	0.47	0.62	0.53	0.44	0.63	8.87	8.99	0.886920433	49	2	20.16460905	6.896551724
MS3_09961	0.47	0.63	0.55	0.44	0.65	9.54	9.39	1.161834245	107	10	44.03292181	34.48275862
MS3_11280	0.47	0.63	0.48	0.39	0.58	8.07	7.97	1.105170942	9	0	3.703703704	0
MS3_01096	0.48	0.63	0.49	0.39	0.6	8.05	7.93	1.127496883	21	0	8.641975309	0
MS3_04147	0.48	0.63	0.54	0.42	0.66	7.74	7.6	1.150273869	6	0	2.469135802	0
MS3_05284	0.48	0.63	0.55	0.42	0.67	8.29	8.4	0.895834124	1	0	0.411522634	0
MS3_05389	0.48	0.63	0.52	0.41	0.63	7.37	7.25	1.127496973	2	0	0.823045267	0
MS3_06258	0.48	0.63	0.56	0.44	0.68	8.66	8.51	1.161834255	16	4	6.58436214	13.79310345
MS3_10188	0.48	0.63	0.51	0.39	0.63	7.12	6.96	1.17351116	10	0	4.115226337	0
MS3_00242	0.49	0.63	0.55	0.45	0.65	9.02	9.18	0.852143786	50	4	20.57613169	13.79310345
MS3_01004	0.49	0.63	0.53	0.41	0.64	9.74	9.94	0.818730752	131	16	53.90946502	55.17241379
MS3_01705	0.49	0.63	0.52	0.42	0.62	6.06	5.99	1.07250906	0	0	0	0
MS3_05896	0.49	0.64	0.48	0.38	0.58	8.16	8.24	0.923116335	0	0	0	0
MS3_06347	0.49	0.63	0.56	0.45	0.67	8.71	8.61	1.105170925	10	1	4.115226337	3.448275862
MS3_07693	0.49	0.64	0.52	0.42	0.63	10.47	10.31	1.173510871	193	21	79.42386831	72.4137931
MS3_07874	0.49	0.63	0.59	0.48	0.71	9.18	9.33	0.860707974	53	8	21.81069959	27.5862069
MS3_09698	0.49	0.63	0.54	0.43	0.65	8.1	8.01	1.094174304	1	0	0.411522634	0
MS3_00663	0.5	0.65	0.55	0.45	0.66	7.6	7.5	1.105170979	2	1	0.823045267	3.448275862
MS3_03130	0.5	0.65	0.59	0.48	0.7	7.75	7.62	1.138828446	2	1	0.823045267	3.448275862
MS3_08283	0.5	0.65	0.52	0.41	0.64	7.86	7.75	1.116278111	4	0	1.646090535	0
MS3_05484	0.51	0.66	0.53	0.41	0.64	7.62	7.51	1.116278137	6	0	2.469135802	0
MS3_09829	0.51	0.66	0.5	0.39	0.6	6.5	6.42	1.083287493	1	0	0.411522634	0
MS3_01318	0.52	0.66	0.56	0.45	0.67	9.04	9.25	0.810584242	79	11	32.51028807	37.93103448
MS3_04595	0.52	0.67	0.57	0.47	0.68	7.77	7.94	0.843664773	29	0	11.93415638	0
MS3_04642	0.52	0.67	0.49	0.39	0.6	9.08	9.18	0.904837416	45	5	18.51851852	17.24137931
MS3_07096	0.52	0.67	0.55	0.44	0.66	7.8	7.89	0.91393116	3	0	1.234567901	0
MS3_08037	0.52	0.67	0.53	0.42	0.64	8.62	8.53	1.094174291	3	0	1.234567901	0
MS3_00610	0.53	0.67	0.54	0.44	0.64	8.85	8.98	0.878095427	25	2	10.28806584	6.896551724
MS3_01105	0.53	0.68	0.51	0.4	0.61	7.54	7.44	1.105170987	1	0	0.411522634	0
MS3_03937	0.53	0.68	0.57	0.48	0.66	9.13	9	1.138828387	55	1	22.63374486	3.448275862
MS3_06807	0.53	0.67	0.55	0.43	0.66	7.67	7.8	0.878095387	5	0	2.057613169	0
MS3_07738	0.53	0.68	0.5	0.39	0.61	8.36	8.24	1.127496868	17	0	6.995884774	0
MS3_08840	0.53	0.67	0.55	0.44	0.66	8.25	8.35	0.904837407	5	0	2.057613169	0
MS3_10811	0.53	0.67	0.54	0.44	0.65	8.49	8.37	1.127496864	20	2	8.230452675	6.896551724
MS3_10931	0.53	0.68	0.54	0.42	0.65	7.94	8.03	0.913931166	2	0	0.823045267	0

MS3_00756	0.54	0.68	0.5	0.4	0.6	9.47	9.6	0.87809543	98	9	40.32921811	31.03448276
MS3_03599	0.54	0.69	0.59	0.48	0.69	10.11	10.01	1.105170918	191	17	78.60082305	58.62068966
MS3_10249	0.54	0.68	0.54	0.43	0.64	8.59	8.67	0.923116342	11	0	4.526748971	0
MS3_00277	0.55	0.69	0.53	0.44	0.63	10.73	10.51	1.246076731	160	15	65.8436214	51.72413793
MS3_00312	0.55	0.69	0.49	0.37	0.61	9.57	9.42	1.161834245	96	12	39.50617284	41.37931034
MS3_01840	0.55	0.69	0.51	0.41	0.6	9.46	9.53	0.932393819	80	7	32.9218107	24.13793103
MS3_05126	0.55	0.69	0.51	0.39	0.63	8.98	9.17	0.82695913	36	4	14.81481481	13.79310345
MS3_11077	0.55	0.69	0.52	0.41	0.63	7.8	7.72	1.083287099	1	0	0.411522634	0
MS3_01257	0.56	0.7	0.54	0.45	0.64	7.82	7.98	0.852143751	33	2	13.58024691	6.896551724
MS3_02041	0.56	0.7	0.52	0.43	0.61	8.16	8.23	0.93239381	0	0	0	0
MS3_03872	0.56	0.7	0.54	0.45	0.62	9.5	9.38	1.127496853	93	4	38.27160494	13.79310345
MS3_09739	0.56	0.7	0.53	0.42	0.64	8.2	8.29	0.913931174	4	1	1.646090535	3.448275862
MS3_00054	0.57	0.71	0.56	0.47	0.66	8.1	8.16	0.941764524	6	0	2.469135802	0
MS3_00449	0.57	0.71	0.54	0.43	0.66	7.82	7.91	0.913931161	2	0	0.823045267	0
MS3_00504	0.57	0.71	0.5	0.4	0.6	8.56	8.48	1.083287075	17	0	6.995884774	0
MS3_03963	0.57	0.71	0.5	0.39	0.6	7.18	7.11	1.072508275	2	0	0.823045267	0
MS3_11226	0.57	0.71	0.57	0.45	0.68	7.99	8.08	0.913931168	0	0	0	0
MS3_00405	0.58	0.72	0.53	0.42	0.63	8.37	8.29	1.083287078	3	0	1.234567901	0
MS3_01386	0.58	0.72	0.46	0.34	0.57	8.25	8.36	0.895834123	11	1	4.526748971	3.448275862
MS3_03041	0.58	0.72	0.49	0.39	0.59	6.67	6.59	1.08328737	1	0	0.411522634	0
MS3_05002	0.58	0.71	0.54	0.43	0.66	8.38	8.46	0.923116339	1	0	0.411522634	0
MS3_05230	0.58	0.72	0.51	0.42	0.59	8.44	8.39	1.051271102	4	0	1.646090535	0
MS3_06994	0.58	0.72	0.57	0.49	0.66	9.45	9.39	1.061836547	69	3	28.39506173	10.34482759
MS3_11293	0.58	0.72	0.55	0.45	0.65	9.45	9.57	0.886920436	95	10	39.09465021	34.48275862
MS3_02172	0.59	0.72	0.52	0.42	0.63	10.02	10.09	0.93239382	152	18	62.55144033	62.06896552
MS3_05447	0.59	0.72	0.59	0.47	0.7	7.58	7.45	1.138828471	7	1	2.880658436	3.448275862
MS3_07037	0.59	0.72	0.51	0.38	0.64	8.49	8.39	1.105170928	2	0	0.823045267	0
MS3_00413	0.6	0.73	0.55	0.44	0.66	7.84	7.76	1.083287097	1	1	0.411522634	3.448275862
MS3_04717	0.6	0.73	0.55	0.46	0.64	7.41	7.49	0.923116296	4	0	1.646090535	0
MS3_05631	0.6	0.73	0.56	0.47	0.64	9.83	9.74	1.094174284	129	8	53.08641975	27.5862069
MS3_09161	0.6	0.73	0.51	0.4	0.62	9.12	9.05	1.072508183	28	0	11.52263374	0
MS3_00787	0.61	0.74	0.51	0.41	0.62	10.67	10.76	0.913931185	233	26	95.88477366	89.65517241
MS3_02476	0.61	0.74	0.55	0.44	0.66	8.38	8.28	1.105170931	9	2	3.703703704	6.896551724
MS3_02504	0.61	0.74	0.52	0.4	0.64	8.44	8.35	1.094174294	9	1	3.703703704	3.448275862
MS3_05761	0.61	0.74	0.56	0.46	0.67	6.26	6.31	0.951229094	0	0	0	0
MS3_06468	0.61	0.74	0.52	0.42	0.61	7.8	7.73	1.072508208	1	0	0.411522634	0
MS3_06769	0.61	0.74	0.53	0.43	0.63	7.91	7.84	1.072508203	2	1	0.823045267	3.448275862

MS3_00361	0.62	0.74	0.51	0.41	0.61	8.87	8.99	0.886920433	55	5	22.63374486	17.24137931
MS3_01435	0.63	0.76	0.51	0.4	0.62	8.14	8.07	1.072508195	4	0	1.646090535	0
MS3_02359	0.63	0.76	0.54	0.43	0.66	7.46	7.53	0.93239378	3	0	1.234567901	0
MS3_02951	0.63	0.76	0.48	0.37	0.58	10.59	10.53	1.061836547	237	25	97.5308642	86.20689655
MS3_03406	0.63	0.76	0.55	0.44	0.65	8.19	8.27	0.923116336	5	0	2.057613169	0
MS3_07587	0.63	0.76	0.52	0.41	0.62	9.84	9.91	0.93239382	133	16	54.73251029	55.17241379
MS3_00665	0.64	0.76	0.53	0.42	0.65	7.08	7.16	0.92311625	2	0	0.823045267	0
MS3_00404	0.65	0.78	0.51	0.41	0.62	8.86	8.91	0.951229423	8	1	3.29218107	3.448275862
MS3_02991	0.65	0.77	0.52	0.42	0.63	9.19	9.09	1.105170921	61	6	25.10288066	20.68965517
MS3_10085	0.65	0.78	0.55	0.45	0.64	9.68	9.59	1.094174285	105	7	43.20987654	24.13793103
MS3_01406	0.66	0.79	0.51	0.41	0.62	9.17	9.1	1.072508183	50	5	20.57613169	17.24137931
MS3_04117	0.66	0.79	0.5	0.4	0.6	6.22	6.16	1.061837082	2	0	0.823045267	0
MS3_05157	0.66	0.79	0.47	0.36	0.58	7.93	7.86	1.072508202	1	0	0.411522634	0
MS3_09233	0.66	0.79	0.52	0.42	0.61	8.83	8.9	0.932393817	18	0	7.407407407	0
MS3_08446	0.67	0.79	0.48	0.37	0.6	8.25	8.19	1.061836556	1	0	0.411522634	0
MS3_04873	0.67	0.79	0.54	0.42	0.66	8.83	8.93	0.904837415	28	4	11.52263374	13.79310345
MS3_05360	0.67	0.79	0.53	0.41	0.64	8.13	8.2	0.932393809	0	0	0	0
MS3_07565	0.67	0.79	0.54	0.44	0.64	8.35	8.29	1.061836554	2	0	0.823045267	0
MS3_08432	0.67	0.79	0.52	0.42	0.63	9.16	9.26	0.904837416	50	5	20.57613169	17.24137931
MS3_08871	0.67	0.79	0.52	0.43	0.61	8.9	8.86	1.040810776	18	0	7.407407407	0
MS3_04817	0.68	0.79	0.56	0.45	0.66	8.01	8.07	0.941764522	3	0	1.234567901	0
MS3_05958	0.68	0.8	0.53	0.43	0.63	8.79	8.87	0.923116343	30	2	12.34567901	6.896551724
MS3_04355	0.69	0.8	0.49	0.39	0.59	8.32	8.38	0.941764527	2	0	0.823045267	0
MS3_04584	0.69	0.81	0.55	0.44	0.65	10.33	10.39	0.941764533	204	25	83.95061728	86.20689655
MS3_04799	0.69	0.8	0.5	0.39	0.62	7.13	7.26	0.878095302	14	2	5.761316872	6.896551724
MS3_01600	0.7	0.82	0.53	0.43	0.63	8.48	8.54	0.941764529	9	0	3.703703704	0
MS3_03079	0.7	0.82	0.51	0.4	0.62	9.29	9.17	1.127496854	105	12	43.20987654	41.37931034
MS3_05332	0.7	0.81	0.58	0.48	0.69	9.27	9.34	0.932393819	50	5	20.57613169	17.24137931
MS3_08162	0.7	0.81	0.53	0.43	0.62	9.14	9.22	0.923116345	57	6	23.45679012	20.68965517
MS3_11076	0.7	0.82	0.49	0.38	0.6	8.92	8.86	1.061836549	30	0	12.34567901	0
MS3_02396	0.71	0.82	0.52	0.41	0.63	8.83	8.88	0.951229423	13	0	5.349794239	0
MS3_06257	0.71	0.83	0.54	0.41	0.66	8.19	8.3	0.895834122	9	2	3.703703704	6.896551724
MS3_06690	0.71	0.82	0.49	0.38	0.61	10.72	10.82	0.904837418	214	23	88.06584362	79.31034483
MS3_07420	0.71	0.82	0.5	0.37	0.62	7.14	7.22	0.923116261	1	1	0.411522634	3.448275862
MS3_09793	0.71	0.83	0.53	0.41	0.64	8.49	8.44	1.051271101	2	0	0.823045267	0
MS3_10588	0.71	0.82	0.58	0.46	0.7	8.36	8.52	0.852143776	42	7	17.28395062	24.13793103
MS3_01964	0.72	0.83	0.48	0.37	0.6	8.21	8.27	0.941764526	0	0	0	0

MS3_06108	0.72	0.83	0.52	0.42	0.63	8.47	8.56	0.913931179	35	1	14.40329218	3.448275862
MS3_08618	0.72	0.83	0.5	0.39	0.61	8.8	8.75	1.051271099	12	0	4.938271605	0
MS3_09188	0.72	0.83	0.51	0.4	0.62	10.75	10.65	1.105170918	239	26	98.35390947	89.65517241
MS3_01780	0.73	0.84	0.52	0.42	0.62	6.17	6.14	1.030454813	0	0	0	0
MS3_04100	0.73	0.84	0.52	0.4	0.64	8.11	8.06	1.051271106	2	0	0.823045267	0
MS3_05427	0.73	0.84	0.54	0.44	0.64	8.3	8.35	0.951229419	7	1	2.880658436	3.448275862
MS3_05437	0.73	0.84	0.54	0.43	0.65	7.85	7.89	0.960789428	2	0	0.823045267	0
MS3_07617	0.73	0.84	0.52	0.39	0.65	8.39	8.32	1.07250819	3	0	1.234567901	0
MS3_07988	0.73	0.84	0.5	0.4	0.6	10.35	10.44	0.913931185	162	20	66.66666667	68.96551724
MS3_08539	0.73	0.84	0.49	0.38	0.6	8.18	8.13	1.051271105	0	0	0	0
MS3_00294	0.74	0.84	0.52	0.42	0.63	8.43	8.47	0.960789436	3	0	1.234567901	0
MS3_02318	0.74	0.84	0.51	0.4	0.62	9.25	9.14	1.116278073	102	11	41.97530864	37.93103448
MS3_03817	0.74	0.85	0.55	0.45	0.64	9.24	9.15	1.094174286	104	7	42.79835391	24.13793103
MS3_07280	0.74	0.85	0.51	0.4	0.63	8.11	8.06	1.051271106	0	0	0	0
MS3_01952	0.75	0.85	0.5	0.39	0.61	8.5	8.46	1.040810778	11	1	4.526748971	3.448275862
MS3_04582	0.75	0.85	0.48	0.35	0.61	8.87	8.92	0.951229423	12	4	4.938271605	13.79310345
MS3_05283	0.75	0.85	0.52	0.42	0.62	8.45	8.4	1.051271101	19	0	7.818930041	0
MS3_06592	0.75	0.85	0.53	0.43	0.64	7.05	6.99	1.061836648	5	1	2.057613169	3.448275862
MS3_00668	0.76	0.86	0.49	0.38	0.6	10.35	10.27	1.083287068	185	22	76.13168724	75.86206897
MS3_02085	0.76	0.86	0.52	0.41	0.63	9.86	9.78	1.083287068	171	18	70.37037037	62.06896552
MS3_04206	0.76	0.86	0.51	0.41	0.6	8.41	8.44	0.970445531	2	0	0.823045267	0
MS3_06868	0.76	0.86	0.5	0.4	0.61	9.75	9.82	0.932393819	125	12	51.44032922	41.37931034
MS3_07195	0.76	0.86	0.51	0.41	0.61	7.84	7.79	1.051271114	2	0	0.823045267	0
MS3_09240	0.76	0.86	0.5	0.41	0.6	8.39	8.36	1.030454537	11	0	4.526748971	0
MS3_09434	0.76	0.86	0.49	0.39	0.6	8.86	8.93	0.932393817	23	1	9.465020576	3.448275862
MS3_11074	0.76	0.85	0.5	0.41	0.6	7.96	7.92	1.040810785	4	0	1.646090535	0
MS3_01664	0.77	0.86	0.51	0.4	0.63	8.12	8.17	0.951229416	5	1	2.057613169	3.448275862
MS3_05587	0.77	0.86	0.53	0.4	0.66	7	7.07	0.932393719	3	1	1.234567901	3.448275862
MS3_06944	0.77	0.86	0.55	0.45	0.64	9.56	9.59	0.970445533	87	6	35.80246914	20.68965517
MS3_07520	0.77	0.86	0.53	0.41	0.65	8.18	8.23	0.951229417	5	1	2.057613169	3.448275862
MS3_08440	0.77	0.86	0.55	0.43	0.67	8.86	8.92	0.941764531	28	3	11.52263374	10.34482759
MS3_08479	0.77	0.86	0.51	0.43	0.6	9.48	9.44	1.040810775	82	5	33.74485597	17.24137931
MS3_07831	0.78	0.87	0.5	0.38	0.61	8.6	8.64	0.960789437	6	1	2.469135802	3.448275862
MS3_09613	0.78	0.87	0.5	0.41	0.59	9.6	9.57	1.030454534	83	4	34.1563786	13.79310345
MS3_10194	0.78	0.87	0.54	0.42	0.66	8.35	8.26	1.094174296	32	4	13.16872428	13.79310345
MS3_10472	0.78	0.87	0.49	0.37	0.6	8.53	8.57	0.960789436	4	0	1.646090535	0
MS3_02453	0.79	0.88	0.53	0.42	0.64	7.76	7.8	0.960789426	1	0	0.411522634	0

MS3_07405	0.79	0.88	0.53	0.4	0.65	8.33	8.27	1.061836554	15	3	6.172839506	10.34482759
MS3_00859	0.8	0.88	0.53	0.41	0.65	6.39	6.34	1.051271408	4	0	1.646090535	0
MS3_02465	0.8	0.88	0.51	0.39	0.62	7.4	7.44	0.960789412	0	0	0	0
MS3_03192	0.8	0.88	0.53	0.43	0.62	8.21	8.24	0.970445529	13	0	5.349794239	0
MS3_08444	0.8	0.88	0.5	0.41	0.59	8.92	8.89	1.030454535	25	0	10.28806584	0
MS3_08504	0.8	0.88	0.53	0.41	0.64	8.18	8.22	0.960789433	4	0	1.646090535	0
MS3_03856	0.81	0.89	0.5	0.41	0.6	8.45	8.48	0.970445531	1	0	0.411522634	0
MS3_04221	0.81	0.89	0.53	0.42	0.64	8.71	8.67	1.040810777	5	1	2.057613169	3.448275862
MS3_08337	0.81	0.89	0.5	0.4	0.61	7.46	7.5	0.960789415	1	1	0.411522634	3.448275862
MS3_08503	0.81	0.89	0.5	0.4	0.61	7.48	7.45	1.030454554	0	0	0	0
MS3_00203	0.82	0.89	0.5	0.38	0.61	8.67	8.63	1.040810777	9	1	3.703703704	3.448275862
MS3_00353	0.82	0.89	0.57	0.47	0.68	9.79	9.85	0.941764533	136	19	55.96707819	65.51724138
MS3_01972	0.82	0.89	0.52	0.38	0.65	8.17	8.22	0.951229417	4	0	1.646090535	0
MS3_01988	0.82	0.89	0.54	0.41	0.67	9.62	9.53	1.094174285	96	11	39.50617284	37.93103448
MS3_02237	0.82	0.89	0.52	0.43	0.61	8.64	8.61	1.030454536	21	1	8.641975309	3.448275862
MS3_07650	0.82	0.89	0.51	0.41	0.6	10.29	10.24	1.051271097	160	19	65.8436214	65.51724138
MS3_07822	0.82	0.89	0.5	0.38	0.61	7.47	7.51	0.960789415	1	0	0.411522634	0
MS3_07885	0.82	0.89	0.5	0.39	0.61	8.17	8.14	1.030454539	2	0	0.823045267	0
MS3_05939	0.83	0.9	0.52	0.41	0.63	8.09	8.12	0.970445528	0	0	0	0
MS3_08159	0.83	0.9	0.54	0.44	0.64	8.22	8.25	0.970445529	7	0	2.880658436	0
MS3_01240	0.84	0.91	0.5	0.4	0.6	8.59	8.62	0.970445532	19	1	7.818930041	3.448275862
MS3_02088	0.84	0.9	0.47	0.35	0.58	8.11	8.14	0.970445528	3	0	1.234567901	0
MS3_07464	0.84	0.9	0.51	0.4	0.63	8.88	8.83	1.051271099	26	1	10.69958848	3.448275862
MS3_07729	0.84	0.9	0.5	0.37	0.63	8.28	8.24	1.04081078	8	0	3.29218107	0
MS3_10116	0.84	0.91	0.5	0.38	0.62	8.87	8.83	1.040810776	24	3	9.87654321	10.34482759
MS3_10572	0.84	0.91	0.53	0.42	0.63	9.35	9.4	0.951229424	81	10	33.33333333	34.48275862
MS3_04266	0.85	0.91	0.54	0.43	0.64	8.96	8.94	1.020201341	16	1	6.58436214	3.448275862
MS3_05125	0.85	0.91	0.47	0.35	0.59	8.02	7.95	1.072508199	34	6	13.99176955	20.68965517
MS3_06147	0.85	0.91	0.5	0.39	0.62	7.79	7.76	1.030454545	0	0	0	0
MS3_07651	0.85	0.91	0.51	0.41	0.61	8.61	8.65	0.960789437	30	2	12.34567901	6.896551724
MS3_10161	0.85	0.91	0.5	0.4	0.61	8.4	8.38	1.020201342	3	0	1.234567901	0
MS3_01124	0.86	0.92	0.49	0.39	0.58	8.66	8.64	1.020201341	5	0	2.057613169	0
MS3_05222	0.86	0.92	0.5	0.39	0.6	9.79	9.81	0.980198673	130	14	53.49794239	48.27586207
MS3_06248	0.86	0.91	0.48	0.39	0.58	8.81	8.85	0.960789438	29	1	11.93415638	3.448275862
MS3_08276	0.86	0.91	0.51	0.4	0.63	8.95	8.91	1.040810776	48	5	19.75308642	17.24137931
MS3_10044	0.86	0.92	0.55	0.45	0.66	6.35	6.38	0.970445361	1	0	0.411522634	0
MS3_03726	0.87	0.92	0.5	0.39	0.62	8.69	8.67	1.020201341	14	2	5.761316872	6.896551724

MS3_03800	0.87	0.92	0.48	0.36	0.6	7.59	7.64	0.951229401	1	1	0.411522634	3.448275862
MS3_05192	0.87	0.92	0.5	0.38	0.63	8.61	8.57	1.040810777	11	2	4.526748971	6.896551724
MS3_06348	0.87	0.92	0.54	0.43	0.66	9.17	9.2	0.970445533	64	10	26.33744856	34.48275862
MS3_09489	0.87	0.92	0.5	0.39	0.61	8.98	8.93	1.051271098	55	5	22.63374486	17.24137931
MS3_02307	0.88	0.93	0.52	0.42	0.62	9.22	9.19	1.030454535	62	4	25.51440329	13.79310345
MS3_03140	0.88	0.93	0.52	0.4	0.63	9.61	9.59	1.02020134	81	11	33.33333333	37.93103448
MS3_03226	0.88	0.93	0.51	0.4	0.63	8.22	8.2	1.020201343	0	0	0	0
MS3_03577	0.88	0.93	0.52	0.4	0.65	8.25	8.22	1.030454538	1	0	0.411522634	0
MS3_00800	0.89	0.93	0.5	0.39	0.61	7.68	7.66	1.020201349	2	0	0.823045267	0
MS3_07347	0.89	0.93	0.54	0.42	0.65	8.67	8.7	0.970445532	15	2	6.172839506	6.896551724
MS3_09569	0.89	0.93	0.53	0.4	0.65	8.73	8.75	0.980198672	11	1	4.526748971	3.448275862
MS3_09652	0.89	0.93	0.52	0.42	0.62	8.07	8.08	0.990049832	1	0	0.411522634	0
MS3_11428	0.89	0.93	0.53	0.42	0.65	9.06	9.08	0.980198673	19	2	7.818930041	6.896551724
MS3_01364	0.9	0.94	0.5	0.39	0.61	10.19	10.23	0.960789439	151	16	62.1399177	55.17241379
MS3_04540	0.9	0.94	0.52	0.41	0.62	6.65	6.64	1.010050201	3	0	1.234567901	0
MS3_05326	0.9	0.94	0.5	0.39	0.61	7.87	7.89	0.980198668	1	0	0.411522634	0
MS3_03863	0.91	0.95	0.52	0.44	0.61	7.65	7.64	1.010050172	0	0	0	0
MS3_04680	0.91	0.95	0.49	0.4	0.58	7.92	7.94	0.980198668	23	1	9.465020576	3.448275862
MS3_09778	0.91	0.95	0.51	0.41	0.61	8.03	8.01	1.020201344	2	0	0.823045267	0
MS3_02202	0.92	0.96	0.51	0.41	0.61	9.09	9.08	1.010050167	30	1	12.34567901	3.448275862
MS3_03933	0.92	0.96	0.49	0.37	0.62	8.7	8.69	1.010050168	11	1	4.526748971	3.448275862
MS3_06649	0.92	0.95	0.53	0.42	0.64	8.66	8.68	0.980198672	23	2	9.465020576	6.896551724
MS3_11273	0.92	0.95	0.5	0.4	0.6	8.65	8.64	1.010050168	7	0	2.880658436	0
MS3_03231	0.93	0.96	0.51	0.41	0.61	7.98	7.97	1.010050169	2	0	0.823045267	0
MS3_04364	0.93	0.96	0.54	0.43	0.65	9.35	9.33	1.02020134	77	9	31.6872428	31.03448276
MS3_05913	0.93	0.96	0.52	0.41	0.63	8.83	8.85	0.980198672	29	3	11.93415638	10.34482759
MS3_08042	0.93	0.96	0.52	0.39	0.64	8.74	8.76	0.980198672	18	4	7.407407407	13.79310345
MS3_09465	0.93	0.96	0.48	0.38	0.59	7.64	7.63	1.010050172	1	0	0.411522634	0
MS3_11239	0.93	0.96	0.51	0.41	0.61	7.79	7.8	0.99004983	1	0	0.411522634	0
MS3_00931	0.94	0.96	0.5	0.42	0.58	9.79	9.8	0.990049834	111	9	45.67901235	31.03448276
MS3_04275	0.94	0.96	0.48	0.38	0.58	8.76	8.76	1	10	0	4.115226337	0
MS3_06551	0.94	0.96	0.51	0.39	0.62	8.66	8.65	1.010050168	14	3	5.761316872	10.34482759
MS3_07125	0.94	0.96	0.51	0.41	0.6	8.42	8.42	1	4	0	1.646090535	0
MS3_08839	0.94	0.96	0.52	0.42	0.61	8.43	8.42	1.010050168	12	0	4.938271605	0
MS3_09640	0.94	0.96	0.53	0.44	0.62	9.12	9.1	1.020201341	61	4	25.10288066	13.79310345
MS3_01585	0.95	0.97	0.52	0.41	0.62	8.52	8.52	1	1	0	0.411522634	0
MS3_04011	0.95	0.97	0.54	0.41	0.66	7.84	7.86	0.980198667	14	4	5.761316872	13.79310345

MS3_05047	0.95	0.97	0.51	0.41	0.61	9.16	9.17	0.990049834	59	5	24.27983539	17.24137931
MS3_06400	0.95	0.97	0.52	0.39	0.64	8.17	8.18	0.990049832	2	0	0.823045267	0
MS3_00006	0.96	0.97	0.51	0.4	0.63	7.9	7.9	1	1	0	0.411522634	0
MS3_02952	0.96	0.97	0.53	0.42	0.63	7.04	7.04	1	1	1	0.411522634	3.448275862
MS3_04474	0.96	0.97	0.51	0.38	0.63	8.5	8.5	1	5	0	2.057613169	0
MS3_06729	0.96	0.97	0.51	0.39	0.62	8.27	8.27	1	7	0	2.880658436	0
MS3_07299	0.96	0.98	0.51	0.39	0.63	7.76	7.77	0.99004983	3	1	1.234567901	3.448275862
MS3_03615	0.97	0.98	0.57	0.44	0.7	7.56	7.57	0.990049828	27	3	11.11111111	10.34482759
MS3_06740	0.97	0.98	0.5	0.39	0.62	8.06	8.06	1	0	0	0	0
MS3_08655	0.97	0.98	0.55	0.42	0.69	7.65	7.66	0.990049829	13	3	5.349794239	10.34482759
MS3_09333	0.97	0.98	0.52	0.41	0.64	8.62	8.63	0.990049833	9	0	3.703703704	0
MS3_02460	0.98	0.98	0.51	0.4	0.62	8.71	8.72	0.990049833	4	0	1.646090535	0
MS3_08216	0.98	0.99	0.54	0.44	0.64	7.27	7.27	1	0	0	0	0
MS3_09473	0.98	0.98	0.51	0.41	0.61	9.26	9.27	0.990049834	67	8	27.57201646	27.5862069
MS3_02593	0.99	0.99	0.5	0.39	0.62	7.97	7.97	1	2	0	0.823045267	0
MS3_05686	0.99	0.99	0.51	0.41	0.62	9.59	9.58	1.010050167	84	8	34.56790123	27.5862069
MS3_00499	1	1	0.52	0.41	0.63	8.51	8.51	1	37	3	15.22633745	10.34482759
MS3_03511	1	1	0.5	0.41	0.6	8.22	8.22	1	2	0	0.823045267	0

*WormBase ParaSite online database, version 14 https://parasite.wormbase.org/Schistosoma_haematobium_prjna78265/Info/Index/

Table S3. Fold change of IgG responses between infected and non-infected (S. haematobium-endemic) populations resulting from urine sample probing of *S. haematobium* protein arrays.

Antigen (WBPS14* accession)	P value	FDR	AUC	AUC Lower CI	AUC Upper CI	Mean infected	Mean non infected	Fold Change	Positive infected	Positive non infected	Positive infected (%)	Positive non infected (%)
MS3_10385	4.20E-14	4.20E-11	0.93	0.85	1	12	7.5	90.01716	103	2	91.15044	8.33333333
MS3_06193	4.30E-10	1.8E-07	0.83	0.75	0.91	11.14	7.75	29.66596	90	7	79.64602	29.1666667
MS3_10186	5.40E-10	1.8E-07	0.88	0.8	0.97	11.68	7.73	51.93538	99	6	87.61062	25
MS3_02553	0.000000017	0.0000043	0.86	0.77	0.94	10.79	8.87	6.820959	107	18	94.69027	75
MS3_01466	0.000000096	0.000019	0.75	0.66	0.84	9.46	6.96	12.1825	59	7	52.21239	29.1666667
MS3_07702	0.00000012	0.00002	0.76	0.67	0.85	8.94	7.43	4.526732	57	3	50.44248	12.5
MS3_04688	0.00000054	0.000077	0.76	0.66	0.86	8.38	6.96	4.137124	46	2	40.70796	8.33333333
MS3_00996	0.00000075	0.000086	0.7	0.61	0.78	9.62	8.87	2.117	98	22	86.72566	91.6666667
MS3_09198	0.00000078	0.000086	0.83	0.73	0.92	10.65	8.65	7.389056	103	11	91.15044	45.8333333
MS3_01597	0.0000056	0.00056	0.78	0.69	0.86	6.94	7.71	0.463013	5	5	4.424779	20.8333333
MS3_07968	0.0000094	0.00084	0.78	0.69	0.87	7.02	8.41	0.249075	19	13	16.81416	54.1666667
MS3_07481	0.000014	0.0012	0.74	0.63	0.85	9.43	7.82	5.002812	77	9	68.14159	37.5
MS3_09207	0.000018	0.0013	0.68	0.57	0.78	8.11	7.02	2.974276	39	2	34.51327	8.33333333
MS3_00805	0.000028	0.002	0.77	0.68	0.86	7.01	8.58	0.208045	23	15	20.35398	62.5
MS3_07178	0.000032	0.0021	0.66	0.57	0.76	7.35	6.33	2.773202	32	0	28.31858	0
MS3_07693	0.000043	0.0027	0.7	0.6	0.81	10.11	10.98	0.418952	99	24	87.61062	100
MS3_05950	0.000064	0.0036	0.72	0.62	0.82	9.04	7.31	5.640656	64	7	56.63717	29.1666667
MS3_02428	0.000065	0.0036	0.75	0.66	0.85	7.92	7.26	1.934793	33	1	29.20354	4.16666667
MS3_05350	0.000073	0.0036	0.77	0.66	0.89	7.23	8.19	0.382893	13	13	11.50442	54.1666667
MS3_07037	0.000074	0.0036	0.74	0.63	0.85	7.58	8.33	0.472366	19	12	16.81416	50
MS3_05192	0.00008	0.0036	0.73	0.63	0.83	7.7	8.39	0.501576	24	10	21.23894	41.6666667
MS3_08283	0.00008	0.0036	0.76	0.66	0.86	7.63	8.85	0.29523	29	15	25.66372	62.5
MS3_05024	0.000084	0.0036	0.77	0.66	0.87	7.44	8.45	0.364219	20	13	17.69912	54.1666667
MS3_00180	0.000089	0.0037	0.68	0.58	0.79	8.24	7.27	2.637946	42	2	37.16814	8.33333333
MS3_01257	0.0001	0.0041	0.7	0.6	0.81	6.74	5.98	2.138287	13	0	11.50442	0
MS3_04820	0.00012	0.0045	0.77	0.66	0.88	8.86	7.81	2.857652	83	7	73.45133	29.1666667
MS3_05739	0.00012	0.0045	0.77	0.67	0.87	6.31	7.1	0.453844	1	2	0.884956	8.33333333
MS3_01857	0.00013	0.0045	0.75	0.65	0.84	9.57	8.36	3.353485	96	14	84.95575	58.3333333
MS3_08087	0.00013	0.0045	0.77	0.65	0.89	7.66	8.71	0.349938	26	17	23.00885	70.8333333
MS3_07405	0.00014	0.0045	0.73	0.62	0.83	7.61	8.43	0.440432	23	13	20.35398	54.1666667
MS3_03509	0.00015	0.0049	0.74	0.64	0.84	9.44	8.38	2.886371	90	13	79.64602	54.1666667

MS3_09779	0.00017	0.0051	0.66	0.55	0.76	7.49	6.55	2.559986	30	0	26.54867	0
MS3_01365	0.00019	0.0057	0.69	0.59	0.79	8.5	7.73	2.159767	57	6	50.44248	25
MS3_05676	0.0002	0.0059	0.74	0.63	0.85	7.8	8.44	0.527292	25	13	22.12389	54.1666667
MS3_00670	0.00021	0.0059	0.73	0.62	0.84	7.79	8.54	0.472366	33	13	29.20354	54.1666667
MS3_02343	0.00024	0.0067	0.74	0.64	0.84	7.04	7.63	0.554327	5	4	4.424779	16.6666667
MS3_00886	0.00028	0.0074	0.7	0.59	0.8	8.66	7.82	2.316367	63	8	55.75221	33.3333333
MS3_03988	0.00041	0.01	0.75	0.64	0.86	7.02	7.78	0.467666	11	6	9.734513	25
MS3_06551	0.00041	0.01	0.72	0.61	0.83	7.77	8.45	0.506617	26	13	23.00885	54.1666667
MS3_01364	0.00052	0.013	0.66	0.57	0.76	7.67	6.77	2.459606	38	2	33.62832	8.33333333
MS3_01749	0.00053	0.013	0.74	0.65	0.83	9.85	8.95	2.459603	105	19	92.92035	79.1666667
MS3_02688	0.0006	0.014	0.74	0.62	0.86	9.35	8.22	3.095657	96	12	84.95575	50
MS3_10485	0.00078	0.018	0.74	0.62	0.87	7.28	8.38	0.332871	16	14	14.15929	58.3333333
MS3_00203	0.0008	0.018	0.71	0.6	0.82	7.65	8.32	0.511708	21	11	18.58407	45.8333333
MS3_03140	0.0008	0.018	0.74	0.63	0.85	8.84	8.23	1.840431	89	9	78.76106	37.5
MS3_09744	0.00085	0.018	0.72	0.61	0.83	8.99	7.93	2.886371	81	9	71.68142	37.5
MS3_07988	0.00097	0.021	0.7	0.59	0.8	9.56	8.56	2.718282	94	16	83.18584	66.6666667
MS3_07617	0.001	0.021	0.71	0.59	0.82	7.71	8.3	0.554327	24	11	21.23894	45.8333333
MS3_08220	0.0011	0.021	0.73	0.61	0.86	9.06	7.99	2.91538	85	9	75.22124	37.5
MS3_05959	0.0012	0.023	0.65	0.56	0.75	8.52	7.81	2.033992	52	4	46.0177	16.6666667
MS3_06608	0.0012	0.023	0.71	0.6	0.83	7.5	8.31	0.444858	24	11	21.23894	45.8333333
MS3_03603	0.0014	0.027	0.72	0.6	0.84	8.18	7.5	1.973878	50	4	44.24779	16.6666667
MS3_09536	0.0014	0.027	0.72	0.59	0.85	6.63	7.39	0.467666	1	3	0.884956	12.5
MS3_04827	0.0015	0.028	0.72	0.6	0.84	7.97	8.57	0.548812	33	16	29.20354	66.6666667
MS3_07158	0.0015	0.027	0.7	0.59	0.81	7.89	8.48	0.554327	29	12	25.66372	50
MS3_08094	0.0017	0.029	0.71	0.59	0.84	8.18	7.61	1.768267	39	3	34.51327	12.5
MS3_04307	0.0017	0.029	0.65	0.54	0.76	8.18	7.11	2.915381	47	4	41.59292	16.6666667
MS3_05952	0.0017	0.029	0.66	0.56	0.77	8.46	7.72	2.095936	56	4	49.55752	16.6666667
MS3_06258	0.0017	0.029	0.71	0.59	0.83	7.55	8.28	0.481909	21	10	18.58407	41.6666667
MS3_09521	0.0018	0.029	0.71	0.6	0.82	7.44	8.24	0.449329	17	11	15.04425	45.8333333
MS3_01852	0.0019	0.031	0.71	0.62	0.81	6.5	7.05	0.576949	3	2	2.654867	8.33333333
MS3_07972	0.0019	0.031	0.65	0.54	0.76	8.31	7.45	2.363161	51	7	45.13274	29.1666667
MS3_06532	0.002	0.031	0.63	0.52	0.75	8.64	7.85	2.203397	56	7	49.55752	29.1666667
MS3_09690	0.002	0.031	0.69	0.59	0.79	8.23	7.76	1.599994	54	3	47.78761	12.5
MS3_01370	0.0021	0.031	0.66	0.56	0.77	8.11	7.31	2.225542	43	3	38.0531	12.5
MS3_02314	0.0022	0.032	0.69	0.57	0.81	8.01	8.51	0.606531	37	15	32.74336	62.5
MS3_00850	0.0022	0.032	0.7	0.58	0.82	7.74	8.27	0.588605	22	12	19.46903	50
MS3_06825	0.0022	0.032	0.69	0.58	0.8	7.58	8.12	0.582748	19	8	16.81416	33.3333333

MS3_07612	0.0022	0.032	0.71	0.62	0.81	8.42	7.81	1.840432	67	7	59.29204	29.1666667
MS3_10017	0.0022	0.032	0.73	0.61	0.85	7.63	8.4	0.463013	28	14	24.77876	58.3333333
MS3_00277	0.0023	0.033	0.68	0.57	0.79	8.45	7.11	3.819046	52	5	46.0177	20.8333333
MS3_08413	0.0026	0.036	0.68	0.57	0.78	7.86	7.34	1.682028	26	1	23.00885	4.16666667
MS3_05002	0.0028	0.038	0.7	0.58	0.82	7.62	8.2	0.559898	23	11	20.35398	45.8333333
MS3_10378	0.0029	0.038	0.7	0.58	0.81	7.48	8.06	0.559898	15	8	13.27434	33.3333333
MS3_06898	0.0031	0.041	0.67	0.57	0.77	7.69	7.2	1.632317	25	0	22.12389	0
MS3_06944	0.0032	0.042	0.71	0.59	0.84	8.34	7.42	2.509291	65	6	57.52212	25
MS3_05913	0.0033	0.042	0.7	0.59	0.81	7.72	7.03	1.993717	29	2	25.66372	8.33333333
MS3_08432	0.0035	0.044	0.7	0.58	0.82	8.16	7.35	2.247909	52	4	46.0177	16.6666667
MS3_08811	0.0038	0.047	0.7	0.57	0.83	7.81	8.4	0.554327	21	12	18.58407	50
MS3_05976	0.004	0.049	0.68	0.56	0.81	6.95	7.56	0.543351	3	4	2.654867	16.6666667
MS3_09070	0.0045	0.055	0.64	0.54	0.75	6.73	6.14	1.803994	9	0	7.964602	0
MS3_07594	0.0047	0.057	0.66	0.56	0.76	7.3	7.69	0.677057	11	1	9.734513	4.16666667
MS3_10785	0.0048	0.058	0.71	0.58	0.83	6.66	7.27	0.54335	3	2	2.654867	8.33333333
MS3_07763	0.0051	0.06	0.68	0.56	0.8	7.5	8.13	0.532592	17	9	15.04425	37.5
MS3_01030	0.0052	0.061	0.67	0.56	0.78	7.58	6.91	1.954239	35	1	30.97345	4.16666667
MS3_00361	0.0053	0.061	0.7	0.58	0.82	8.26	7.37	2.43513	58	4	51.32743	16.6666667
MS3_01870	0.0053	0.061	0.69	0.56	0.82	7	7.71	0.491644	11	8	9.734513	33.3333333
MS3_02256	0.0054	0.061	0.69	0.57	0.81	7.99	7.51	1.616075	31	4	27.43363	16.6666667
MS3_01193	0.0055	0.061	0.65	0.53	0.78	7.65	7.04	1.840432	26	2	23.00885	8.33333333
MS3_05425	0.0057	0.063	0.7	0.58	0.82	8.56	7.94	1.858928	74	8	65.48673	33.3333333
MS3_05730	0.006	0.066	0.67	0.57	0.78	9.58	8.87	2.033991	95	17	84.0708	70.8333333
No hits	0.0061	0.066	0.67	0.56	0.78	7.03	7.5	0.625002	7	2	6.19469	8.33333333
MS3_05718	0.0063	0.067	0.67	0.57	0.78	7.12	6.38	2.09594	18	1	15.9292	4.16666667
MS3_09700	0.0063	0.067	0.69	0.58	0.8	7.45	7.96	0.600495	16	9	14.15929	37.5
MS3_05539	0.0065	0.068	0.68	0.57	0.8	7.49	8.17	0.506617	18	10	15.9292	41.6666667
MS3_10083	0.0067	0.069	0.66	0.55	0.77	7.8	8.36	0.571209	35	11	30.97345	45.8333333
MS3_01780	0.0068	0.069	0.69	0.58	0.8	6.04	6.49	0.637626	1	0	0.884956	0
MS3_03041	0.0068	0.069	0.68	0.56	0.79	6.43	6.89	0.631283	1	0	0.884956	0
MS3_01585	0.007	0.07	0.67	0.55	0.78	7.82	8.17	0.704688	20	8	17.69912	33.3333333
MS3_02805	0.0071	0.07	0.68	0.56	0.8	8.12	7.48	1.896481	49	5	43.36283	20.8333333
MS3_10184	0.0071	0.07	0.66	0.55	0.77	7.56	6.75	2.24791	36	3	31.85841	12.5
MS3_01337	0.0072	0.07	0.67	0.55	0.78	8.02	7.44	1.786039	39	4	34.51327	16.6666667
MS3_07347	0.0073	0.07	0.67	0.55	0.79	7.64	8.16	0.59452	19	9	16.81416	37.5
MS3_02539	0.0077	0.073	0.67	0.55	0.78	7.66	8.19	0.588605	29	9	25.66372	37.5
MS3_06736	0.0078	0.073	0.67	0.55	0.8	8.12	7.52	1.822119	42	5	37.16814	20.8333333

MS3_05222	0.0079	0.073	0.69	0.58	0.8	8.43	7.58	2.339647	65	8	57.52212	33.3333333
MS3_05496	0.0079	0.073	0.68	0.57	0.79	7.05	7.62	0.565525	9	6	7.964602	25
MS3_03429	0.008	0.073	0.66	0.55	0.77	8.21	7.66	1.733253	53	5	46.90265	20.8333333
MS3_07650	0.008	0.073	0.68	0.56	0.8	8.71	7.88	2.293319	76	9	67.25664	37.5
MS3_06868	0.0085	0.077	0.69	0.55	0.82	8.98	8.21	2.159766	82	11	72.56637	45.8333333
MS3_08455	0.0086	0.077	0.6	0.49	0.72	8.06	7.48	1.786039	34	5	30.0885	20.8333333
MS3_01938	0.0089	0.079	0.69	0.57	0.8	8.94	8.45	1.632316	86	13	76.10619	54.1666667
MS3_04083	0.0097	0.085	0.66	0.56	0.77	10.93	10.5	1.537258	112	24	99.11504	100
MS3_04193	0.0099	0.085	0.69	0.58	0.79	8.29	7.79	1.648721	61	5	53.9823	20.8333333
MS3_04437	0.0099	0.085	0.68	0.56	0.8	7.86	7.45	1.506818	26	2	23.00885	8.33333333
MS3_08618	0.0099	0.085	0.68	0.55	0.8	7.83	8.25	0.657047	24	11	21.23894	45.8333333
MS3_00498	0.01	0.085	0.68	0.57	0.79	8.86	8.17	1.993716	81	11	71.68142	45.8333333
MS3_01141	0.01	0.085	0.67	0.54	0.8	7.06	7.87	0.444858	13	11	11.50442	45.8333333
MS3_02162	0.01	0.085	0.67	0.55	0.78	8.05	7.53	1.682028	43	5	38.0531	20.8333333
MS3_05283	0.01	0.085	0.66	0.55	0.78	7.18	7.74	0.571209	13	6	11.50442	25
MS3_08954	0.01	0.085	0.66	0.53	0.78	7.11	6.46	1.915544	18	2	15.9292	8.33333333
MS3_00808	0.011	0.086	0.68	0.58	0.79	8.75	8.28	1.599994	78	10	69.02655	41.6666667
MS3_04262	0.011	0.086	0.67	0.56	0.78	8.28	7.72	1.750673	59	4	52.21239	16.6666667
MS3_08840	0.011	0.086	0.67	0.56	0.78	8.15	7.71	1.552707	51	5	45.13274	20.8333333
MS3_08975	0.011	0.086	0.58	0.48	0.68	7.83	7.28	1.733254	35	1	30.97345	4.16666667
MS3_09000	0.011	0.086	0.65	0.53	0.76	8.48	7.95	1.698932	54	10	47.78761	41.6666667
MS3_09287	0.011	0.086	0.66	0.55	0.77	8.03	7.47	1.750673	44	3	38.93805	12.5
MS3_10729	0.011	0.086	0.66	0.54	0.78	7.71	8.16	0.637628	19	9	16.81416	37.5
MS3_09396	0.012	0.089	0.66	0.55	0.76	7.87	7.38	1.632317	36	3	31.85841	12.5
MS3_09632	0.012	0.089	0.61	0.51	0.72	7.05	6.64	1.506819	11	1	9.734513	4.16666667
MS3_09692	0.012	0.092	0.69	0.55	0.82	6.44	7.08	0.527291	3	2	2.654867	8.33333333
MS3_00812	0.013	0.094	0.68	0.56	0.79	8.39	7.77	1.858928	63	6	55.75221	25
MS3_02442	0.013	0.095	0.66	0.54	0.79	8.33	7.6	2.075081	56	9	49.55752	37.5
MS3_04117	0.013	0.098	0.67	0.53	0.81	6.3	7.16	0.423161	6	6	5.309735	25
MS3_05322	0.013	0.096	0.67	0.55	0.8	7.91	7.46	1.568312	22	3	19.46903	12.5
MS3_01840	0.014	0.1	0.67	0.55	0.78	8.87	8.25	1.858928	81	13	71.68142	54.1666667
MS3_02758	0.014	0.1	0.67	0.55	0.79	7.79	8.27	0.618783	26	11	23.00885	45.8333333
MS3_05734	0.014	0.1	0.66	0.55	0.77	7.25	7.69	0.644036	16	4	14.15929	16.6666667
MS3_00257	0.015	0.1	0.66	0.54	0.77	7.68	7.2	1.616075	24	2	21.23894	8.33333333
MS3_01483	0.015	0.1	0.64	0.53	0.76	7.72	8.13	0.66365	31	9	27.43363	37.5
MS3_04962	0.015	0.1	0.63	0.52	0.74	7.86	8.23	0.690734	27	10	23.89381	41.6666667
MS3_03372	0.016	0.11	0.66	0.54	0.78	8.07	7.42	1.915541	51	5	45.13274	20.8333333

MS3_09846	0.016	0.11	0.68	0.55	0.81	7.62	6.72	2.459606	38	4	33.62832	16.6666667
MS3_11293	0.016	0.11	0.67	0.55	0.8	8.14	7.37	2.159767	53	7	46.90265	29.1666667
MS3_00859	0.017	0.11	0.66	0.53	0.78	6.04	6.5	0.631281	0	0	0	0
MS3_01339	0.017	0.11	0.66	0.55	0.76	8.18	7.68	1.648721	54	4	47.78761	16.6666667
MS3_04800	0.017	0.11	0.68	0.56	0.8	7.98	7.34	1.896481	42	3	37.16814	12.5
MS3_07422	0.017	0.11	0.65	0.53	0.77	7.57	7.96	0.677057	14	6	12.38938	25
MS3_09089	0.017	0.11	0.67	0.54	0.79	6.5	6.95	0.637627	3	0	2.654867	0
MS3_00756	0.018	0.12	0.65	0.53	0.77	8.32	7.61	2.033992	64	9	56.63717	37.5
MS3_05280	0.018	0.12	0.65	0.53	0.76	8.39	7.98	1.506818	61	8	53.9823	33.3333333
MS3_06147	0.018	0.12	0.67	0.56	0.78	7.04	7.41	0.690734	6	2	5.309735	8.33333333
MS3_10440	0.018	0.12	0.66	0.54	0.78	7.45	8.02	0.565525	24	8	21.23894	33.3333333
MS3_10772	0.018	0.12	0.67	0.55	0.79	6.94	7.47	0.588605	9	3	7.964602	12.5
MS3_00151	0.019	0.12	0.64	0.52	0.75	7.17	7.64	0.625002	6	3	5.309735	12.5
MS3_01542	0.019	0.12	0.65	0.52	0.78	9.15	8.46	1.993716	86	13	76.10619	54.1666667
MS3_02593	0.019	0.12	0.66	0.53	0.79	7.34	7.83	0.612626	10	6	8.849558	25
MS3_03872	0.019	0.12	0.66	0.55	0.77	8.12	7.45	1.954238	56	6	49.55752	25
MS3_05284	0.019	0.12	0.66	0.54	0.78	7.48	7.93	0.637628	17	8	15.04425	33.3333333
MS3_08144	0.019	0.12	0.66	0.54	0.78	6.8	7.27	0.625002	3	2	2.654867	8.33333333
MS3_09233	0.019	0.12	0.65	0.54	0.75	7.88	7.43	1.568313	36	2	31.85841	8.33333333
MS3_05677	0.02	0.12	0.65	0.51	0.79	8.63	7.85	2.181473	64	10	56.63717	41.6666667
MS3_00934	0.021	0.12	0.66	0.54	0.79	6.27	6.8	0.588604	1	2	0.884956	8.33333333
MS3_00006	0.021	0.12	0.66	0.53	0.78	7.31	7.82	0.600495	11	7	9.734513	29.1666667
MS3_04053	0.021	0.12	0.65	0.53	0.76	8	8.43	0.650509	38	14	33.62832	58.3333333
MS3_09684	0.021	0.12	0.56	0.44	0.68	7.9	7.38	1.682028	31	2	27.43363	8.33333333
MS3_09829	0.021	0.12	0.66	0.54	0.78	6.21	6.68	0.625001	2	1	1.769912	4.16666667
MS3_01871	0.022	0.13	0.65	0.52	0.78	7.58	8.03	0.637628	17	9	15.04425	37.5
MS3_01937	0.022	0.13	0.65	0.52	0.77	7.82	7.37	1.568313	29	4	25.66372	16.6666667
MS3_03569	0.022	0.13	0.65	0.53	0.77	7.84	8.27	0.650509	30	12	26.54867	50
MS3_05050	0.022	0.13	0.64	0.52	0.75	7.05	6.53	1.68203	11	1	9.734513	4.16666667
MS3_07918	0.022	0.13	0.66	0.53	0.79	8.5	7.81	1.993716	65	9	57.52212	37.5
MS3_09489	0.023	0.13	0.65	0.53	0.76	7.65	7.06	1.803989	34	5	30.0885	20.8333333
MS3_09942	0.023	0.13	0.65	0.51	0.79	8.38	7.64	2.095936	59	10	52.21239	41.6666667
MS3_00779	0.024	0.13	0.66	0.54	0.78	8.26	7.82	1.552707	61	6	53.9823	25
MS3_06877	0.024	0.13	0.65	0.53	0.76	8.34	7.72	1.858928	62	8	54.86726	33.3333333
MS3_10459	0.024	0.13	0.62	0.48	0.75	7.91	7.33	1.786039	28	4	24.77876	16.6666667
MS3_11526	0.024	0.13	0.66	0.53	0.78	7.81	7.09	2.054434	46	4	40.70796	16.6666667
MS3_00880	0.025	0.14	0.65	0.53	0.77	7.03	6.48	1.733256	10	1	8.849558	4.16666667

MS3_08162	0.025	0.14	0.65	0.53	0.77	7.43	6.79	1.896483	28	2	24.77876	8.33333333
MS3_00844	0.026	0.14	0.71	0.59	0.83	7.24	7.74	0.60653	8	5	7.079646	20.8333333
MS3_03576	0.026	0.14	0.66	0.53	0.78	7.61	8.12	0.600495	22	9	19.46903	37.5
MS3_04025	0.026	0.14	0.65	0.53	0.77	7.7	8.03	0.718924	21	7	18.58407	29.1666667
MS3_06283	0.027	0.14	0.65	0.53	0.77	7.84	8.25	0.66365	30	11	26.54867	45.8333333
MS3_00569	0.028	0.15	0.65	0.53	0.77	7.59	8.09	0.606531	25	10	22.12389	41.6666667
MS3_03818	0.028	0.15	0.66	0.55	0.77	6.28	6.68	0.670319	1	1	0.884956	4.16666667
MS3_04598	0.028	0.15	0.66	0.53	0.8	7.56	8.13	0.565525	20	12	17.69912	50
MS3_09283	0.028	0.15	0.67	0.55	0.79	7.54	8.17	0.532592	15	8	13.27434	33.3333333
MS3_08636	0.029	0.15	0.63	0.51	0.75	7.44	7.06	1.462285	15	0	13.27434	0
MS3_10900	0.029	0.15	0.65	0.52	0.79	6.66	7.05	0.677056	0	1	0	4.16666667
MS3_09276	0.03	0.15	0.64	0.53	0.76	8.11	7.68	1.537258	47	5	41.59292	20.8333333
MS3_00499	0.03	0.16	0.66	0.52	0.8	8.14	7.47	1.954238	49	7	43.36283	29.1666667
MS3_03571	0.03	0.15	0.64	0.51	0.76	6.98	7.39	0.66365	5	2	4.424779	8.33333333
MS3_01705	0.031	0.16	0.66	0.52	0.8	6.11	6.58	0.625	1	1	0.884956	4.16666667
MS3_06223	0.031	0.16	0.65	0.52	0.78	6.36	6.77	0.663649	1	0	0.884956	0
MS3_06276	0.031	0.16	0.66	0.54	0.79	8.51	8.08	1.537258	66	6	58.40708	25
MS3_09903	0.031	0.16	0.65	0.53	0.77	7.43	6.83	1.82212	24	2	21.23894	8.33333333
MS3_02202	0.032	0.16	0.63	0.51	0.76	8.28	7.87	1.506818	51	7	45.13274	29.1666667
MS3_05516	0.032	0.16	0.64	0.52	0.75	7.17	6.54	1.877613	19	2	16.81416	8.33333333
MS3_08024	0.032	0.16	0.64	0.52	0.76	7.33	7.74	0.66365	15	6	13.27434	25
MS3_09626	0.032	0.16	0.64	0.52	0.76	7.81	8.21	0.67032	28	12	24.77876	50
MS3_10956	0.032	0.16	0.65	0.53	0.77	7.96	7.36	1.822119	45	4	39.82301	16.6666667
MS3_06380	0.033	0.16	0.66	0.55	0.77	7.7	8.13	0.650509	23	8	20.35398	33.3333333
MS3_06488	0.033	0.16	0.66	0.52	0.79	8.08	7.45	1.877611	45	5	39.82301	20.8333333
MS3_07337	0.033	0.16	0.64	0.53	0.76	6.51	6.97	0.631283	4	3	3.539823	12.5
MS3_08613	0.033	0.16	0.64	0.51	0.77	8.07	8.53	0.631284	43	14	38.0531	58.3333333
MS3_11103	0.033	0.16	0.66	0.53	0.79	7.49	6.82	1.954239	25	3	22.12389	12.5
MS3_00663	0.034	0.16	0.65	0.52	0.78	7.16	7.56	0.67032	8	2	7.079646	8.33333333
MS3_07994	0.034	0.16	0.64	0.49	0.78	7.95	7.24	2.033992	40	8	35.39823	33.3333333
MS3_08004	0.034	0.16	0.65	0.53	0.77	7.87	7.38	1.632317	39	4	34.51327	16.6666667
MS3_11280	0.034	0.16	0.64	0.52	0.77	7.11	7.45	0.71177	7	2	6.19469	8.33333333
MS3_06914	0.035	0.16	0.65	0.53	0.76	6.46	6.9	0.644035	3	2	2.654867	8.33333333
MS3_07273	0.035	0.16	0.67	0.53	0.81	7.58	8.11	0.588605	18	11	15.9292	45.8333333
MS3_00223	0.037	0.17	0.64	0.51	0.76	7.79	7.3	1.632317	30	5	26.54867	20.8333333
MS3_03863	0.037	0.17	0.66	0.52	0.79	7.19	7.59	0.67032	5	4	4.424779	16.6666667
MS3_09993	0.037	0.17	0.67	0.54	0.79	7.71	8.19	0.618783	24	10	21.23894	41.6666667

MS3_05910	0.038	0.17	0.65	0.55	0.76	7.41	7.81	0.67032	18	7	15.9292	29.1666667
MS3_10044	0.038	0.17	0.65	0.54	0.75	6.31	6.61	0.740817	3	0	2.654867	0
MS3_11076	0.038	0.17	0.63	0.51	0.75	8.48	8.02	1.584074	66	9	58.40708	37.5
MS3_10671	0.039	0.18	0.64	0.5	0.77	7.35	6.79	1.750674	23	3	20.35398	12.5
MS3_01761	0.04	0.18	0.63	0.52	0.75	8.01	7.67	1.404948	41	5	36.28319	20.8333333
MS3_05389	0.04	0.18	0.61	0.47	0.76	6.78	7.26	0.618783	4	6	3.539823	25
MS3_07403	0.04	0.18	0.66	0.55	0.77	6.37	6.73	0.697675	3	0	2.654867	0
MS3_05495	0.041	0.18	0.63	0.51	0.75	7.98	8.35	0.690734	32	11	28.31858	45.8333333
MS3_02928	0.042	0.18	0.63	0.51	0.76	8.18	8.51	0.718924	45	14	39.82301	58.3333333
MS3_06211	0.042	0.18	0.65	0.51	0.79	7.52	6.93	1.80399	16	4	14.15929	16.6666667
MS3_06719	0.042	0.18	0.65	0.53	0.78	7.57	8.05	0.618783	23	8	20.35398	33.3333333
MS3_00891	0.043	0.19	0.63	0.52	0.75	6.78	7.14	0.697676	2	2	1.769912	8.33333333
MS3_02356	0.044	0.19	0.61	0.49	0.74	8.37	7.97	1.491825	54	8	47.78761	33.3333333
MS3_05939	0.044	0.19	0.65	0.52	0.78	7.53	7.93	0.67032	13	7	11.50442	29.1666667
MS3_06101	0.044	0.19	0.65	0.51	0.78	7.99	7.58	1.506818	40	5	35.39823	20.8333333
MS3_06500	0.044	0.19	0.64	0.53	0.76	7.39	7.78	0.677057	16	5	14.15929	20.8333333
MS3_09333	0.044	0.19	0.63	0.52	0.75	7.77	7.42	1.419068	24	1	21.23894	4.16666667
MS3_00787	0.045	0.19	0.62	0.5	0.74	9.61	9.92	0.733447	105	24	92.92035	100
MS3_03269	0.046	0.19	0.63	0.52	0.74	7.72	7.23	1.632317	42	2	37.16814	8.33333333
MS3_06431	0.046	0.19	0.63	0.5	0.75	7.58	7.92	0.71177	12	5	10.61947	20.8333333
MS3_07411	0.046	0.19	0.64	0.51	0.77	6.66	7.12	0.631283	3	3	2.654867	12.5
MS3_08907	0.046	0.19	0.62	0.5	0.75	7.23	6.79	1.552708	15	1	13.27434	4.16666667
MS3_02637	0.047	0.2	0.65	0.51	0.78	7.61	7.03	1.786039	27	5	23.89381	20.8333333
MS3_05047	0.048	0.2	0.63	0.51	0.75	7.18	6.67	1.665293	21	1	18.58407	4.16666667
MS3_00702	0.049	0.2	0.64	0.5	0.77	7.76	7.33	1.537258	27	3	23.89381	12.5
MS3_06680	0.049	0.2	0.65	0.53	0.77	6.07	6.57	0.606529	2	1	1.769912	4.16666667
MS3_06707	0.049	0.2	0.62	0.49	0.75	7.56	7.98	0.657047	23	8	20.35398	33.3333333
MS3_07885	0.049	0.2	0.63	0.51	0.75	7.52	7.82	0.740818	14	5	12.38938	20.8333333
MS3_11411	0.05	0.2	0.66	0.53	0.78	8.33	7.49	2.316368	51	7	45.13274	29.1666667
MS3_03963	0.051	0.2	0.65	0.52	0.78	6.67	7.08	0.66365	2	3	1.769912	12.5
MS3_04493	0.051	0.2	0.63	0.49	0.76	7.31	7.69	0.683861	10	7	8.849558	29.1666667
MS3_08533	0.051	0.2	0.64	0.52	0.76	7.4	7.72	0.726149	12	7	10.61947	29.1666667
MS3_04896	0.053	0.21	0.64	0.51	0.77	8.17	7.78	1.476981	47	6	41.59292	25
MS3_10305	0.053	0.21	0.62	0.51	0.74	8.1	7.78	1.377128	46	6	40.70796	25
MS3_05125	0.054	0.21	0.45	0.32	0.57	7.18	6.72	1.584075	18	0	15.9292	0
MS3_09443	0.054	0.21	0.64	0.52	0.76	7.48	7.81	0.718924	16	4	14.15929	16.6666667
MS3_04221	0.055	0.21	0.61	0.48	0.74	7.7	8.07	0.690734	26	8	23.00885	33.3333333

MS3_05484	0.055	0.21	0.65	0.52	0.78	6.88	7.26	0.683861	2	3	1.769912	12.5
MS3_10292	0.055	0.21	0.61	0.49	0.73	7.75	8.06	0.733447	27	7	23.89381	29.1666667
MS3_02176	0.056	0.21	0.63	0.51	0.75	8.31	7.99	1.377128	57	7	50.44248	29.1666667
MS3_06690	0.056	0.21	0.61	0.48	0.75	9.42	8.87	1.733253	98	15	86.72566	62.5
MS3_09952	0.056	0.21	0.63	0.52	0.75	7.48	7.85	0.690734	15	5	13.27434	20.8333333
MS3_05602	0.057	0.22	0.6	0.49	0.72	7.54	7.21	1.390968	19	2	16.81416	8.33333333
MS3_08903	0.057	0.22	0.64	0.52	0.76	6.6	7.02	0.657046	6	1	5.309735	4.16666667
MS3_03091	0.06	0.23	0.64	0.52	0.77	7.47	7.86	0.677057	17	7	15.04425	29.1666667
MS3_02157	0.061	0.23	0.58	0.47	0.69	7.87	8.17	0.740818	35	6	30.97345	25
MS3_02807	0.061	0.23	0.62	0.51	0.74	7.58	7.05	1.698933	36	4	31.85841	16.6666667
MS3_06748	0.061	0.23	0.63	0.51	0.75	7.48	6.98	1.648722	32	2	28.31858	8.33333333
MS3_08216	0.061	0.23	0.62	0.5	0.74	6.86	7.22	0.697676	3	5	2.654867	20.8333333
MS3_10931	0.061	0.23	0.65	0.5	0.79	7.25	7.66	0.66365	5	6	4.424779	25
MS3_05908	0.062	0.23	0.63	0.5	0.76	7.86	7.47	1.476981	29	4	25.66372	16.6666667
MS3_09961	0.062	0.23	0.62	0.49	0.74	8.43	7.9	1.698932	68	9	60.17699	37.5
MS3_05600	0.063	0.23	0.63	0.5	0.76	6.41	6.88	0.625001	3	1	2.654867	4.16666667
MS3_08169	0.063	0.23	0.61	0.49	0.73	7.11	6.65	1.584076	16	1	14.15929	4.16666667
MS3_07737	0.065	0.24	0.64	0.52	0.76	9	8.6	1.491825	86	13	76.10619	54.1666667
MS3_01777	0.065	0.24	0.63	0.52	0.74	7.93	7.61	1.377128	41	4	36.28319	16.6666667
MS3_07854	0.065	0.24	0.62	0.49	0.75	7.17	7.54	0.690734	9	4	7.964602	16.6666667
MS3_10486	0.065	0.24	0.63	0.5	0.76	8.55	8.04	1.665291	74	8	65.48673	33.3333333
MS3_01348	0.066	0.24	0.6	0.48	0.71	7.42	7.67	0.778801	7	3	6.19469	12.5
MS3_00383	0.067	0.24	0.62	0.5	0.74	7.85	7.37	1.616075	37	5	32.74336	20.8333333
MS3_05631	0.067	0.24	0.62	0.5	0.73	8.15	7.55	1.822119	54	6	47.78761	25
MS3_06462	0.067	0.24	0.62	0.49	0.75	8.79	8.18	1.840432	76	12	67.25664	50
MS3_02172	0.068	0.24	0.6	0.48	0.73	9.23	8.72	1.665291	93	14	82.30088	58.3333333
MS3_02375	0.068	0.24	0.61	0.49	0.73	8.36	7.99	1.447735	59	12	52.21239	50
MS3_02393	0.068	0.24	0.64	0.51	0.77	7.19	7.57	0.683861	9	4	7.964602	16.6666667
MS3_11139	0.069	0.24	0.65	0.53	0.77	8.02	7.54	1.616075	53	4	46.90265	16.6666667
MS3_00800	0.071	0.25	0.62	0.49	0.75	7.1	7.58	0.618783	14	8	12.38938	33.3333333
MS3_03726	0.071	0.25	0.63	0.49	0.76	7.76	8.12	0.697676	25	9	22.12389	37.5
MS3_08042	0.072	0.25	0.6	0.48	0.73	7.83	8.17	0.71177	33	10	29.20354	41.6666667
MS3_03304	0.074	0.25	0.61	0.49	0.72	8.06	7.75	1.363425	41	7	36.28319	29.1666667
MS3_02991	0.075	0.26	0.63	0.51	0.75	8.3	7.88	1.521962	60	8	53.09735	33.3333333
MS3_07125	0.075	0.26	0.61	0.48	0.73	7.52	7.89	0.690734	22	7	19.46903	29.1666667
MS3_10194	0.075	0.26	0.56	0.45	0.67	7.82	7.41	1.506818	34	5	30.0885	20.8333333
MS3_05960	0.076	0.26	0.63	0.51	0.75	8.01	7.41	1.822119	39	4	34.51327	16.6666667

MS3_09161	0.076	0.26	0.58	0.47	0.7	8.42	8.14	1.32313	52	9	46.0177	37.5
MS3_00939	0.077	0.26	0.62	0.5	0.74	6.78	7.08	0.740818	3	1	2.654867	4.16666667
MS3_02499	0.077	0.26	0.62	0.48	0.76	7.57	7.19	1.462285	15	1	13.27434	4.16666667
MS3_07824	0.078	0.26	0.6	0.47	0.72	8.65	8.33	1.377128	71	13	62.83186	54.1666667
MS3_09190	0.078	0.26	0.61	0.49	0.74	7.64	7.3	1.404948	23	2	20.35398	8.33333333
MS3_06918	0.079	0.26	0.62	0.5	0.75	7.47	7	1.599995	27	3	23.89381	12.5
MS3_06928	0.08	0.26	0.62	0.49	0.74	8.16	7.75	1.506818	46	6	40.70796	25
MS3_07874	0.08	0.26	0.61	0.48	0.74	8.08	7.57	1.665291	49	7	43.36283	29.1666667
MS3_08037	0.08	0.26	0.61	0.49	0.73	8	7.68	1.377128	32	3	28.31858	12.5
MS3_08725	0.08	0.26	0.62	0.5	0.74	7.58	7.13	1.568313	27	5	23.89381	20.8333333
MS3_10713	0.08	0.26	0.62	0.49	0.75	7.68	7.1	1.786039	36	4	31.85841	16.6666667
MS3_02041	0.081	0.26	0.61	0.49	0.72	7.4	7.08	1.377128	16	1	14.15929	4.16666667
MS3_02346	0.081	0.26	0.64	0.53	0.75	6.73	7.04	0.733446	3	0	2.654867	0
MS3_03096	0.083	0.27	0.61	0.48	0.73	7.55	8.04	0.612626	35	11	30.97345	45.8333333
MS3_04261	0.083	0.27	0.6	0.49	0.72	7.43	7.05	1.462285	25	2	22.12389	8.33333333
MS3_04158	0.084	0.27	0.64	0.51	0.77	7.83	8.22	0.677057	33	14	29.20354	58.3333333
MS3_09644	0.084	0.27	0.62	0.5	0.74	7.18	7.52	0.71177	15	3	13.27434	12.5
MS3_06257	0.085	0.27	0.64	0.5	0.79	7.26	6.76	1.648723	15	4	13.27434	16.6666667
MS3_01302	0.086	0.27	0.63	0.51	0.75	6.73	7.08	0.704688	8	2	7.079646	8.33333333
MS3_03206	0.086	0.27	0.64	0.5	0.77	7.04	6.54	1.648723	12	2	10.61947	8.33333333
MS3_05150	0.086	0.27	0.62	0.5	0.74	6.89	7.21	0.726149	3	1	2.654867	4.16666667
MS3_08398	0.086	0.27	0.61	0.48	0.73	8.35	8.03	1.377128	56	8	49.55752	33.3333333
MS3_08996	0.086	0.27	0.63	0.5	0.77	7.22	7.84	0.537944	28	12	24.77876	50
MS3_10499	0.086	0.27	0.61	0.48	0.73	8.08	7.76	1.377128	42	5	37.16814	20.8333333
MS3_05686	0.087	0.27	0.59	0.46	0.71	8.19	7.84	1.419068	39	5	34.51327	20.8333333
MS3_09253	0.087	0.27	0.54	0.43	0.65	6.68	6.35	1.39097	13	0	11.50442	0
MS3_09229	0.088	0.27	0.6	0.48	0.72	8.62	8.31	1.363425	74	14	65.48673	58.3333333
MS3_07395	0.089	0.27	0.61	0.48	0.74	7.75	8.12	0.690734	33	10	29.20354	41.6666667
MS3_08689	0.089	0.27	0.62	0.5	0.74	8.36	8.61	0.778801	54	15	47.78761	62.5
MS3_08391	0.09	0.28	0.58	0.47	0.7	7.8	8.11	0.733447	35	8	30.97345	33.3333333
MS3_11059	0.091	0.28	0.62	0.5	0.74	7.95	7.42	1.698933	51	6	45.13274	25
MS3_04157	0.092	0.28	0.62	0.49	0.75	7.83	7.43	1.491825	37	5	32.74336	20.8333333
MS3_10591	0.094	0.29	0.61	0.47	0.74	6.14	6.42	0.755782	0	0	0	0
No hits	0.095	0.29	0.61	0.49	0.74	6.62	6.19	1.537261	4	1	3.539823	4.16666667
MS3_00178	0.095	0.29	0.6	0.48	0.72	7.5	7.18	1.377128	15	2	13.27434	8.33333333
MS3_07757	0.095	0.29	0.62	0.5	0.75	7.16	7.48	0.726149	9	2	7.964602	8.33333333
MS3_01771	0.096	0.29	0.63	0.51	0.75	8.4	8.09	1.363425	61	11	53.9823	45.8333333

MS3_10811	0.096	0.29	0.63	0.5	0.76	7.4	7.75	0.704688	12	7	10.61947	29.1666667
MS3_08663	0.097	0.29	0.59	0.47	0.71	7.83	7.55	1.32313	22	3	19.46903	12.5
MS3_02538	0.098	0.29	0.63	0.5	0.75	7.66	8.09	0.650509	28	9	24.77876	37.5
MS3_04564	0.099	0.29	0.61	0.48	0.73	6.46	6.91	0.637627	3	2	2.654867	8.33333333
No hits	0.1	0.3	0.6	0.48	0.71	6.96	6.53	1.537259	15	2	13.27434	8.33333333
MS3_00508	0.1	0.3	0.6	0.47	0.72	7.9	7.4	1.648722	39	6	34.51327	25
MS3_06126	0.1	0.3	0.61	0.48	0.74	8	8.3	0.740818	37	10	32.74336	41.6666667
MS3_07096	0.1	0.3	0.6	0.49	0.71	7.11	6.73	1.462286	15	1	13.27434	4.16666667
MS3_08625	0.1	0.3	0.61	0.49	0.72	7.02	6.71	1.363426	6	0	5.309735	0
MS3_10036	0.1	0.3	0.62	0.5	0.75	7.23	7.61	0.683861	18	6	15.9292	25
MS3_02486	0.11	0.32	0.61	0.48	0.74	7.03	7.3	0.763379	4	2	3.539823	8.33333333
MS3_02641	0.11	0.31	0.59	0.48	0.71	7.71	7.49	1.246077	20	0	17.69912	0
MS3_03461	0.11	0.32	0.6	0.47	0.73	7.41	7.01	1.491825	21	3	18.58407	12.5
MS3_03534	0.11	0.31	0.6	0.47	0.74	8.37	8.67	0.740818	53	14	46.90265	58.3333333
MS3_03768	0.11	0.31	0.5	0.35	0.64	6.92	8.15	0.292292	8	6	7.079646	25
MS3_04540	0.11	0.32	0.63	0.51	0.75	6.41	6.7	0.748263	2	2	1.769912	8.33333333
MS3_05520	0.11	0.32	0.63	0.49	0.77	7.5	7.81	0.733447	13	6	11.50442	25
MS3_06112	0.11	0.32	0.63	0.48	0.77	7.6	7.08	1.682028	26	4	23.00885	16.6666667
MS3_06559	0.11	0.31	0.6	0.48	0.73	7.25	7.56	0.733447	10	5	8.849558	20.8333333
MS3_06994	0.11	0.31	0.62	0.48	0.76	8.31	7.84	1.599994	59	7	52.21239	29.1666667
MS3_08479	0.11	0.31	0.58	0.47	0.7	7.78	7.27	1.665292	38	3	33.62832	12.5
MS3_02899	0.12	0.33	0.59	0.45	0.72	7.79	8.06	0.763379	19	8	16.81416	33.3333333
MS3_00447	0.12	0.33	0.61	0.48	0.75	8.17	7.91	1.29693	45	6	39.82301	25
MS3_02085	0.12	0.33	0.6	0.47	0.73	9.22	8.84	1.462285	95	16	84.0708	66.6666667
MS3_05219	0.12	0.33	0.62	0.49	0.75	7.92	7.63	1.336428	29	4	25.66372	16.6666667
MS3_05761	0.12	0.33	0.61	0.48	0.73	6.22	6.52	0.740817	1	1	0.884956	4.16666667
MS3_09086	0.12	0.34	0.61	0.48	0.74	6.88	7.17	0.748263	3	2	2.654867	8.33333333
MS3_10161	0.12	0.34	0.59	0.46	0.73	7.78	7.4	1.462285	29	4	25.66372	16.6666667
MS3_10820	0.12	0.34	0.62	0.5	0.74	7.07	7.36	0.748263	10	2	8.849558	8.33333333
MS3_00242	0.13	0.35	0.62	0.49	0.75	7.97	7.49	1.616075	48	7	42.47788	29.1666667
MS3_00412	0.13	0.35	0.61	0.48	0.73	8.12	7.86	1.29693	43	6	38.0531	25
MS3_01964	0.13	0.36	0.6	0.48	0.71	7.2	7.48	0.755784	11	3	9.734513	12.5
MS3_02289	0.13	0.35	0.61	0.48	0.75	7.87	8.13	0.771052	24	11	21.23894	45.8333333
MS3_03400	0.13	0.36	0.6	0.48	0.73	8.14	7.91	1.2586	38	5	33.62832	20.8333333
MS3_03992	0.13	0.36	0.62	0.49	0.76	7.62	7.97	0.704688	20	11	17.69912	45.8333333
MS3_05351	0.13	0.35	0.6	0.49	0.71	6.52	6.8	0.755783	3	1	2.654867	4.16666667
MS3_06167	0.13	0.36	0.42	0.3	0.55	6.88	6.49	1.476983	14	1	12.38938	4.16666667

MS3_06740	0.13	0.35	0.59	0.46	0.72	7.92	7.65	1.309965	34	6	30.0885	25
MS3_07419	0.13	0.36	0.6	0.49	0.72	7.69	8.04	0.704688	25	8	22.12389	33.3333333
MS3_08399	0.13	0.36	0.6	0.47	0.72	7.44	6.97	1.599995	38	4	33.62832	16.6666667
MS3_08891	0.13	0.36	0.61	0.49	0.74	7.03	7.34	0.733447	8	4	7.079646	16.6666667
MS3_09175	0.13	0.36	0.61	0.48	0.74	6.71	7.05	0.71177	5	4	4.424779	16.6666667
MS3_09426	0.13	0.36	0.6	0.48	0.71	6.77	7.07	0.740818	5	3	4.424779	12.5
MS3_02838	0.14	0.37	0.6	0.48	0.72	8.02	7.8	1.246077	36	5	31.85841	20.8333333
MS3_03119	0.14	0.37	0.59	0.47	0.72	7.53	7.23	1.349859	15	2	13.27434	8.33333333
MS3_03625	0.14	0.37	0.59	0.47	0.71	7.73	7.48	1.284026	23	2	20.35398	8.33333333
MS3_04268	0.14	0.37	0.61	0.48	0.73	6.99	7.27	0.755783	7	1	6.19469	4.16666667
MS3_04799	0.14	0.37	0.63	0.51	0.76	6.78	7.1	0.726149	9	1	7.964602	4.16666667
MS3_05142	0.14	0.36	0.62	0.48	0.76	7.89	8.19	0.740818	31	10	27.43363	41.6666667
MS3_06080	0.14	0.38	0.6	0.47	0.73	7.59	7.9	0.733447	21	7	18.58407	29.1666667
MS3_06649	0.14	0.38	0.64	0.51	0.78	8.38	7.87	1.665291	57	7	50.44248	29.1666667
MS3_06745	0.14	0.37	0.56	0.43	0.69	7.96	7.73	1.2586	28	4	24.77876	16.6666667
No hits	0.15	0.39	0.59	0.45	0.73	7.8	7.35	1.568313	33	6	29.20354	25
MS3_01218	0.15	0.38	0.61	0.49	0.74	7.99	8.23	0.786628	34	10	30.0885	41.6666667
MS3_01318	0.15	0.39	0.59	0.46	0.73	8.35	7.91	1.552707	58	11	51.32743	45.8333333
MS3_01504	0.15	0.39	0.6	0.48	0.72	7.56	7.81	0.778801	22	5	19.46903	20.8333333
MS3_01600	0.15	0.39	0.59	0.46	0.71	8.29	7.92	1.447735	57	9	50.44248	37.5
MS3_01972	0.15	0.39	0.6	0.49	0.71	7.88	7.59	1.336428	40	3	35.39823	12.5
MS3_02681	0.15	0.38	0.58	0.45	0.71	7.87	7.57	1.349859	31	6	27.43363	25
MS3_03054	0.15	0.39	0.6	0.46	0.75	8.36	8.68	0.726149	62	14	54.86726	58.3333333
MS3_04227	0.15	0.38	0.59	0.47	0.71	8.06	7.82	1.271249	43	5	38.0531	20.8333333
MS3_06161	0.15	0.38	0.58	0.46	0.71	8.1	7.8	1.349859	49	6	43.36283	25
MS3_08440	0.15	0.38	0.6	0.47	0.73	7.76	8.08	0.726149	24	10	21.23894	41.6666667
MS3_09415	0.15	0.38	0.62	0.49	0.74	7.54	7.82	0.755784	18	6	15.9292	25
MS3_00785	0.16	0.39	0.6	0.47	0.73	7.22	6.79	1.537259	22	3	19.46903	12.5
MS3_02460	0.16	0.4	0.59	0.46	0.72	8	7.73	1.309965	31	4	27.43363	16.6666667
MS3_03127	0.16	0.39	0.61	0.49	0.73	6.93	7.2	0.763379	7	0	6.19469	0
MS3_03270	0.16	0.39	0.61	0.48	0.73	7.79	8.03	0.786628	24	8	21.23894	33.3333333
MS3_05370	0.16	0.4	0.61	0.49	0.74	7.04	7.29	0.778801	7	1	6.19469	4.16666667
MS3_05391	0.16	0.4	0.6	0.46	0.74	7.32	7.64	0.726149	12	8	10.61947	33.3333333
MS3_06769	0.16	0.4	0.59	0.47	0.7	7.39	7.15	1.271249	14	2	12.38938	8.33333333
MS3_08655	0.16	0.4	0.59	0.46	0.72	7.05	7.37	0.726149	9	5	7.964602	20.8333333
MS3_09569	0.16	0.4	0.58	0.47	0.69	7.84	8.05	0.810584	30	7	26.54867	29.1666667
MS3_09620	0.16	0.4	0.59	0.48	0.7	7.93	7.71	1.246077	39	4	34.51327	16.6666667

MS3_09739	0.16	0.39	0.62	0.48	0.75	7.42	7.67	0.778801	9	5	7.964602	20.8333333
MS3_10116	0.16	0.39	0.6	0.48	0.71	8.42	8.15	1.309964	64	9	56.63717	37.5
MS3_10513	0.16	0.4	0.59	0.45	0.73	7.53	7.28	1.284026	14	3	12.38938	12.5
MS3_10588	0.16	0.4	0.61	0.49	0.73	6.71	6.18	1.698937	26	3	23.00885	12.5
MS3_10590	0.16	0.4	0.6	0.46	0.73	7.22	6.86	1.43333	13	3	11.50442	12.5
MS3_11376	0.16	0.39	0.6	0.46	0.73	7.82	8.07	0.778801	24	9	21.23894	37.5
MS3_00316	0.17	0.4	0.59	0.44	0.73	6.79	7.1	0.733447	3	2	2.654867	8.33333333
MS3_02999	0.17	0.4	0.61	0.48	0.73	7.08	6.71	1.447736	18	3	15.9292	12.5
MS3_03641	0.17	0.41	0.55	0.43	0.67	8.82	9.1	0.755784	77	17	68.14159	70.8333333
MS3_03695	0.17	0.4	0.6	0.47	0.72	6.26	5.93	1.390973	9	0	7.964602	0
MS3_04279	0.17	0.4	0.56	0.45	0.68	7.52	7.21	1.363425	27	3	23.89381	12.5
MS3_04347	0.17	0.4	0.6	0.48	0.72	8.38	8.61	0.794534	58	17	51.32743	70.8333333
MS3_09231	0.17	0.4	0.59	0.44	0.74	7.6	7.9	0.740818	20	10	17.69912	41.6666667
MS3_10803	0.17	0.4	0.61	0.47	0.76	8.55	8.92	0.690734	76	16	67.25664	66.6666667
MS3_11544	0.17	0.4	0.59	0.47	0.71	7.95	7.62	1.390968	42	6	37.16814	25
MS3_10847	0.18	0.42	0.58	0.44	0.72	8.51	8.11	1.491825	70	11	61.9469	45.8333333
MS3_01328	0.18	0.42	0.58	0.44	0.72	8.4	8.02	1.462285	67	12	59.29204	50
MS3_01516	0.18	0.42	0.6	0.47	0.72	7.49	7.79	0.740818	25	7	22.12389	29.1666667
MS3_01527	0.18	0.41	0.6	0.47	0.74	7.24	7.64	0.67032	18	8	15.9292	33.3333333
MS3_01833	0.18	0.42	0.57	0.45	0.69	7.23	7.59	0.697676	26	8	23.00885	33.3333333
MS3_01952	0.18	0.42	0.56	0.43	0.68	7.65	7.86	0.810584	12	6	10.61947	25
MS3_02136	0.18	0.42	0.59	0.46	0.72	7.69	7.26	1.537258	38	7	33.62832	29.1666667
MS3_02489	0.18	0.42	0.59	0.47	0.72	7.36	7.63	0.763379	10	3	8.849558	12.5
MS3_03789	0.18	0.42	0.54	0.43	0.64	7.42	7.1	1.377128	24	1	21.23894	4.16666667
MS3_05038	0.18	0.42	0.6	0.47	0.73	7.4	7.04	1.43333	27	3	23.89381	12.5
MS3_05203	0.18	0.42	0.6	0.48	0.72	7.58	7.32	1.29693	25	4	22.12389	16.6666667
MS3_05216	0.18	0.42	0.61	0.47	0.75	7.77	7.36	1.506818	40	6	35.39823	25
MS3_07487	0.18	0.42	0.61	0.48	0.74	7.82	7.55	1.309965	27	4	23.89381	16.6666667
MS3_07905	0.18	0.42	0.43	0.31	0.56	6.73	7.06	0.718923	10	2	8.849558	8.33333333
MS3_09640	0.18	0.42	0.57	0.44	0.71	7.69	7.29	1.491825	26	6	23.00885	25
MS3_00196	0.19	0.43	0.59	0.46	0.72	7.73	8.23	0.606531	28	10	24.77876	41.6666667
MS3_01004	0.19	0.43	0.59	0.45	0.72	8.82	9.12	0.740818	79	19	69.9115	79.1666667
MS3_01686	0.19	0.43	0.58	0.45	0.7	7.46	7.24	1.246077	7	2	6.19469	8.33333333
MS3_01898	0.19	0.43	0.58	0.46	0.71	8.33	8.58	0.778801	58	18	51.32743	75
MS3_04550	0.19	0.43	0.58	0.45	0.7	7.33	7.58	0.778801	11	5	9.734513	20.8333333
MS3_05040	0.19	0.43	0.59	0.45	0.73	7.59	7.89	0.740818	22	8	19.46903	33.3333333
MS3_05465	0.19	0.43	0.57	0.42	0.72	8.09	7.8	1.336428	39	9	34.51327	37.5

MS3_08059	0.19	0.43	0.58	0.45	0.71	6.67	6.94	0.763379	4	2	3.539823	8.33333333
MS3_08361	0.19	0.43	0.6	0.47	0.73	6.97	6.62	1.419069	14	2	12.38938	8.33333333
MS3_08480	0.19	0.43	0.58	0.45	0.72	9.6	9.23	1.447735	104	18	92.0354	75
MS3_09290	0.19	0.43	0.59	0.45	0.73	6.74	7.1	0.697676	8	4	7.079646	16.6666667
MS3_09662	0.19	0.43	0.6	0.47	0.73	6.61	6.88	0.763379	7	2	6.19469	8.33333333
MS3_09810	0.19	0.43	0.6	0.48	0.72	8.83	8.48	1.419068	80	12	70.79646	50
MS3_10600	0.19	0.43	0.58	0.47	0.7	6.96	6.66	1.34986	15	2	13.27434	8.33333333
MS3_11509	0.19	0.43	0.59	0.46	0.72	7.89	7.64	1.284026	34	6	30.0885	25
MS3_00668	0.2	0.43	0.58	0.46	0.7	8.31	7.97	1.404948	57	10	50.44248	41.6666667
MS3_01014	0.2	0.44	0.59	0.46	0.71	6.85	6.56	1.336429	10	1	8.849558	4.16666667
MS3_02155	0.2	0.44	0.57	0.43	0.7	7.57	7.77	0.818731	13	6	11.50442	25
MS3_05387	0.2	0.44	0.58	0.45	0.71	6.89	7.17	0.755783	6	3	5.309735	12.5
MS3_06327	0.2	0.44	0.59	0.47	0.71	6.6	6.87	0.763379	4	2	3.539823	8.33333333
MS3_06583	0.2	0.44	0.57	0.45	0.7	7.27	6.92	1.419068	21	3	18.58407	12.5
MS3_08504	0.2	0.44	0.57	0.45	0.68	7.47	7.7	0.794534	23	4	20.35398	16.6666667
MS3_09119	0.2	0.44	0.63	0.52	0.74	7.74	8.02	0.755784	24	8	21.23894	33.3333333
MS3_01051	0.21	0.45	0.6	0.47	0.74	7.88	8.1	0.802519	26	12	23.00885	50
MS3_01153	0.21	0.45	0.6	0.47	0.73	7.21	7.5	0.748263	11	4	9.734513	16.6666667
MS3_01333	0.21	0.46	0.57	0.43	0.71	6.05	6.35	0.740816	0	1	0	4.16666667
MS3_01710	0.21	0.45	0.6	0.47	0.73	7.69	7.92	0.794534	18	6	15.9292	25
MS3_04011	0.21	0.45	0.58	0.45	0.71	6.68	6.34	1.40495	4	2	3.539823	8.33333333
MS3_04375	0.21	0.46	0.58	0.46	0.71	7.17	7.46	0.748263	13	4	11.50442	16.6666667
MS3_07105	0.21	0.45	0.6	0.46	0.73	7.2	7.5	0.740818	14	5	12.38938	20.8333333
MS3_09510	0.21	0.45	0.6	0.48	0.71	7.36	7.01	1.419068	33	3	29.20354	12.5
MS3_10148	0.22	0.46	0.59	0.47	0.71	8.3	8.02	1.32313	61	12	53.9823	50
MS3_01611	0.22	0.46	0.58	0.46	0.7	7.83	8.04	0.810584	32	9	28.31858	37.5
MS3_04526	0.22	0.47	0.56	0.42	0.7	7.08	7.47	0.677057	16	6	14.15929	25
MS3_04595	0.22	0.46	0.59	0.47	0.71	7.55	7.24	1.363425	26	3	23.00885	12.5
MS3_04932	0.22	0.47	0.56	0.44	0.69	7.12	7.44	0.726149	20	5	17.69912	20.8333333
MS3_05289	0.22	0.47	0.58	0.45	0.72	7.75	7.96	0.810584	20	8	17.69912	33.3333333
MS3_08539	0.22	0.46	0.56	0.43	0.68	7.53	7.77	0.786628	15	6	13.27434	25
MS3_03817	0.23	0.47	0.59	0.46	0.72	8.09	7.73	1.43333	51	7	45.13274	29.1666667
MS3_04355	0.23	0.48	0.58	0.44	0.73	7.67	7.44	1.2586	17	3	15.04425	12.5
MS3_04873	0.23	0.47	0.57	0.44	0.71	8.19	7.92	1.309965	50	9	44.24779	37.5
MS3_05337	0.23	0.47	0.59	0.47	0.71	7.54	7.75	0.810584	19	5	16.81416	20.8333333
MS3_06248	0.23	0.47	0.59	0.47	0.72	8.22	7.92	1.349859	57	8	50.44248	33.3333333
MS3_09160	0.23	0.49	0.58	0.44	0.73	7.03	7.25	0.802519	6	1	5.309735	4.16666667

MS3_09828	0.23	0.48	0.61	0.51	0.72	7.42	7.61	0.826959	17	3	15.04425	12.5
MS3_11484	0.24	0.49	0.59	0.46	0.71	7.18	6.85	1.390969	23	3	20.35398	12.5
MS3_00452	0.24	0.49	0.58	0.45	0.71	7.82	8.01	0.826959	24	6	21.23894	25
MS3_01016	0.24	0.49	0.6	0.48	0.72	7.69	7.37	1.377128	37	3	32.74336	12.5
MS3_01114	0.24	0.49	0.59	0.46	0.72	7.12	7.36	0.786628	6	3	5.309735	12.5
MS3_01245	0.24	0.49	0.57	0.45	0.69	7.55	7.74	0.826959	15	4	13.27434	16.6666667
MS3_03933	0.24	0.49	0.57	0.42	0.73	7.67	7.94	0.763379	19	10	16.81416	41.6666667
MS3_04063	0.24	0.49	0.6	0.46	0.74	7.18	7.46	0.755784	8	3	7.079646	12.5
MS3_06108	0.24	0.49	0.57	0.44	0.7	7.59	7.23	1.43333	33	5	29.20354	20.8333333
MS3_06449	0.24	0.49	0.58	0.45	0.7	7.91	7.69	1.246077	32	5	28.31858	20.8333333
MS3_06828	0.24	0.49	0.6	0.47	0.72	6.9	7.21	0.733447	13	3	11.50442	12.5
MS3_06832	0.24	0.49	0.58	0.45	0.7	7.07	7.29	0.802519	8	3	7.079646	12.5
MS3_09473	0.24	0.49	0.58	0.45	0.71	7.06	6.73	1.390969	17	2	15.04425	8.33333333
No hits	0.25	0.49	0.58	0.45	0.71	7.75	7.42	1.390968	40	6	35.39823	25
MS3_01105	0.25	0.49	0.58	0.46	0.7	6.94	6.68	1.296931	14	1	12.38938	4.16666667
MS3_01286	0.25	0.49	0.6	0.49	0.71	6.48	6.68	0.81873	5	0	4.424779	0
MS3_02234	0.25	0.5	0.58	0.46	0.71	7.3	7.56	0.771051	18	6	15.9292	25
MS3_03381	0.25	0.49	0.59	0.46	0.72	7.45	7.68	0.794534	12	6	10.61947	25
MS3_04285	0.25	0.49	0.58	0.45	0.7	7.6	7.19	1.506818	31	5	27.43363	20.8333333
MS3_04767	0.25	0.5	0.59	0.45	0.73	7.96	7.75	1.233678	31	5	27.43363	20.8333333
MS3_05000	0.25	0.49	0.44	0.3	0.59	6.89	7.14	0.7788	5	5	4.424779	20.8333333
MS3_05230	0.25	0.5	0.6	0.44	0.75	7.79	8.03	0.786628	15	9	13.27434	37.5
MS3_08509	0.25	0.5	0.62	0.49	0.74	6.24	5.95	1.336431	4	1	3.539823	4.16666667
MS3_00900	0.26	0.51	0.58	0.45	0.72	7.29	6.93	1.43333	24	4	21.23894	16.6666667
MS3_03824	0.26	0.51	0.56	0.45	0.68	7.17	6.98	1.20925	12	1	10.61947	4.16666667
MS3_04147	0.26	0.52	0.58	0.46	0.7	6.8	7.01	0.810584	6	0	5.309735	0
MS3_07213	0.26	0.51	0.6	0.48	0.71	6.98	7.29	0.733447	15	2	13.27434	8.33333333
MS3_07729	0.26	0.51	0.58	0.47	0.7	7.58	7.79	0.810584	24	7	21.23894	29.1666667
MS3_08000	0.26	0.5	0.58	0.46	0.7	7.21	7.43	0.802519	6	1	5.309735	4.16666667
MS3_09958	0.26	0.5	0.58	0.46	0.69	7.2	6.89	1.363426	24	2	21.23894	8.33333333
MS3_08446	0.27	0.52	0.58	0.46	0.7	7.58	7.38	1.221403	18	3	15.9292	12.5
MS3_00312	0.27	0.53	0.45	0.31	0.59	8.87	8.56	1.363425	86	15	76.10619	62.5
MS3_03577	0.27	0.53	0.57	0.44	0.69	7.79	7.55	1.271249	35	4	30.97345	16.6666667
MS3_03599	0.27	0.52	0.58	0.46	0.71	8.38	8.61	0.794534	59	17	52.21239	70.8333333
MS3_04774	0.27	0.52	0.58	0.44	0.72	6.72	6.49	1.258601	6	1	5.309735	4.16666667
MS3_11226	0.27	0.52	0.56	0.42	0.71	7.23	7.46	0.794533	9	4	7.964602	16.6666667
MS3_00054	0.28	0.53	0.56	0.43	0.69	7.38	7.57	0.826959	7	4	6.19469	16.6666667

MS3_02087	0.28	0.53	0.53	0.41	0.66	8.03	7.81	1.246077	34	4	30.0885	16.6666667
MS3_02160	0.28	0.53	0.55	0.41	0.68	7.06	7.27	0.810584	7	3	6.19469	12.5
MS3_03775	0.28	0.53	0.58	0.44	0.71	7.81	7.51	1.349859	43	7	38.0531	29.1666667
MS3_05735	0.28	0.53	0.56	0.45	0.67	7.98	7.77	1.233678	47	5	41.59292	20.8333333
MS3_06592	0.28	0.53	0.57	0.44	0.71	6.63	6.84	0.810584	5	0	4.424779	0
MS3_09073	0.28	0.53	0.57	0.44	0.71	6.72	6.92	0.81873	5	0	4.424779	0
MS3_09427	0.28	0.53	0.58	0.44	0.71	7.19	7.38	0.826959	5	2	4.424779	8.33333333
MS3_09638	0.28	0.53	0.57	0.44	0.7	6.75	7.01	0.771051	5	3	4.424779	12.5
MS3_10489	0.28	0.53	0.57	0.43	0.71	7.25	7.45	0.818731	9	2	7.964602	8.33333333
MS3_11074	0.28	0.53	0.58	0.43	0.73	7.39	7.61	0.802519	10	6	8.849558	25
MS3_00294	0.29	0.55	0.56	0.42	0.7	7.85	7.64	1.233678	28	6	24.77876	25
MS3_01934	0.29	0.54	0.57	0.44	0.7	6.51	6.71	0.81873	5	1	4.424779	4.16666667
MS3_02494	0.29	0.54	0.57	0.44	0.71	7.23	7.4	0.843665	6	2	5.309735	8.33333333
MS3_05586	0.29	0.55	0.55	0.44	0.66	7.64	7.84	0.818731	29	7	25.66372	29.1666667
MS3_07944	0.29	0.54	0.58	0.46	0.7	7.6	7.83	0.794534	26	8	23.00885	33.3333333
MS3_11537	0.3	0.55	0.58	0.46	0.7	8.38	8.22	1.173511	60	9	53.09735	37.5
MS3_00440	0.3	0.55	0.56	0.45	0.67	7.31	7.49	0.83527	14	2	12.38938	8.33333333
MS3_00931	0.3	0.55	0.47	0.34	0.6	8.02	7.66	1.43333	40	7	35.39823	29.1666667
MS3_01386	0.3	0.56	0.58	0.46	0.71	7.7	7.9	0.818731	23	7	20.35398	29.1666667
MS3_01406	0.3	0.55	0.55	0.42	0.67	8.41	8.23	1.197217	60	11	53.09735	45.8333333
MS3_02545	0.3	0.55	0.57	0.46	0.68	7.49	7.68	0.826959	22	5	19.46903	20.8333333
MS3_03776	0.3	0.55	0.56	0.42	0.7	7.04	7.32	0.755783	11	6	9.734513	25
MS3_04981	0.3	0.55	0.57	0.45	0.7	7.33	7.05	1.32313	23	3	20.35398	12.5
MS3_05945	0.3	0.55	0.57	0.44	0.7	7.35	7.58	0.794533	16	4	14.15929	16.6666667
MS3_06539	0.3	0.56	0.56	0.43	0.69	6.04	6.27	0.794532	1	1	0.884956	4.16666667
MS3_07390	0.3	0.55	0.57	0.44	0.71	6.86	6.5	1.433331	17	3	15.04425	12.5
MS3_08262	0.3	0.55	0.55	0.44	0.66	7.48	7.3	1.197218	24	1	21.23894	4.16666667
MS3_10736	0.3	0.55	0.53	0.42	0.64	7.59	7.39	1.221403	22	3	19.46903	12.5
MS3_01049	0.31	0.56	0.57	0.46	0.68	7.82	8.01	0.826959	32	7	28.31858	29.1666667
MS3_01988	0.31	0.56	0.57	0.44	0.7	7.66	7.38	1.32313	32	5	28.31858	20.8333333
MS3_02504	0.31	0.56	0.48	0.35	0.6	7.96	8.14	0.83527	41	7	36.28319	29.1666667
MS3_06214	0.31	0.57	0.57	0.44	0.69	7.78	7.59	1.20925	26	2	23.00885	8.33333333
MS3_06348	0.31	0.56	0.59	0.47	0.7	7.27	7	1.309965	21	2	18.58407	8.33333333
MS3_06471	0.31	0.56	0.55	0.42	0.68	7.79	7.59	1.221403	23	5	20.35398	20.8333333
MS3_10187	0.31	0.56	0.57	0.46	0.68	7.86	7.59	1.309965	47	8	41.59292	33.3333333
MS3_09353	0.32	0.57	0.6	0.45	0.74	7.79	7.97	0.83527	19	10	16.81416	41.6666667
MS3_00143	0.32	0.57	0.58	0.44	0.71	8.04	8.21	0.843665	29	13	25.66372	54.1666667

MS3_00148	0.32	0.57	0.57	0.46	0.69	8.91	8.68	1.2586	76	16	67.25664	66.6666667
MS3_00403	0.32	0.57	0.58	0.45	0.72	7.89	8.07	0.83527	27	10	23.89381	41.6666667
MS3_01478	0.32	0.57	0.56	0.43	0.68	7.01	6.77	1.27125	13	2	11.50442	8.33333333
MS3_02318	0.32	0.57	0.45	0.31	0.6	8.44	8.09	1.419068	63	13	55.75221	54.1666667
MS3_03453	0.32	0.57	0.56	0.43	0.69	7.18	7.39	0.810584	13	4	11.50442	16.6666667
MS3_04364	0.32	0.57	0.59	0.47	0.7	8.15	7.97	1.197217	52	6	46.0177	25
MS3_04920	0.32	0.57	0.6	0.49	0.71	7.74	7.94	0.818731	26	6	23.00885	25
MS3_06243	0.32	0.57	0.54	0.41	0.67	7.03	7.25	0.802519	9	4	7.964602	16.6666667
MS3_07061	0.32	0.57	0.56	0.43	0.7	7.29	7.47	0.83527	8	2	7.079646	8.33333333
MS3_09188	0.32	0.57	0.62	0.49	0.76	9.82	10.13	0.733447	101	23	89.38053	95.8333333
MS3_10002	0.32	0.57	0.58	0.46	0.71	7.59	7.33	1.29693	35	4	30.97345	16.6666667
MS3_01425	0.33	0.57	0.54	0.41	0.67	6.92	7.23	0.733447	14	4	12.38938	16.6666667
MS3_03350	0.33	0.58	0.58	0.45	0.71	6.99	7.19	0.818731	8	2	7.079646	8.33333333
MS3_04609	0.33	0.58	0.55	0.41	0.7	7.63	7.83	0.818731	18	7	15.9292	29.1666667
MS3_09273	0.33	0.57	0.56	0.43	0.69	6.85	7.01	0.852144	2	1	1.769912	4.16666667
MS3_09286	0.33	0.57	0.58	0.46	0.7	7.39	7.1	1.336428	34	2	30.0885	8.33333333
MS3_11428	0.33	0.57	0.54	0.41	0.66	8.19	8.36	0.843665	50	10	44.24779	41.6666667
MS3_00286	0.34	0.59	0.56	0.44	0.68	7.56	7.3	1.29693	40	4	35.39823	16.6666667
MS3_00769	0.34	0.58	0.55	0.43	0.67	7.3	7.13	1.185305	13	1	11.50442	4.16666667
MS3_01650	0.34	0.58	0.56	0.44	0.68	7.36	7.07	1.336428	37	5	32.74336	20.8333333
MS3_01668	0.34	0.58	0.54	0.43	0.66	8.17	7.95	1.246077	52	8	46.0177	33.3333333
MS3_03856	0.34	0.58	0.59	0.47	0.72	7.5	7.33	1.185305	8	2	7.079646	8.33333333
MS3_05427	0.34	0.58	0.57	0.43	0.7	7.62	7.79	0.843665	15	5	13.27434	20.8333333
MS3_07520	0.34	0.58	0.58	0.45	0.7	7.66	7.84	0.83527	24	6	21.23894	25
MS3_07565	0.34	0.58	0.58	0.45	0.72	7.54	7.74	0.818731	12	5	10.61947	20.8333333
MS3_07685	0.34	0.58	0.56	0.43	0.68	7.13	7.38	0.778801	17	6	15.04425	25
MS3_09465	0.34	0.59	0.57	0.44	0.7	7.15	7.32	0.843665	5	2	4.424779	8.33333333
MS3_01124	0.35	0.6	0.58	0.44	0.73	7.83	8.04	0.810584	26	10	23.00885	41.6666667
MS3_05587	0.35	0.6	0.57	0.44	0.69	6.73	6.94	0.810584	7	2	6.19469	8.33333333
MS3_08503	0.35	0.59	0.54	0.42	0.65	7.27	7.43	0.852144	9	2	7.964602	8.33333333
MS3_09110	0.35	0.59	0.57	0.44	0.7	7.8	7.62	1.197217	29	4	25.66372	16.6666667
MS3_09457	0.35	0.59	0.55	0.4	0.7	7.24	7.48	0.786628	11	7	9.734513	29.1666667
MS3_09619	0.35	0.59	0.57	0.45	0.69	8.08	7.8	1.32313	54	9	47.78761	37.5
MS3_00560	0.36	0.6	0.59	0.47	0.71	6.94	7.14	0.818731	12	2	10.61947	8.33333333
MS3_01313	0.36	0.6	0.54	0.43	0.65	8.53	8.67	0.869358	62	17	54.86726	70.8333333
MS3_03427	0.36	0.6	0.55	0.43	0.67	6.98	6.79	1.20925	10	1	8.849558	4.16666667
MS3_05715	0.36	0.6	0.57	0.43	0.72	7.4	7.62	0.802519	13	6	11.50442	25

MS3_06704	0.36	0.6	0.57	0.44	0.7	8.06	8.22	0.852144	37	11	32.74336	45.8333333
MS3_09652	0.36	0.6	0.56	0.42	0.69	7.6	7.44	1.173511	10	3	8.849558	12.5
MS3_09793	0.36	0.6	0.57	0.42	0.71	7.81	8	0.826959	31	11	27.43363	45.8333333
MS3_00353	0.37	0.61	0.57	0.44	0.7	8.4	8.12	1.32313	68	10	60.17699	41.6666667
MS3_01261	0.37	0.61	0.56	0.45	0.67	7.67	7.41	1.29693	44	7	38.93805	29.1666667
MS3_01905	0.37	0.61	0.55	0.4	0.7	7.62	7.81	0.826959	16	8	14.15929	33.3333333
MS3_04559	0.37	0.61	0.46	0.33	0.59	7.65	7.83	0.83527	17	5	15.04425	20.8333333
MS3_05836	0.37	0.61	0.54	0.41	0.68	6.74	6.92	0.83527	3	2	2.654867	8.33333333
MS3_06430	0.37	0.61	0.56	0.42	0.69	7.42	7.62	0.818731	15	6	13.27434	25
MS3_07738	0.37	0.61	0.55	0.43	0.68	7.28	7.05	1.2586	19	2	16.81416	8.33333333
MS3_08530	0.37	0.61	0.56	0.42	0.7	7.03	7.28	0.778801	15	6	13.27434	25
MS3_08805	0.37	0.61	0.56	0.41	0.7	7.89	8.07	0.83527	25	8	22.12389	33.3333333
MS3_09271	0.37	0.61	0.51	0.41	0.61	6.59	6.45	1.150275	6	0	5.309735	0
MS3_01658	0.38	0.62	0.57	0.45	0.69	6.48	6.66	0.83527	7	1	6.19469	4.16666667
MS3_04269	0.38	0.62	0.57	0.45	0.7	8.23	8.04	1.20925	55	8	48.67257	33.3333333
MS3_04778	0.38	0.62	0.57	0.44	0.7	7.29	7.05	1.27125	18	3	15.9292	12.5
MS3_05595	0.38	0.61	0.57	0.44	0.7	6.18	5.97	1.233681	1	0	0.884956	0
MS3_06299	0.38	0.61	0.56	0.42	0.71	6.8	6.98	0.83527	4	1	3.539823	4.16666667
MS3_06889	0.38	0.62	0.55	0.41	0.69	7.31	7.55	0.786628	17	6	15.04425	25
MS3_08161	0.38	0.62	0.57	0.44	0.7	7.93	7.67	1.29693	45	7	39.82301	29.1666667
MS3_08498	0.38	0.62	0.56	0.43	0.7	7.87	8.05	0.83527	28	8	24.77876	33.3333333
No hits	0.39	0.62	0.55	0.41	0.7	7.39	7.13	1.29693	20	6	17.69912	25
No hits	0.39	0.62	0.56	0.44	0.68	7.47	7.26	1.233678	26	3	23.00885	12.5
MS3_02653	0.39	0.62	0.55	0.43	0.67	7.26	7.11	1.161834	15	1	13.27434	4.16666667
MS3_02709	0.39	0.62	0.56	0.42	0.69	6.97	7.16	0.826959	7	3	6.19469	12.5
MS3_05326	0.39	0.62	0.58	0.44	0.72	7.37	7.18	1.20925	11	4	9.734513	16.6666667
MS3_05958	0.39	0.62	0.56	0.43	0.69	7.07	6.82	1.284026	22	3	19.46903	12.5
MS3_07420	0.39	0.62	0.55	0.43	0.67	7.05	6.9	1.161835	7	1	6.19469	4.16666667
MS3_07569	0.39	0.62	0.47	0.34	0.6	8.4	8.19	1.233678	50	11	44.24779	45.8333333
MS3_07593	0.39	0.63	0.53	0.38	0.68	8.47	8.22	1.284025	75	12	66.37168	50
MS3_08943	0.39	0.62	0.47	0.35	0.59	7.86	7.71	1.161834	31	5	27.43363	20.8333333
MS3_09735	0.39	0.62	0.55	0.43	0.66	7.14	6.9	1.27125	21	1	18.58407	4.16666667
MS3_10177	0.39	0.62	0.56	0.44	0.68	7.65	7.51	1.150274	18	2	15.9292	8.33333333
MS3_03295	0.4	0.63	0.56	0.43	0.7	7.48	7.21	1.309965	31	6	27.43363	25
MS3_07473	0.4	0.64	0.47	0.35	0.6	9.57	9.29	1.32313	99	18	87.61062	75
MS3_07831	0.4	0.63	0.55	0.4	0.7	7.68	7.88	0.818731	25	8	22.12389	33.3333333
MS3_08999	0.4	0.63	0.56	0.43	0.7	7.99	7.84	1.161834	35	8	30.97345	33.3333333

MS3_01289	0.41	0.64	0.57	0.43	0.7	7.62	7.37	1.284026	34	6	30.0885	25
MS3_01899	0.41	0.65	0.56	0.44	0.68	7.36	7.54	0.83527	23	5	20.35398	20.8333333
MS3_09778	0.41	0.64	0.56	0.43	0.68	7.38	7.54	0.852144	18	3	15.9292	12.5
MS3_10471	0.41	0.64	0.57	0.44	0.69	7.54	7.67	0.878095	13	4	11.50442	16.6666667
MS3_05754	0.42	0.66	0.54	0.4	0.67	7.06	7.23	0.843665	6	3	5.309735	12.5
MS3_07294	0.42	0.66	0.56	0.42	0.69	7.47	7.23	1.271249	36	6	31.85841	25
MS3_10209	0.42	0.66	0.47	0.35	0.6	7.03	7.31	0.755783	18	5	15.9292	20.8333333
MS3_10493	0.42	0.65	0.55	0.42	0.69	7.51	7.74	0.794534	26	8	23.00885	33.3333333
MS3_10619	0.42	0.65	0.55	0.42	0.68	7.43	7.21	1.246077	22	3	19.46903	12.5
MS3_00048	0.43	0.66	0.51	0.38	0.64	7.91	7.75	1.173511	26	6	23.00885	25
MS3_03193	0.43	0.66	0.56	0.43	0.68	7.79	7.64	1.161834	31	4	27.43363	16.6666667
MS3_05447	0.43	0.66	0.55	0.43	0.68	7.18	7.32	0.869358	6	1	5.309735	4.16666667
MS3_06069	0.43	0.66	0.59	0.45	0.72	8.18	8.36	0.83527	50	13	44.24779	54.1666667
MS3_06400	0.43	0.66	0.55	0.42	0.68	7.54	7.34	1.221403	31	7	27.43363	29.1666667
MS3_07280	0.43	0.66	0.55	0.43	0.67	7.65	7.49	1.173511	30	4	26.54867	16.6666667
MS3_07531	0.43	0.66	0.55	0.41	0.7	7.49	7.24	1.284026	33	7	29.20354	29.1666667
MS3_08808	0.43	0.66	0.56	0.42	0.7	7.28	7.03	1.284026	23	4	20.35398	16.6666667
MS3_10472	0.43	0.66	0.57	0.43	0.71	7.92	7.77	1.161834	26	5	23.00885	20.8333333
MS3_00703	0.44	0.67	0.55	0.42	0.68	7.02	7.18	0.852144	4	2	3.539823	8.33333333
MS3_04100	0.44	0.67	0.55	0.42	0.67	7.2	7.36	0.852144	10	3	8.849558	12.5
MS3_05530	0.44	0.67	0.54	0.41	0.68	6.74	6.98	0.786627	10	5	8.849558	20.8333333
MS3_06482	0.44	0.67	0.55	0.42	0.68	7.92	8.17	0.778801	47	13	41.59292	54.1666667
MS3_06732	0.44	0.67	0.54	0.42	0.67	7.45	7.2	1.284026	31	6	27.43363	25
MS3_06950	0.44	0.67	0.56	0.43	0.7	7.12	7.3	0.83527	8	4	7.079646	16.6666667
MS3_09128	0.44	0.67	0.56	0.42	0.7	7.26	7.47	0.810584	18	7	15.9292	29.1666667
MS3_10510	0.44	0.67	0.56	0.44	0.68	7.77	7.55	1.246077	38	7	33.62832	29.1666667
MS3_02674	0.45	0.67	0.58	0.46	0.7	6.81	6.94	0.878095	8	1	7.079646	4.16666667
MS3_02734	0.45	0.67	0.55	0.42	0.68	7	6.79	1.233679	16	3	14.15929	12.5
MS3_03084	0.45	0.67	0.58	0.44	0.71	8.57	8.75	0.83527	73	17	64.60177	70.8333333
MS3_04887	0.45	0.68	0.47	0.33	0.6	7.22	7.39	0.843665	12	3	10.61947	12.5
MS3_06979	0.45	0.67	0.53	0.4	0.66	6.74	6.9	0.852143	2	1	1.769912	4.16666667
MS3_07370	0.45	0.67	0.55	0.42	0.68	7.4	7.25	1.161834	16	3	14.15929	12.5
MS3_07467	0.45	0.68	0.57	0.45	0.7	7.79	7.58	1.233678	47	8	41.59292	33.3333333
MS3_07637	0.45	0.67	0.56	0.42	0.7	7.22	7.38	0.852144	9	4	7.964602	16.6666667
MS3_08472	0.45	0.67	0.52	0.4	0.64	7.91	8.15	0.786628	50	13	44.24779	54.1666667
MS3_02856	0.46	0.68	0.56	0.44	0.68	7.51	7.3	1.233678	42	6	37.16814	25
MS3_04179	0.46	0.69	0.55	0.42	0.69	8.1	8.21	0.895834	39	10	34.51327	41.6666667

MS3_05614	0.46	0.68	0.57	0.44	0.7	8.35	8.25	1.105171	57	10	50.44248	41.6666667
MS3_09683	0.46	0.68	0.61	0.48	0.74	7.48	7.17	1.363425	34	5	30.0885	20.8333333
MS3_10492	0.46	0.68	0.55	0.41	0.68	7.79	7.6	1.20925	36	7	31.85841	29.1666667
MS3_05213	0.47	0.69	0.54	0.42	0.66	6.99	7.18	0.826959	14	2	12.38938	8.33333333
MS3_07195	0.47	0.69	0.55	0.42	0.68	7.33	7.12	1.233678	25	5	22.12389	20.8333333
MS3_09406	0.47	0.69	0.56	0.44	0.69	7.76	7.63	1.138828	24	4	21.23894	16.6666667
MS3_10397	0.47	0.7	0.56	0.43	0.7	7.2	7.05	1.161834	10	2	8.849558	8.33333333
MS3_10607	0.47	0.7	0.53	0.4	0.66	6.4	6.61	0.810583	4	1	3.539823	4.16666667
MS3_00676	0.48	0.7	0.53	0.38	0.69	6.51	6.72	0.810584	2	5	1.769912	20.8333333
MS3_02804	0.48	0.7	0.53	0.39	0.66	8.05	7.86	1.20925	46	7	40.70796	29.1666667
MS3_03615	0.48	0.7	0.49	0.37	0.61	6.69	6.48	1.233679	16	3	14.15929	12.5
MS3_04453	0.48	0.7	0.53	0.4	0.67	7.8	7.64	1.173511	29	6	25.66372	25
MS3_05639	0.48	0.7	0.54	0.42	0.67	8.1	8.2	0.904837	40	8	35.39823	33.3333333
MS3_07716	0.48	0.7	0.56	0.43	0.69	7.18	7.07	1.116278	7	1	6.19469	4.16666667
MS3_07795	0.48	0.7	0.54	0.41	0.67	6.62	6.85	0.794533	7	1	6.19469	4.16666667
MS3_08692	0.48	0.7	0.55	0.42	0.68	7.5	7.29	1.233678	27	4	23.89381	16.6666667
MS3_10297	0.48	0.7	0.46	0.35	0.58	7.26	7.11	1.161834	21	2	18.58407	8.33333333
MS3_10753	0.48	0.7	0.55	0.42	0.67	7.46	7.26	1.221403	32	6	28.31858	25
MS3_05252	0.49	0.71	0.63	0.52	0.75	7.79	7.57	1.246077	28	2	24.77876	8.33333333
MS3_06075	0.49	0.71	0.55	0.41	0.69	7.68	7.81	0.878095	17	6	15.04425	25
MS3_08826	0.49	0.71	0.47	0.34	0.6	6.86	6.72	1.150274	10	2	8.849558	8.33333333
MS3_10225	0.49	0.71	0.55	0.43	0.67	8.2	8.02	1.197217	56	8	49.55752	33.3333333
MS3_04311	0.5	0.71	0.55	0.42	0.68	6.75	6.58	1.185306	8	2	7.079646	8.33333333
MS3_08460	0.5	0.71	0.57	0.44	0.7	7.33	7.11	1.246077	27	4	23.89381	16.6666667
MS3_10141	0.5	0.71	0.55	0.41	0.68	7.18	7.32	0.869358	10	2	8.849558	8.33333333
MS3_01001	0.5	0.71	0.47	0.34	0.6	7.52	7.39	1.138828	20	1	17.69912	4.16666667
MS3_02855	0.5	0.71	0.53	0.41	0.65	7.46	7.58	0.88692	15	3	13.27434	12.5
MS3_03405	0.5	0.71	0.57	0.43	0.71	7.65	7.78	0.878095	17	5	15.04425	20.8333333
MS3_05437	0.5	0.71	0.55	0.4	0.7	7.61	7.47	1.150274	12	7	10.61947	29.1666667
MS3_06507	0.5	0.71	0.56	0.43	0.69	7.12	6.92	1.221403	16	3	14.15929	12.5
MS3_07822	0.5	0.71	0.56	0.43	0.68	7.17	7.05	1.127497	10	3	8.849558	12.5
MS3_10943	0.5	0.71	0.58	0.46	0.71	7.31	7.45	0.869358	13	2	11.50442	8.33333333
MS3_11429	0.5	0.71	0.56	0.43	0.7	7.95	7.83	1.127497	30	4	26.54867	16.6666667
MS3_01664	0.51	0.72	0.55	0.42	0.68	7.47	7.61	0.869358	19	6	16.81416	25
MS3_02453	0.51	0.72	0.54	0.4	0.67	6.79	6.93	0.869358	2	2	1.769912	8.33333333
MS3_02474	0.51	0.72	0.53	0.41	0.66	7.87	7.78	1.094174	24	5	21.23894	20.8333333
MS3_04286	0.51	0.71	0.56	0.42	0.7	6.38	6.16	1.246079	6	4	5.309735	16.6666667

MS3_10249	0.51	0.72	0.56	0.43	0.69	7.93	8.06	0.878095	32	11	28.31858	45.8333333
MS3_10721	0.51	0.72	0.58	0.45	0.71	7.84	7.96	0.88692	24	8	21.23894	33.3333333
MS3_00719	0.52	0.73	0.55	0.42	0.69	7.41	7.55	0.869358	16	6	14.15929	25
MS3_00404	0.53	0.74	0.53	0.38	0.68	7.8	7.91	0.895834	22	6	19.46903	25
MS3_00876	0.53	0.74	0.56	0.43	0.69	7.54	7.44	1.105171	14	2	12.38938	8.33333333
MS3_05157	0.53	0.74	0.52	0.39	0.65	7.33	7.2	1.138829	12	3	10.61947	12.5
MS3_07600	0.53	0.74	0.56	0.42	0.69	7.68	7.56	1.127497	15	4	13.27434	16.6666667
MS3_08737	0.53	0.74	0.54	0.41	0.66	7.79	7.94	0.860708	21	6	18.58407	25
MS3_09305	0.53	0.74	0.53	0.38	0.67	8.03	7.92	1.116278	38	9	33.62832	37.5
MS3_02044	0.54	0.74	0.57	0.43	0.7	7.95	8.11	0.852144	40	10	35.39823	41.6666667
MS3_06022	0.54	0.74	0.57	0.46	0.68	7.48	7.59	0.895834	21	4	18.58407	16.6666667
MS3_08726	0.54	0.74	0.53	0.4	0.66	7.28	7.14	1.150274	13	4	11.50442	16.6666667
MS3_09970	0.54	0.74	0.58	0.46	0.7	7.28	7.42	0.869358	19	3	16.81416	12.5
MS3_10998	0.54	0.75	0.55	0.41	0.69	7.24	7.46	0.802519	22	8	19.46903	33.3333333
MS3_11432	0.54	0.75	0.53	0.4	0.67	7.07	7.25	0.83527	19	5	16.81416	20.8333333
MS3_07465	0.55	0.75	0.52	0.38	0.66	7.6	7.48	1.127497	18	5	15.9292	20.8333333
MS3_10188	0.55	0.76	0.61	0.49	0.72	6.89	7.01	0.88692	13	0	11.50442	0
MS3_02685	0.56	0.76	0.56	0.43	0.68	8.27	8.1	1.185305	64	11	56.63717	45.8333333
MS3_03192	0.56	0.76	0.48	0.34	0.62	7.28	7.42	0.869358	13	5	11.50442	20.8333333
MS3_03417	0.56	0.77	0.55	0.43	0.66	8.19	8.28	0.913931	48	13	42.47788	54.1666667
MS3_06468	0.56	0.77	0.54	0.41	0.66	7.08	6.98	1.105171	7	1	6.19469	4.16666667
MS3_06677	0.56	0.77	0.54	0.41	0.67	7.42	7.53	0.895834	16	5	14.15929	20.8333333
MS3_08159	0.56	0.76	0.52	0.39	0.65	7.34	7.49	0.860708	17	5	15.04425	20.8333333
MS3_05011	0.57	0.77	0.55	0.41	0.69	7.58	7.4	1.197217	33	6	29.20354	25
MS3_05126	0.57	0.77	0.56	0.43	0.68	7.78	7.61	1.185305	24	4	21.23894	16.6666667
MS3_10085	0.57	0.77	0.55	0.42	0.68	7.36	7.54	0.83527	24	8	21.23894	33.3333333
MS3_00449	0.58	0.78	0.52	0.4	0.65	7.44	7.57	0.878095	23	5	20.35398	20.8333333
MS3_00625	0.58	0.78	0.56	0.43	0.7	6.71	6.82	0.895834	5	2	4.424779	8.33333333
MS3_05646	0.58	0.78	0.48	0.34	0.61	7.05	7.16	0.895834	6	2	5.309735	8.33333333
MS3_05748	0.58	0.78	0.52	0.39	0.66	7.91	8	0.913931	22	8	19.46903	33.3333333
MS3_07606	0.58	0.78	0.49	0.37	0.61	7.84	7.99	0.860708	44	10	38.93805	41.6666667
MS3_08157	0.58	0.78	0.56	0.42	0.7	7.76	7.87	0.895834	18	7	15.9292	29.1666667
MS3_08276	0.58	0.78	0.54	0.41	0.67	7.61	7.46	1.161834	36	7	31.85841	29.1666667
MS3_11247	0.58	0.78	0.55	0.41	0.69	7.75	7.64	1.116278	22	5	19.46903	20.8333333
MS3_03171	0.59	0.78	0.54	0.41	0.67	7.68	7.57	1.116278	19	4	16.81416	16.6666667
MS3_05026	0.59	0.79	0.54	0.4	0.68	7.78	7.61	1.185305	40	7	35.39823	29.1666667
MS3_06668	0.59	0.78	0.56	0.44	0.67	8.14	8.05	1.094174	52	8	46.0177	33.3333333

MS3_08925	0.59	0.79	0.54	0.41	0.66	7.13	6.98	1.161835	19	4	16.81416	16.6666667
MS3_10423	0.59	0.78	0.56	0.42	0.7	8.39	8.51	0.88692	52	17	46.0177	70.8333333
MS3_11273	0.59	0.79	0.55	0.41	0.69	7.81	7.7	1.116278	29	6	25.66372	25
MS3_02237	0.6	0.79	0.51	0.38	0.64	7.68	7.58	1.105171	25	3	22.12389	12.5
MS3_02396	0.6	0.79	0.53	0.39	0.68	7.72	7.82	0.904837	17	6	15.04425	25
MS3_03655	0.6	0.79	0.55	0.41	0.69	7.61	7.74	0.878095	24	8	21.23894	33.3333333
MS3_04386	0.6	0.79	0.55	0.41	0.68	7.53	7.64	0.895834	17	7	15.04425	29.1666667
MS3_04680	0.6	0.79	0.53	0.4	0.66	7.9	7.77	1.138828	40	9	35.39823	37.5
MS3_08008	0.6	0.79	0.46	0.31	0.61	7.24	7.08	1.173511	22	3	19.46903	12.5
MS3_09780	0.6	0.79	0.52	0.39	0.66	7.1	7.24	0.869358	16	6	14.15929	25
MS3_11250	0.6	0.79	0.54	0.41	0.67	7.3	7.13	1.185305	29	6	25.66372	25
MS3_01643	0.61	0.8	0.49	0.37	0.62	7.97	7.88	1.094174	30	5	26.54867	20.8333333
MS3_02944	0.61	0.8	0.49	0.35	0.62	8.02	7.93	1.094174	33	7	29.20354	29.1666667
MS3_04275	0.61	0.79	0.54	0.4	0.68	7.71	7.6	1.116278	22	5	19.46903	20.8333333
MS3_05352	0.61	0.8	0.52	0.4	0.63	8.27	8.36	0.913931	55	15	48.67257	62.5
MS3_07590	0.61	0.8	0.55	0.42	0.68	7.36	7.21	1.161834	24	5	21.23894	20.8333333
MS3_09296	0.61	0.8	0.49	0.35	0.63	7.91	7.77	1.150274	34	8	30.0885	33.3333333
MS3_01096	0.62	0.8	0.52	0.39	0.66	7.53	7.44	1.094174	14	4	12.38938	16.6666667
MS3_02359	0.62	0.8	0.5	0.37	0.62	7.07	6.98	1.094174	7	0	6.19469	0
MS3_02952	0.62	0.8	0.53	0.39	0.67	6.83	6.92	0.913931	4	1	3.539823	4.16666667
MS3_05555	0.62	0.8	0.52	0.39	0.64	6.5	6.4	1.105171	3	0	2.654867	0
MS3_05896	0.62	0.8	0.53	0.4	0.66	7.48	7.56	0.923116	16	4	14.15929	16.6666667
MS3_07304	0.62	0.8	0.54	0.39	0.68	7.52	7.63	0.895834	18	8	15.9292	33.3333333
MS3_11239	0.62	0.8	0.48	0.35	0.61	7.03	6.95	1.083287	2	0	1.769912	0
MS3_03443	0.63	0.81	0.52	0.38	0.66	7.96	7.85	1.116278	43	9	38.0531	37.5
MS3_04781	0.63	0.81	0.53	0.4	0.66	7.91	7.82	1.094174	32	6	28.31858	25
MS3_06834	0.63	0.81	0.53	0.41	0.66	6.25	6.36	0.895833	4	0	3.539823	0
MS3_08366	0.63	0.81	0.53	0.42	0.64	7.38	7.28	1.105171	22	2	19.46903	8.33333333
MS3_08444	0.63	0.81	0.53	0.39	0.67	8	7.91	1.094174	29	7	25.66372	29.1666667
MS3_08593	0.63	0.81	0.54	0.41	0.67	6.69	6.56	1.138829	10	3	8.849558	12.5
MS3_02086	0.64	0.81	0.53	0.4	0.67	7.87	7.72	1.161834	50	10	44.24779	41.6666667
MS3_03079	0.64	0.81	0.53	0.39	0.66	7.81	7.66	1.161834	42	9	37.16814	37.5
MS3_05016	0.64	0.81	0.53	0.38	0.67	7.87	7.97	0.904837	31	10	27.43363	41.6666667
MS3_06798	0.64	0.81	0.45	0.34	0.57	7.01	7.11	0.904837	9	3	7.964602	12.5
MS3_10898	0.64	0.81	0.54	0.4	0.67	8.06	7.91	1.161834	49	9	43.36283	37.5
MS3_01983	0.65	0.82	0.51	0.39	0.64	8.36	8.43	0.932394	57	14	50.44248	58.3333333
MS3_02001	0.65	0.82	0.54	0.42	0.67	7.15	7.02	1.138829	22	3	19.46903	12.5

MS3_03511	0.65	0.82	0.52	0.37	0.66	7.31	7.41	0.904837	8	3	7.079646	12.5
MS3_06746	0.65	0.82	0.55	0.45	0.66	7.43	7.32	1.116278	37	3	32.74336	12.5
MS3_10022	0.65	0.82	0.53	0.39	0.68	7.15	7.24	0.913931	7	1	6.19469	4.16666667
MS3_11161	0.65	0.83	0.47	0.34	0.6	7.16	7.07	1.094174	8	2	7.079646	8.33333333
MS3_01775	0.66	0.83	0.53	0.41	0.66	7.27	7.36	0.913931	14	2	12.38938	8.33333333
MS3_04717	0.66	0.83	0.52	0.41	0.64	6.99	6.92	1.072508	8	1	7.079646	4.16666667
MS3_05170	0.66	0.83	0.52	0.38	0.65	7.74	7.62	1.127497	33	8	29.20354	33.3333333
MS3_06789	0.66	0.83	0.52	0.39	0.65	7.81	7.74	1.072508	29	7	25.66372	29.1666667
MS3_08019	0.66	0.83	0.55	0.41	0.69	7.39	7.25	1.150274	26	5	23.00885	20.8333333
MS3_04642	0.67	0.84	0.49	0.36	0.62	7.09	7.21	0.88692	21	5	18.58407	20.8333333
MS3_07002	0.67	0.84	0.54	0.41	0.67	7.82	7.9	0.923116	23	7	20.35398	29.1666667
MS3_11045	0.67	0.84	0.52	0.4	0.65	6.45	6.33	1.127498	8	1	7.079646	4.16666667
MS3_01353	0.68	0.85	0.51	0.36	0.65	7.57	7.66	0.913931	13	5	11.50442	20.8333333
MS3_01922	0.68	0.85	0.53	0.39	0.66	7.17	7.06	1.116278	18	3	15.9292	12.5
MS3_04276	0.68	0.85	0.54	0.4	0.67	7.4	7.32	1.083287	9	4	7.964602	16.6666667
MS3_06403	0.68	0.85	0.46	0.34	0.58	6.6	6.69	0.913931	5	1	4.424779	4.16666667
MS3_07045	0.68	0.85	0.51	0.39	0.62	7.46	7.38	1.083287	17	3	15.04425	12.5
MS3_10935	0.68	0.85	0.5	0.36	0.65	7.31	7.42	0.895834	9	4	7.964602	16.6666667
MS3_01627	0.69	0.85	0.47	0.33	0.6	7.42	7.31	1.116278	25	4	22.12389	16.6666667
MS3_06669	0.69	0.85	0.53	0.39	0.68	7.63	7.5	1.138828	35	9	30.97345	37.5
MS3_07345	0.69	0.85	0.53	0.4	0.65	7.15	7.04	1.116278	17	3	15.04425	12.5
MS3_09240	0.69	0.85	0.55	0.41	0.69	7.83	7.9	0.932394	26	8	23.00885	33.3333333
MS3_10288	0.69	0.85	0.49	0.36	0.62	8.11	8.18	0.932394	50	10	44.24779	41.6666667
MS3_00076	0.7	0.85	0.53	0.39	0.67	7.65	7.72	0.932394	13	5	11.50442	20.8333333
MS3_01558	0.7	0.86	0.54	0.41	0.68	6.95	7.02	0.932394	7	0	6.19469	0
MS3_02476	0.7	0.86	0.53	0.39	0.67	7.46	7.39	1.072508	12	4	10.61947	16.6666667
MS3_05999	0.7	0.85	0.53	0.39	0.68	7.53	7.4	1.138828	34	9	30.0885	37.5
MS3_08937	0.7	0.86	0.48	0.35	0.61	7.55	7.43	1.127497	37	7	32.74336	29.1666667
MS3_09826	0.7	0.86	0.53	0.39	0.67	8.09	8.17	0.923116	50	11	44.24779	45.8333333
MS3_01693	0.71	0.86	0.56	0.43	0.69	7.02	6.9	1.127497	14	2	12.38938	8.33333333
MS3_02027	0.71	0.87	0.53	0.39	0.66	7.2	7.09	1.116278	24	5	21.23894	20.8333333
MS3_03231	0.71	0.87	0.49	0.35	0.62	7.3	7.23	1.072508	9	2	7.964602	8.33333333
MS3_07374	0.71	0.87	0.53	0.41	0.65	7.16	7.07	1.094174	25	4	22.12389	16.6666667
MS3_02048	0.72	0.87	0.52	0.39	0.64	7.26	7.18	1.083287	11	2	9.734513	8.33333333
MS3_05360	0.72	0.87	0.49	0.36	0.61	7.32	7.37	0.951229	9	2	7.964602	8.33333333
MS3_06347	0.72	0.87	0.56	0.42	0.71	7.73	7.66	1.072508	18	5	15.9292	20.8333333
MS3_08178	0.72	0.87	0.51	0.36	0.66	7.31	7.38	0.932394	9	3	7.964602	12.5

MS3_09274	0.72	0.87	0.48	0.36	0.61	7.02	7.11	0.913931	13	4	11.50442	16.6666667
MS3_10028	0.72	0.87	0.53	0.41	0.65	7.52	7.45	1.072508	23	4	20.35398	16.6666667
MS3_00450	0.73	0.88	0.48	0.34	0.63	7.76	7.82	0.941765	19	7	16.81416	29.1666667
MS3_03130	0.73	0.88	0.55	0.42	0.68	7.17	7.23	0.941764	7	0	6.19469	0
MS3_03558	0.73	0.88	0.54	0.4	0.68	7.53	7.6	0.932394	15	4	13.27434	16.6666667
MS3_07156	0.73	0.88	0.53	0.4	0.65	6.76	6.82	0.941764	5	1	4.424779	4.16666667
MS3_07509	0.73	0.88	0.55	0.4	0.7	8.01	8.09	0.923116	36	11	31.85841	45.8333333
MS3_08607	0.73	0.88	0.53	0.41	0.65	7.77	7.82	0.951229	26	5	23.00885	20.8333333
MS3_08871	0.73	0.88	0.5	0.38	0.63	7.99	8.05	0.941765	41	7	36.28319	29.1666667
MS3_00405	0.74	0.88	0.53	0.41	0.64	7.59	7.54	1.051271	23	2	20.35398	8.33333333
MS3_01053	0.74	0.88	0.47	0.33	0.61	6.87	6.8	1.072508	6	2	5.309735	8.33333333
MS3_01240	0.74	0.88	0.52	0.39	0.64	7.48	7.54	0.941765	21	5	18.58407	20.8333333
MS3_01435	0.74	0.88	0.55	0.43	0.67	7.87	7.8	1.072508	40	6	35.39823	25
MS3_02050	0.74	0.88	0.48	0.35	0.61	8.12	8.06	1.061837	45	11	39.82301	45.8333333
MS3_04342	0.74	0.88	0.53	0.41	0.66	7.69	7.59	1.105171	40	5	35.39823	20.8333333
MS3_08776	0.74	0.88	0.55	0.41	0.69	7.9	7.84	1.061837	26	7	23.00885	29.1666667
MS3_08823	0.74	0.88	0.51	0.37	0.64	7.49	7.42	1.072508	12	3	10.61947	12.5
MS3_00004	0.75	0.88	0.55	0.4	0.7	7.75	7.82	0.932394	21	8	18.58407	33.3333333
MS3_00047	0.75	0.88	0.53	0.41	0.65	7.74	7.65	1.094174	46	9	40.70796	37.5
MS3_00862	0.75	0.88	0.51	0.39	0.63	7.14	7.23	0.913931	23	3	20.35398	12.5
MS3_02787	0.75	0.88	0.53	0.42	0.65	8	7.93	1.072508	34	9	30.0885	37.5
MS3_03226	0.75	0.88	0.49	0.36	0.62	7.68	7.74	0.941765	24	5	21.23894	20.8333333
MS3_04617	0.75	0.88	0.5	0.38	0.62	6.41	6.35	1.061837	5	0	4.424779	0
MS3_08953	0.75	0.88	0.54	0.42	0.65	7.51	7.57	0.941765	18	3	15.9292	12.5
MS3_10221	0.75	0.88	0.53	0.4	0.66	7.67	7.6	1.072508	24	4	21.23894	16.6666667
MS3_03424	0.76	0.89	0.58	0.45	0.7	7.57	7.62	0.951229	18	2	15.9292	8.33333333
MS3_03938	0.76	0.89	0.53	0.41	0.65	6.76	6.81	0.951229	5	0	4.424779	0
MS3_04582	0.76	0.89	0.53	0.41	0.65	8.22	8.18	1.040811	48	9	42.47788	37.5
MS3_08926	0.76	0.89	0.53	0.4	0.66	7.52	7.42	1.105171	33	6	29.20354	25
MS3_00183	0.77	0.89	0.53	0.4	0.66	8.13	8.04	1.094174	61	11	53.9823	45.8333333
MS3_02407	0.77	0.89	0.53	0.4	0.66	7.32	7.23	1.094174	24	5	21.23894	20.8333333
MS3_03814	0.77	0.89	0.54	0.4	0.67	7.57	7.48	1.094174	39	8	34.51327	33.3333333
MS3_05034	0.77	0.89	0.51	0.37	0.65	7.27	7.19	1.083287	17	6	15.04425	25
MS3_06368	0.77	0.89	0.49	0.36	0.62	6.62	6.7	0.923116	8	2	7.079646	8.33333333
MS3_08717	0.77	0.89	0.53	0.4	0.67	8.3	8.24	1.061837	57	10	50.44248	41.6666667
MS3_11077	0.77	0.89	0.5	0.38	0.63	7.14	7.19	0.951229	4	2	3.539823	8.33333333
MS3_00066	0.78	0.89	0.54	0.39	0.68	7.74	7.81	0.932394	23	8	20.35398	33.3333333

MS3_01422	0.78	0.89	0.57	0.46	0.67	7.27	7.19	1.083287	22	3	19.46903	12.5
MS3_01902	0.78	0.89	0.55	0.42	0.68	7.68	7.74	0.941765	17	5	15.04425	20.8333333
MS3_03047	0.78	0.89	0.48	0.34	0.62	7.33	7.25	1.083287	25	5	22.12389	20.8333333
MS3_03301	0.78	0.89	0.53	0.38	0.67	7.15	7.07	1.083287	16	7	14.15929	29.1666667
MS3_06125	0.78	0.89	0.49	0.36	0.61	7.61	7.55	1.061837	28	7	24.77876	29.1666667
MS3_06296	0.78	0.89	0.53	0.39	0.66	7.66	7.57	1.094174	32	8	28.31858	33.3333333
MS3_07363	0.78	0.89	0.48	0.34	0.62	6.99	7.08	0.913931	12	5	10.61947	20.8333333
MS3_07686	0.78	0.89	0.53	0.39	0.66	8.03	7.95	1.083287	55	11	48.67257	45.8333333
MS3_09546	0.78	0.89	0.51	0.37	0.64	8.1	8.05	1.051271	38	9	33.62832	37.5
MS3_10421	0.78	0.89	0.53	0.4	0.65	8.52	8.57	0.951229	70	18	61.9469	75
MS3_03662	0.79	0.9	0.52	0.39	0.66	7.57	7.62	0.951229	17	5	15.04425	20.8333333
MS3_08158	0.79	0.9	0.52	0.39	0.65	7.93	7.97	0.960789	29	6	25.66372	25
MS3_09879	0.79	0.9	0.52	0.38	0.65	7.01	6.96	1.051271	4	0	3.539823	0
MS3_06149	0.8	0.9	0.51	0.38	0.64	7.92	8	0.923116	47	12	41.59292	50
MS3_00504	0.8	0.9	0.52	0.38	0.67	7.87	7.81	1.061837	25	9	22.12389	37.5
MS3_03937	0.8	0.9	0.49	0.37	0.61	6.83	6.9	0.932394	14	2	12.38938	8.33333333
MS3_06424	0.8	0.91	0.53	0.4	0.66	8.27	8.22	1.051271	54	10	47.78761	41.6666667
MS3_09613	0.8	0.91	0.49	0.37	0.61	8.48	8.52	0.960789	64	11	56.63717	45.8333333
MS3_04178	0.81	0.92	0.49	0.35	0.63	6.24	6.3	0.941764	3	1	2.654867	4.16666667
MS3_04267	0.81	0.92	0.51	0.39	0.63	7.11	7.18	0.932394	22	3	19.46903	12.5
MS3_07126	0.81	0.91	0.52	0.4	0.64	7.43	7.47	0.960789	16	2	14.15929	8.33333333
MS3_08210	0.81	0.91	0.55	0.4	0.69	7.43	7.37	1.061837	15	5	13.27434	20.8333333
MS3_08337	0.81	0.91	0.49	0.36	0.62	7.14	7.19	0.951229	7	3	6.19469	12.5
MS3_10687	0.81	0.91	0.53	0.39	0.67	8.02	7.98	1.040811	32	8	28.31858	33.3333333
MS3_01104	0.82	0.92	0.53	0.4	0.67	7.38	7.31	1.072508	28	6	24.77876	25
MS3_02307	0.82	0.92	0.53	0.39	0.66	7.44	7.37	1.072508	32	6	28.31858	25
MS3_02425	0.82	0.92	0.52	0.38	0.66	7.52	7.45	1.072508	31	9	27.43363	37.5
MS3_08839	0.82	0.92	0.52	0.4	0.65	7.81	7.85	0.960789	26	7	23.00885	29.1666667
MS3_10475	0.82	0.92	0.53	0.4	0.67	7.69	7.73	0.960789	23	6	20.35398	25
MS3_01262	0.83	0.92	0.5	0.37	0.64	7.54	7.5	1.040811	23	5	20.35398	20.8333333
MS3_06947	0.83	0.92	0.5	0.35	0.65	7.81	7.85	0.960789	25	8	22.12389	33.3333333
MS3_07892	0.83	0.92	0.52	0.4	0.65	6.52	6.48	1.040811	5	0	4.424779	0
MS3_08160	0.83	0.92	0.52	0.38	0.65	7.59	7.52	1.072508	28	7	24.77876	29.1666667
MS3_08450	0.83	0.92	0.5	0.37	0.63	7.27	7.33	0.941764	20	6	17.69912	25
MS3_08727	0.83	0.92	0.53	0.42	0.65	6.96	6.99	0.970445	3	0	2.654867	0
MS3_09682	0.83	0.92	0.54	0.42	0.67	8.21	8.15	1.061837	60	11	53.09735	45.8333333
MS3_10138	0.83	0.92	0.49	0.36	0.61	8.55	8.51	1.040811	62	15	54.86726	62.5

MS3_10572	0.83	0.92	0.53	0.38	0.68	6.99	6.93	1.061837	11	6	9.734513	25
MS3_00147	0.84	0.92	0.51	0.36	0.65	7.45	7.4	1.051271	16	4	14.15929	16.6666667
MS3_00881	0.84	0.92	0.51	0.39	0.63	6.91	6.86	1.051271	14	1	12.38938	4.16666667
MS3_01764	0.84	0.92	0.51	0.4	0.62	7.73	7.68	1.051271	44	8	38.93805	33.3333333
MS3_02747	0.84	0.92	0.53	0.39	0.67	6.69	6.62	1.072508	12	3	10.61947	12.5
MS3_04646	0.84	0.92	0.52	0.41	0.64	8.41	8.45	0.960789	54	14	47.78761	58.3333333
MS3_06009	0.84	0.92	0.53	0.4	0.66	6.91	6.96	0.951229	12	1	10.61947	4.16666667
MS3_07299	0.84	0.92	0.5	0.39	0.6	7.57	7.6	0.970446	21	1	18.58407	4.16666667
MS3_07464	0.84	0.92	0.53	0.4	0.65	6.92	6.87	1.051271	14	3	12.38938	12.5
MS3_00604	0.85	0.92	0.53	0.4	0.66	7.66	7.61	1.051271	33	6	29.20354	25
MS3_02954	0.85	0.92	0.5	0.36	0.64	7.46	7.5	0.960789	10	5	8.849558	20.8333333
MS3_03853	0.85	0.92	0.53	0.39	0.67	6.48	6.51	0.970445	2	0	1.769912	0
MS3_04817	0.85	0.92	0.53	0.39	0.67	7.48	7.51	0.970446	13	4	11.50442	16.6666667
MS3_07406	0.85	0.92	0.53	0.4	0.66	6.42	6.46	0.960789	5	1	4.424779	4.16666667
MS3_08929	0.85	0.93	0.48	0.35	0.62	7.49	7.52	0.970446	16	5	14.15929	20.8333333
MS3_08945	0.85	0.92	0.53	0.4	0.65	7.25	7.2	1.051271	28	3	24.77876	12.5
MS3_10816	0.85	0.92	0.49	0.35	0.63	7.37	7.31	1.061837	18	6	15.9292	25
MS3_01276	0.86	0.93	0.52	0.38	0.66	7.41	7.38	1.030455	13	4	11.50442	16.6666667
MS3_03420	0.86	0.93	0.53	0.41	0.64	7.97	8	0.970446	39	9	34.51327	37.5
MS3_07799	0.86	0.93	0.49	0.36	0.62	7.89	7.92	0.970446	28	7	24.77876	29.1666667
MS3_08176	0.86	0.93	0.48	0.35	0.62	7.64	7.61	1.030455	12	3	10.61947	12.5
MS3_09691	0.86	0.93	0.5	0.37	0.63	8.55	8.5	1.051271	72	15	63.71681	62.5
MS3_01653	0.87	0.93	0.51	0.38	0.64	7.58	7.54	1.040811	26	7	23.00885	29.1666667
MS3_02275	0.87	0.93	0.53	0.4	0.66	7.29	7.24	1.051271	24	4	21.23894	16.6666667
MS3_02752	0.87	0.93	0.52	0.39	0.66	7.21	7.16	1.051271	24	6	21.23894	25
MS3_02951	0.87	0.93	0.52	0.39	0.65	9.1	9.07	1.030455	87	17	76.99115	70.8333333
MS3_03419	0.87	0.93	0.53	0.39	0.67	8.5	8.46	1.040811	71	12	62.83186	50
MS3_03979	0.87	0.94	0.48	0.36	0.61	7.17	7.2	0.970446	7	0	6.19469	0
MS3_08105	0.87	0.93	0.5	0.36	0.64	6.8	6.84	0.960789	11	3	9.734513	12.5
MS3_00494	0.88	0.94	0.52	0.38	0.66	6.46	6.42	1.040811	5	2	4.424779	8.33333333
MS3_02088	0.88	0.94	0.49	0.36	0.62	7.46	7.48	0.980199	12	3	10.61947	12.5
MS3_03385	0.88	0.94	0.53	0.42	0.63	7.45	7.47	0.980199	16	1	14.15929	4.16666667
MS3_03918	0.88	0.94	0.48	0.35	0.62	7.55	7.52	1.030455	17	4	15.04425	16.6666667
MS3_03976	0.88	0.94	0.49	0.36	0.62	7.91	7.87	1.040811	38	11	33.62832	45.8333333
MS3_09634	0.88	0.94	0.51	0.36	0.66	8.09	8.05	1.040811	37	10	32.74336	41.6666667
MS3_09698	0.88	0.94	0.52	0.39	0.66	7.24	7.22	1.020201	7	3	6.19469	12.5
MS3_00610	0.89	0.94	0.52	0.4	0.65	7.5	7.54	0.960789	28	6	24.77876	25

MS3_04206	0.89	0.95	0.5	0.39	0.62	7.77	7.75	1.020201	25	6	22.12389	25
MS3_04584	0.89	0.94	0.5	0.36	0.63	9.15	9.11	1.040811	93	19	82.30088	79.1666667
MS3_09865	0.89	0.94	0.49	0.36	0.63	8.53	8.57	0.960789	59	14	52.21239	58.3333333
MS3_04266	0.9	0.95	0.52	0.37	0.67	8.05	8.07	0.980199	34	10	30.0885	41.6666667
MS3_07816	0.9	0.95	0.51	0.38	0.64	7.3	7.27	1.030455	25	6	22.12389	25
MS3_10252	0.9	0.95	0.52	0.39	0.65	7.43	7.46	0.970446	23	6	20.35398	25
MS3_03406	0.91	0.95	0.49	0.37	0.61	7.47	7.44	1.030455	22	2	19.46903	8.33333333
MS3_03513	0.91	0.95	0.49	0.37	0.61	6.29	6.27	1.020201	5	0	4.424779	0
MS3_04225	0.91	0.95	0.49	0.36	0.62	7.26	7.29	0.970446	24	7	21.23894	29.1666667
MS3_07587	0.91	0.95	0.5	0.37	0.62	8.92	8.95	0.970446	87	20	76.99115	83.3333333
MS3_01636	0.92	0.96	0.5	0.36	0.63	7.48	7.5	0.980199	16	5	14.15929	20.8333333
MS3_02465	0.92	0.96	0.5	0.37	0.63	6.73	6.7	1.030455	5	2	4.424779	8.33333333
MS3_03800	0.92	0.96	0.57	0.45	0.69	7.16	7.11	1.051271	25	2	22.12389	8.33333333
MS3_03802	0.92	0.96	0.54	0.38	0.69	6.7	6.67	1.030455	8	3	7.079646	12.5
MS3_03977	0.92	0.96	0.5	0.37	0.63	7.44	7.47	0.970446	33	7	29.20354	29.1666667
MS3_04474	0.92	0.96	0.5	0.36	0.64	7.84	7.82	1.020201	32	6	28.31858	25
MS3_07372	0.92	0.96	0.51	0.38	0.65	7.31	7.36	0.951229	28	7	24.77876	29.1666667
MS3_07823	0.92	0.96	0.54	0.42	0.66	7.72	7.7	1.020201	26	5	23.00885	20.8333333
MS3_01095	0.93	0.96	0.5	0.38	0.61	7.47	7.45	1.020201	25	2	22.12389	8.33333333
MS3_05332	0.93	0.97	0.5	0.37	0.62	8.01	7.99	1.020201	44	7	38.93805	29.1666667
MS3_05911	0.93	0.96	0.51	0.38	0.64	7.11	7.09	1.020201	18	5	15.9292	20.8333333
MS3_00665	0.94	0.97	0.5	0.37	0.63	7.28	7.26	1.020201	14	2	12.38938	8.33333333
MS3_02141	0.94	0.97	0.51	0.36	0.66	8.02	8.04	0.980199	31	8	27.43363	33.3333333
MS3_02368	0.94	0.97	0.49	0.36	0.63	7.31	7.29	1.020201	10	4	8.849558	16.6666667
MS3_02690	0.94	0.97	0.59	0.48	0.69	6.98	6.96	1.020201	16	1	14.15929	4.16666667
MS3_04449	0.94	0.97	0.54	0.42	0.65	7.71	7.7	1.01005	48	5	42.47788	20.8333333
MS3_00287	0.95	0.97	0.51	0.38	0.65	7.55	7.54	1.01005	21	6	18.58407	25
MS3_00413	0.95	0.98	0.52	0.39	0.65	7.22	7.23	0.99005	13	3	11.50442	12.5
MS3_03618	0.95	0.97	0.53	0.38	0.68	6.27	6.29	0.980199	3	1	2.654867	4.16666667
MS3_06538	0.95	0.97	0.51	0.39	0.63	8.09	8.08	1.01005	44	9	38.93805	37.5
MS3_06807	0.96	0.98	0.54	0.42	0.66	7.27	7.28	0.99005	17	1	15.04425	4.16666667
MS3_07651	0.96	0.99	0.51	0.38	0.64	7.17	7.16	1.01005	13	3	11.50442	12.5
MS3_09076	0.96	0.98	0.53	0.4	0.65	7.12	7.13	0.99005	10	2	8.849558	8.33333333
MS3_01445	0.97	0.99	0.54	0.43	0.64	6.87	6.87	1	13	1	11.50442	4.16666667
MS3_05077	0.97	0.99	0.54	0.41	0.66	8.3	8.29	1.01005	47	15	41.59292	62.5
MS3_06729	0.97	0.99	0.49	0.38	0.6	7.63	7.64	0.99005	27	2	23.89381	8.33333333
MS3_07010	0.97	0.99	0.5	0.37	0.64	7.74	7.75	0.99005	39	7	34.51327	29.1666667

MS3_08415	0.97	0.99	0.5	0.39	0.61	7.61	7.61	1	23	3	20.35398	12.5
MS3_09371	0.97	0.99	0.51	0.36	0.65	7.53	7.54	0.99005	17	5	15.04425	20.8333333
MS3_09434	0.97	0.99	0.52	0.38	0.66	7.5	7.49	1.01005	25	7	22.12389	29.1666667
MS3_07231	0.98	0.99	0.52	0.39	0.65	7.48	7.48	1	27	6	23.89381	25
MS3_08723	0.98	0.99	0.5	0.38	0.62	7.43	7.43	1	15	2	13.27434	8.33333333
MS3_00187	0.99	1	0.51	0.37	0.65	7.61	7.61	1	16	4	14.15929	16.6666667
MS3_01160	0.99	1	0.51	0.37	0.65	7.55	7.55	1	23	5	20.35398	20.8333333
MS3_01274	0.99	1	0.51	0.38	0.65	7.85	7.85	1	35	8	30.97345	33.3333333
MS3_03101	0.99	1	0.48	0.36	0.6	7.57	7.58	0.99005	34	4	30.0885	16.6666667
MS3_05226	0.99	1	0.53	0.41	0.65	7.84	7.84	1	26	4	23.00885	16.6666667
MS3_05953	0.99	1	0.5	0.37	0.63	8.17	8.17	1	38	9	33.62832	37.5
MS3_04499	1	1	0.51	0.38	0.63	7.46	7.46	1	23	2	20.35398	8.33333333
MS3_05837	1	1	0.49	0.37	0.6	8.4	8.4	1	65	17	57.52212	70.8333333
MS3_09124	1	1	0.48	0.35	0.6	6.78	6.79	0.99005	5	2	4.424779	8.33333333
MS3_10193	1	1	0.5	0.37	0.63	7.2	7.2	1	5	1	4.424779	4.16666667
MS3_10345	1	1	0.49	0.36	0.62	8.14	8.14	1	59	13	52.21239	54.1666667

*WormBase ParaSite online database, version 14 https://parasite.wormbase.org/Schistosoma_haematobium_prjna78265/Info/Index/

Figure S1: Schematic of PoC-ICT design. The conjugate pad (orange) was coated with 10 OD of gold-conjugated mouse anti-human IgG (to capture any human IgG present in the applied serum), 1.0 mg/ml of recombinant antigen (*Sh*-TSP-2 in this example) was sprayed at the test line (to capture any anti-*Sh*-TSP-2 human IgG/anti-human IgG gold-conjugate complex) and 1.0 mg/ml anti-mouse IgG was sprayed at the control line (to capture anti-human IgG gold-conjugate and serve as an internal validation). For each strip, a band at the test and control lines was considered a positive result, a band at the control line only was considered a negative result and a test was considered invalid if there was no band at the control line.

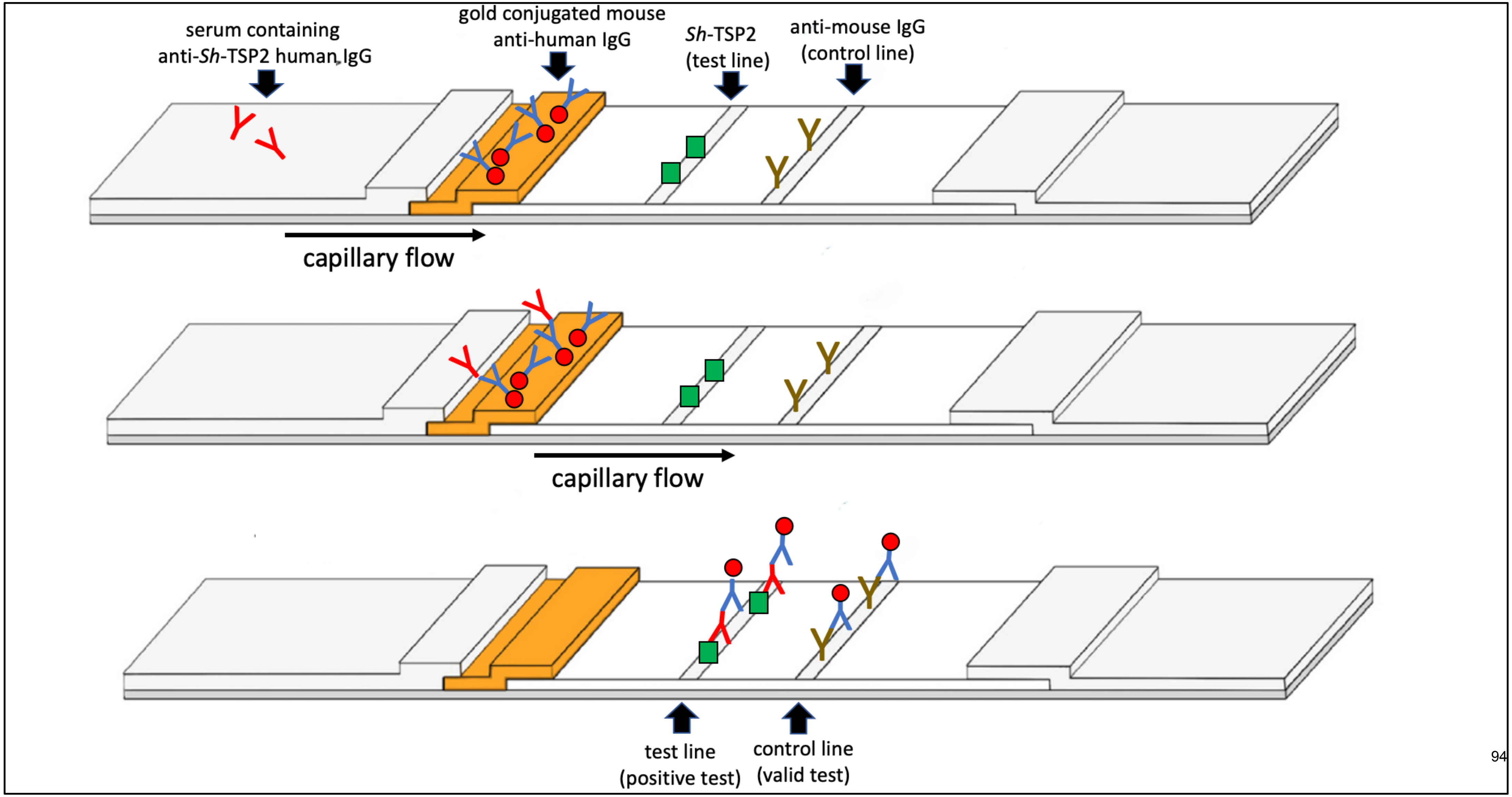


Figure S2. Scatterplot showing correlation of *S. haematobium* infection intensity (urine egg burden) with individual mean SI of all spots resulting from probing of *S. haematobium* protein arrays with different diagnostic fluids. (A) Serum. (B) Urine.

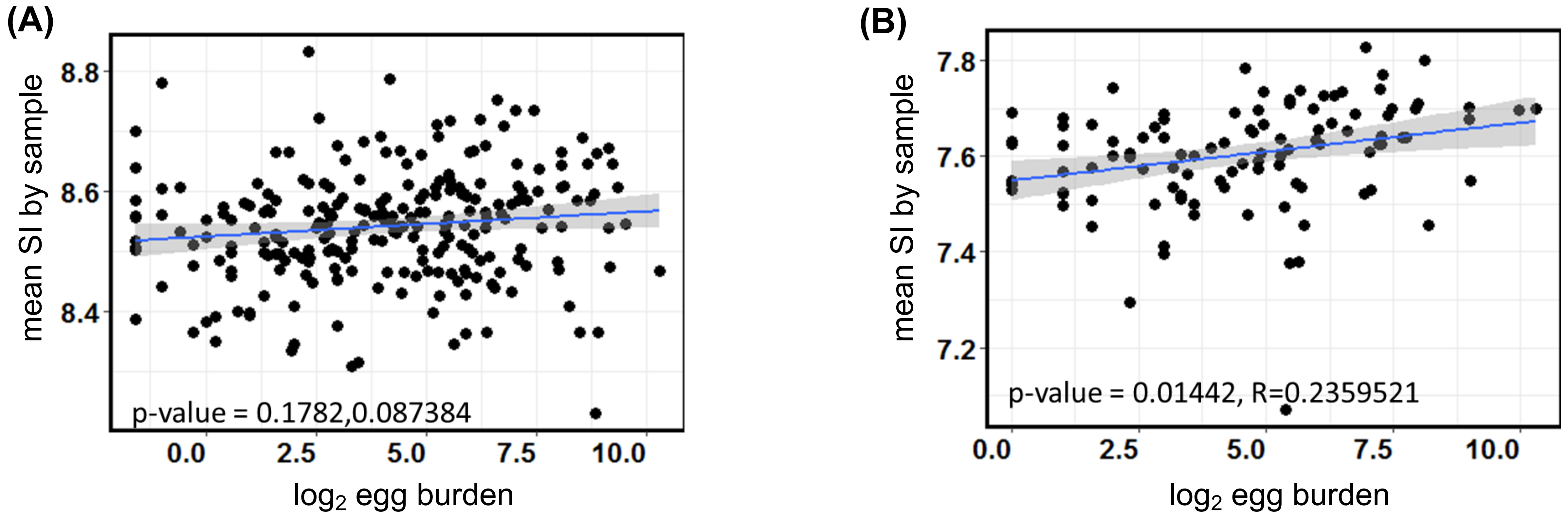


Figure S3. Receiver operating characteristic curve showing diagnostic performance (area under the curve - AUC) of the minimal antibody signature in each diagnostic fluid. (A) Serum. (B) Urine.

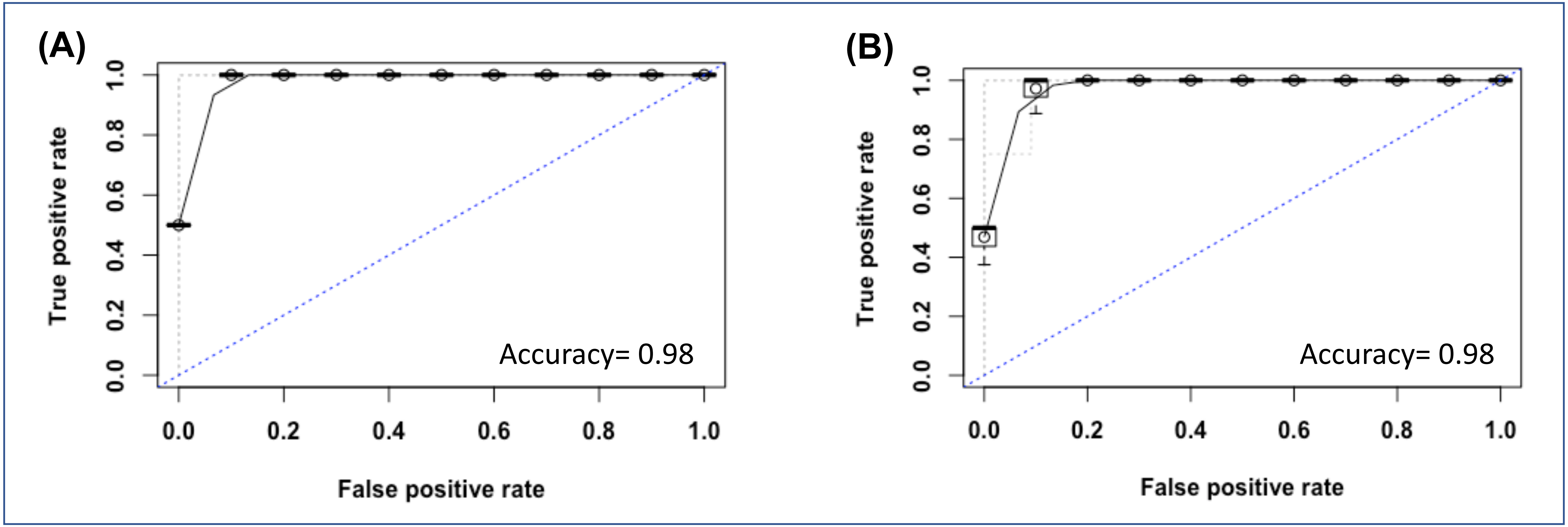
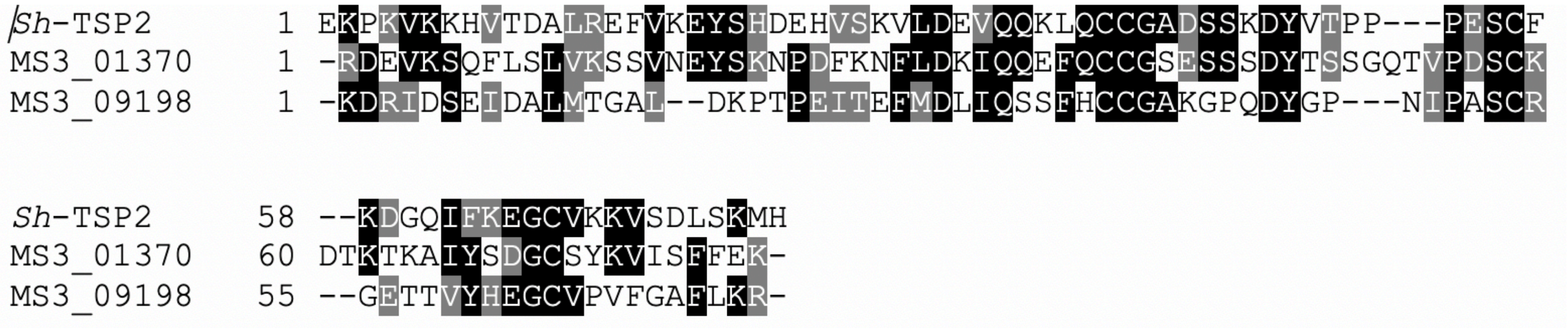


Figure S4. (A) Amino acid alignment of *S. haematobium* TSPs and (B) percent identity matrix showing level of identity between *S. haematobium* TSPs .

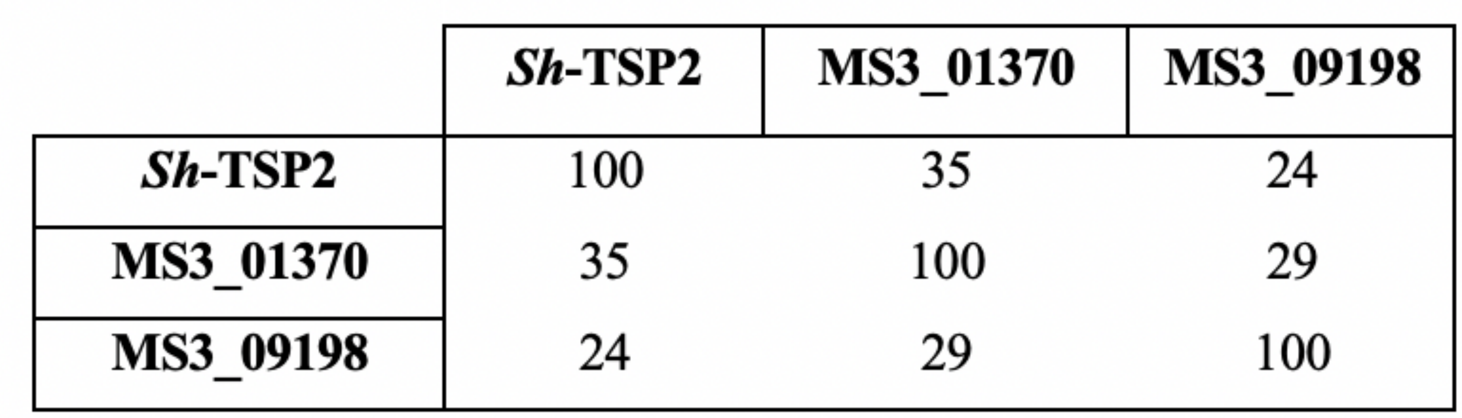
(A)



```
Sh-TSP2        1 EKPKVKKHVTDALREFVKEYSHDEHVSKVLDEVQQKLQCCGADSSKDYVTPP---PESCF
MS3_01370      1 -RDEVKSQFLSLVKSSVNEYSKNPDFKNFLDKIQQEFQCCGSESSSDYTSSGQTVPDSCK
MS3_09198      1 -KDRIDSEIDALMTGAL--DKPTPEITEFMDLIQSSFHCCGAKGPQDYGP---NIPASCR

Sh-TSP2       58 --KDGQIFKEGCVKKVSDLSKMH
MS3_01370     60 DTKTKAIYSDGCSYKVISFFEK-
MS3_09198     55 --GETTVYHEGCVPVFGAFLKR-
```

(B)



	***Sh*-TSP2**	**MS3_01370**	**MS3_09198**
***Sh*-TSP2**	100	35	24
MS3_01370	35	100	29
MS3_09198	24	29	100

Figure S5. Antibody responses to combinations of cell-based recombinant versions of top-ranked proteins generated by ELISA with human urine from *S. haematobium*-endemic populations. (A) anti-MS3_10385 + anti-MS3_10186 + anti-MS3_09198 IgG response. (B) anti-MS3_10385 + anti-MS3_09198 + anti-MS3_01370 + anti-*Sh*-TSP-2 IgG response. (C) anti-MS3_09198 + anti-MS3_01370 + anti *Sh*-TSP-2 IgG response. (D) anti-MS3_01370 IgG response + anti-*Sh*-TSP-2 IgG response. Egg-positive subjects were characterized (WHO stratification) as either having a high (≥50 eggs per 10 ml urine) or low (1-49 eggs per 10 ml urine) infection. “egg -ve/CAA +ve” = egg negative subjects who are classified as positive (infected) by the more sensitive circulating anodic antigen (CAA) detection test. “egg -ve/CAA -ve” = egg negative subjects who are confirmed as antigen negative by the CAA detection test. “non-end. -ve” = subjects from a non-endemic area. Plotted data represent the responses of both the Zimbabwe (black symbols) and Zanzibar (red symbols) cohorts. Reactivity cutoffs were determined as the average plus 3SD of the values of the non-endemic negative group (red dotted line). Significance of responses between each infected group and the non-infected group were analysed by Student’s *t* test *p≤0.05, **p≤0.01, ***p≤0.001, ****p≤0.0001.

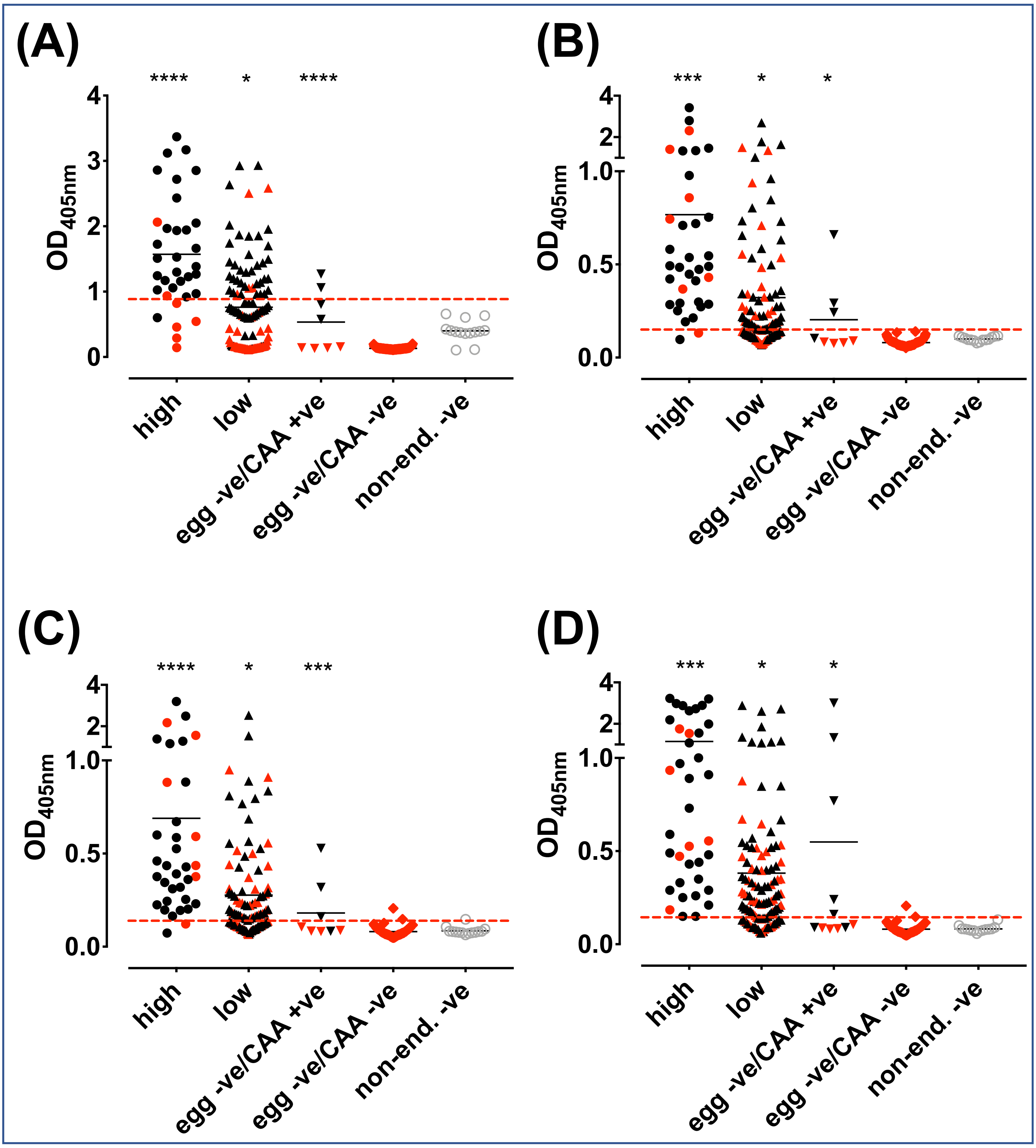


Table S4: Diagnostic accuracy of antigen combinations using urine of individuals from *Schistosoma haematobium*-endemic populations determined by ELISA.

Antigen combination	AUC in cohort (95% CI)		
	Zimbabwe	**Zanzibar**	**All**
MS3_10385 + MS3_10186 + MS3_09198	0·94 (0·89-0·98)	0·63 (0·48-0·80)	0·70 (0·61-0·79)
MS3_10385 + MS3_09198 + MS3_01370 + *Sh*-TSP2	0·93 (0·87-0·98)	0·79 (0·70-0·88)	0·88 (0·83-0·93)
MS3_09198 + MS3_01370 + *Sh*-TSP2	0·94 (0·89-1·00)	0·92 (0·85-0·99)	0·93 (0·87-0·98)
MS3_01370 + *Sh*-TSP2	0·97 (0·93-1·00)	0·92 (0·86-0·98)	0·95 (0·91-0·99)

Figure S6. Frequency of recognition (FoR) patterns based on IgG ELISA responses to combinations of cell-based recombinant versions of top-ranked proteins and *Sh*-SEA using urine from infected individuals in *S. haematobium*-endemic populations. Samples have been sorted from left to right by decreasing egg burden. For each antigen, black bars represent recognition by a sample from the Zimbabwe cohort, red bars represent recognition by a sample from the Zanzibar cohort and white bars denote no recognition (below the cutoff determined by ELISA), regardless of cohort. "Combination 1" = MS3_10385 + MS3_10186 + MS3_09198, "combination 2" = MS3_10385 + MS3_09198 + MS3_01370 + *Sh*-TSP-2, "combination 3" = MS3_09198 + MS3_01370 + *Sh*-TSP-2, "combination 4" = MS3_01370 + *Sh*-TSP-2. FoR percentages among the infected populations (sensitivity) are displayed on the right-hand side of the pattern. "Zim" = Zimbabwe cohort, "Zan" = Zanzibar cohort, "all" = samples from both cohorts combined. To facilitate proper comparison, the dataset has been trimmed to exclude any samples not assayed for all four recombinant antigen combinations (n=148).

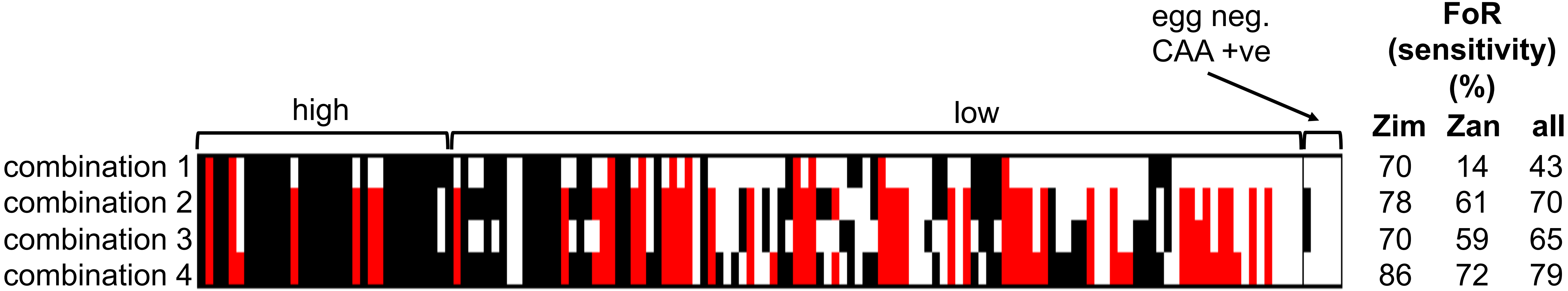


Figure S7. Serum IgG ELISAs showing recognition of *S. haematobium* diagnostic antigens by other schistosome species. (A) *Sh*-TSP2. (B) MS3_01370. “Sh” = *S. haematobium*-infected serum samples from the Gabon cohort used previously in this study. “Sm” = *S. mansoni*-infected serum samples. “Sj” = *S. japonicum*-infected serum samples. “non-end. -ve” = serum samples from a non-endemic area used previously in this study.

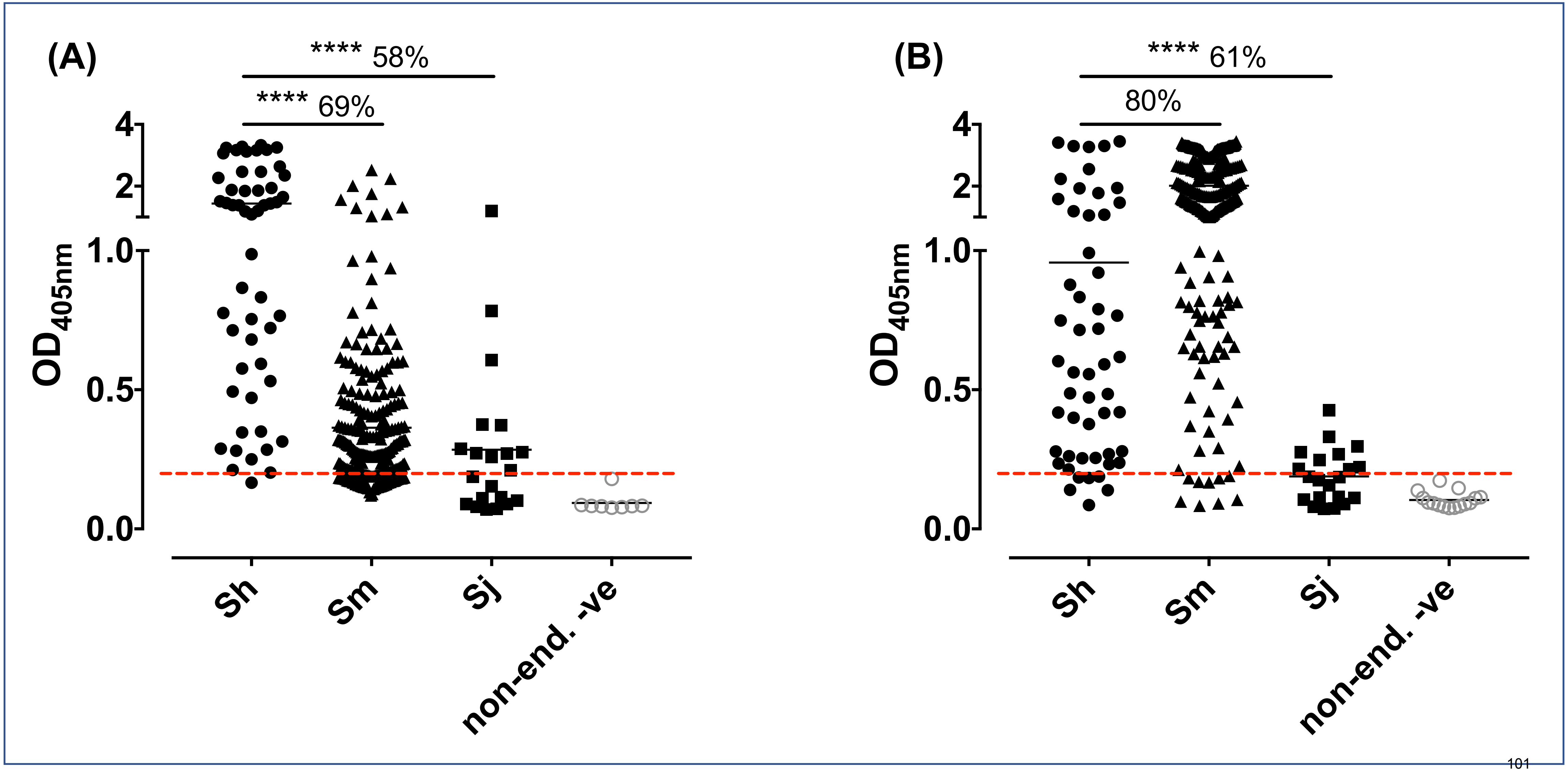
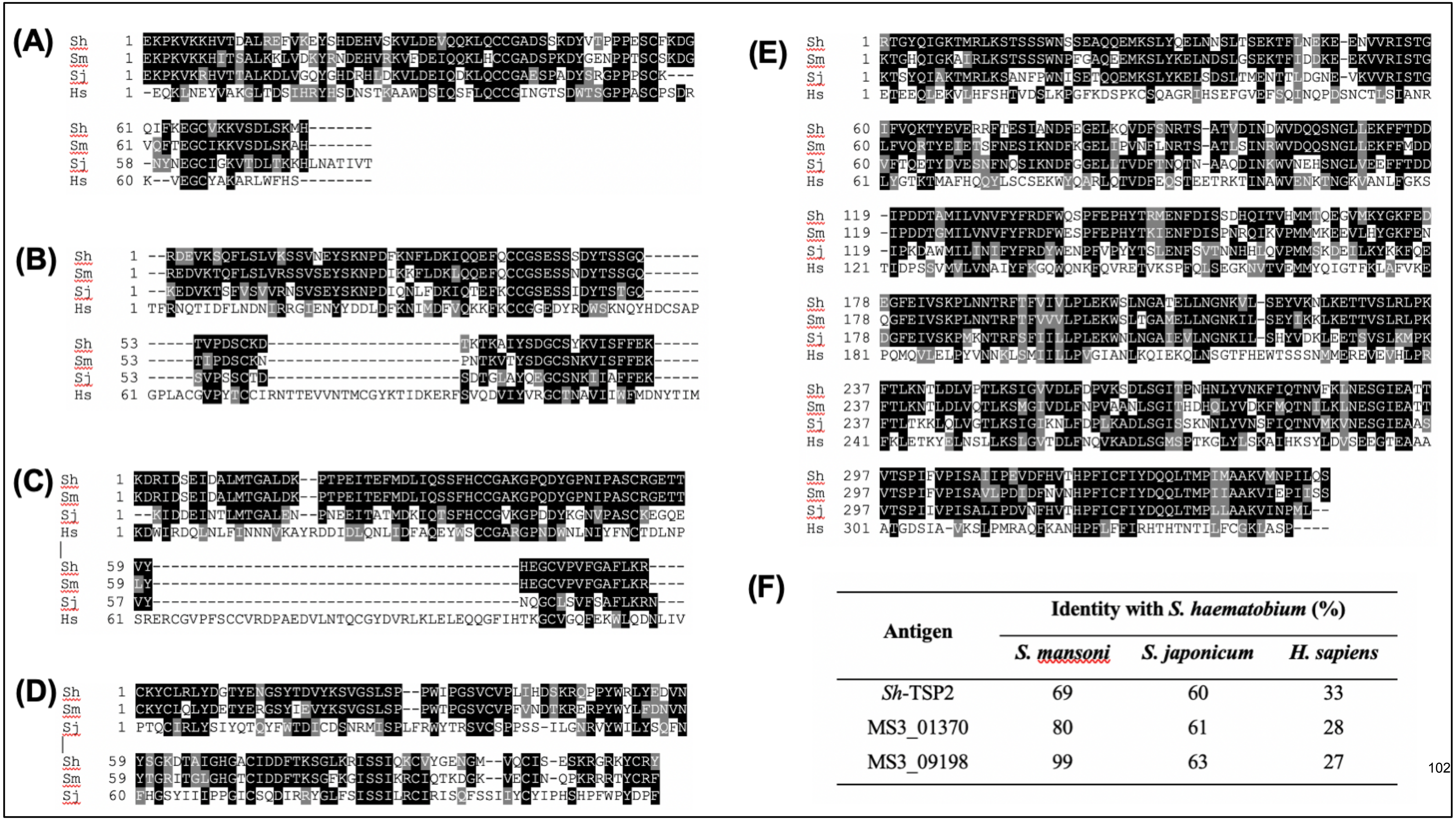


Figure S8. Amino acid alignment of *S. haematobium* diagnostic antigens and homologs from *S. mansoni*, *S. japonicum* and *H. sapiens*. (A) *Sh*-TSP2. (B) MS3_01370. (C) MS3_09198. (D) MS3_10186. (E) MS3_10385. (F) Percent homology table of the diagnostic antigens and their homologs. "Sh" = *S. haematobium*, "Sm" = *S. mansoni*, "Sj" = *S. japonicum* and "Hs" = *Homo sapiens*.



Antigen	Identity with *S. haematobium* (%)		
	S. mansoni	*S. japonicum*	*H. sapiens*
Sh-TSP2	69	60	33
MS3_01370	80	61	28
MS3_09198	99	63	27