

ZeptoMetrix taxa

Adenovirus Type 1
Adenovirus Type 3
Adenovirus Type 31

Influenza A H1N1 pandemic A/NY/ 02/2009

Influenza A
H3N2 A/
Brisbane/
10/07

Metapneumonia virus 8

Parainfluenza Type 1

Parainfluenza Type 4

Rhinovirus 1A

Influenza A
H1N1 A/
New
Caledonia /
20/1999

Coronavirus 229E

Coronavirus HKU1

CoronavirusNL43

Coronavirus OC43

Influenza B
B/Florida
02/06

Parainfluenza Type 3

Discussion

type 2
BOM

	inStrain option1								inStrain option2								inStrain option3								
	RVI-				RVI-				RVI-				RVI-				RVI-								
	veSEQ	seq	ll 3pl	ll 8pl	veSEQ	seq	ll 3pl	ll 8pl	veSEQ	seq	ll 3pl	ll 8pl	veSEQ	seq	ll 3pl	ll 8pl	veSEQ	seq	ll 3pl	ll 8pl					
Human adenovirus 1	0.312	0.076	1.572	1.478					0.311	0.076	1.570	1.476				0.001	0.333	0.078	1.592	1.495					0.001
Human adenovirus 2			0.089	0.085					0.015	0.005	0.089	0.085					0.016	0.005	0.090	0.085					
Human adenovirus 5			0.081	0.072					0.012	0.003	0.081	0.072					0.013	0.003	0.083	0.073					
Human adenovirus 7	24.587	23.797	23.564	23.153					24.527	23.755	23.541	23.139		0.001	0.001	0.001	25.082	23.910	23.584	23.173		0.002	0.002	0.002	
Human adenovirus A									0.021	0.002	0.001	0.001					0.004	0.002							
Human mastadenovirus A									0.017	0.003		0.001					0.004	0.002		0.001					
Human adenovirus B1	71.165	68.576	71.705	72.122					71.073	68.528	71.645	72.095		0.001	0.003	0.006	70.531	68.604	71.638	72.103		0.002	0.004	0.008	
Human adenovirus B2		0.111		0.046					0.008	0.114	0.038	0.045					0.001	0.087	0.036	0.043					
Human adenovirus C			0.091	0.091					0.010	0.005	0.090	0.091					0.011	0.005	0.092	0.092					
Human adenovirus E											0.001														
Human adenovirus type 35		0.070							0.025	0.078	0.022	0.020					0.001	0.022	0.011	0.011					
FLU A (H1N1 CAL) sgm 1	0.422	0.936	0.355	0.375	0.018	0.010	0.006		0.420	0.936	0.355	0.374	0.015	0.019	0.009	0.006	0.453	0.945	0.357	0.374		0.014	0.010	0.007	
FLU A (H1N1 CAL) sgm 2	0.446	1.333	0.385	0.422					0.443	1.338	0.385	0.422					0.477	1.352	0.386	0.421					
FLU A (H1N1 CAL) sgm 3	0.464	0.882	0.242	0.266					0.461	0.884	0.242	0.266					0.489	0.891	0.242	0.265					
FLU A (H1N1 CAL) sgm 4	0.376	0.745	0.291	0.284					0.376	0.752	0.290	0.284					0.397	0.741	0.289	0.283					
FLU A (H1N1 CAL) sgm 5	0.313	0.646	0.315	0.325					0.312	0.649	0.317	0.327					0.337	0.650	0.312	0.323					
FLU A (H1N1 CAL) sgm 6	0.212	0.538	0.201	0.207					0.211	0.542	0.201	0.208					0.221	0.532	0.202	0.207					
FLU A (H1N1 CAL) sgm 7	0.294	0.479	0.209	0.197					0.293	0.483	0.208	0.197					0.314	0.479	0.210	0.196					
FLU A (H1N1 CAL) sgm 8	0.175	0.354	0.106	0.113					0.187	0.357	0.106	0.113					0.170	0.342	0.105	0.113					
FLU A (H3N2 NY) sgm 1													0.015	0.009	0.002	0.001					0.002	0.001			
FLU A (H3N2 NY) sgm 2	0.010	0.011							0.011	0.012	0.001						0.007	0.008	0.001						
FLU A (H3N2 NY) sgm 3													0.008	0.001		0.001									
FLU A (H3N2 NY) sgm 4	0.092	0.140	0.060	0.061					0.091	0.142	0.060	0.061					0.095	0.124	0.056	0.059					
FLU A (H3N2 NY) sgm 5															0.001										
FLU A (H3N2 NY) sgm 6	0.036	0.067	0.038	0.036					0.040	0.069	0.037	0.036					0.037	0.062	0.036	0.035					
FLU A (H3N2 NY) sgm 7													0.030	0.008	0.002	0.002									
FLU A (H3N2 NY) sgm 8							0.004									0.004									0.005
Human metapneumovirus									0.004																
Human parainfluenza 1	0.062	0.159	0.070	0.073					0.063	0.160	0.071	0.073					0.055	0.147	0.067	0.069					
Human parainfluenza 4a	0.069	0.320	0.128	0.124					0.072	0.333	0.128	0.125					0.058	0.264	0.115	0.110					
Human rhinovirus 1	0.117	0.098							0.116	0.098	0.002	0.002													
SARS-Cov2	0.044	0.115	0.103	0.054					0.044	0.115	0.103	0.054			0.001		0.046	0.115	0.103	0.054				0.001	
FLU A (H1N1 PRI) sgm 1	0.296	0.137	0.082	0.078	2.627	0.216	0.079	0.098	0.327	0.141	0.083	0.078	2.445	0.258	0.100	0.116	0.284	0.127	0.080	0.077	0.120	0.062	0.011	0.013	
FLU A (H1N1 PRI) sgm 2	0.069	0.056	0.121	0.150	0.106	0.029	0.089	0.090	0.079	0.056	0.121	0.151	0.218	0.030	0.118	0.116	0.049	0.055	0.114	0.144		0.008	0.004	0.007	
FLU A (H1N1 PRI) sgm 3	0.077	0.093	0.089	0.074	0.239	0.160	0.039	0.046	0.076	0.093	0.089	0.074	0.248	0.169	0.042	0.046	0.080	0.091	0.087	0.072	0.024	0.095	0.020	0.030	
FLU A (H1N1 PRI) sgm 4							0.033	0.035					0.008	0.010	0.055	0.060								0.003	
FLU A (H1N1 PRI) sgm 5	0.095	0.081	0.064	0.075	0.327	0.152	0.017	0.028	0.097	0.080	0.064	0.075	0.376	0.142	0.018	0.027	0.097	0.082	0.063	0.075	0.168	0.123	0.011	0.008	
FLU A (H1N1 PRI) sgm 6														0.002	0.019	0.015									
FLU A (H1N1 PRI) sgm 7	0.127	0.122	0.020	0.021	1.901	0.328	0.095	0.087	0.126	0.123	0.019	0.021	1.753	0.351	0.098	0.096	0.137	0.122	0.020	0.021	2.004	0.299	0.097	0.087	
FLU A (H1N1 PRI) sgm 8	0.035	0.039	0.016	0.010	0.071	0.092	0.008	0.010	0.038	0.039	0.016	0.010	0.098	0.103	0.010	0.012	0.037	0.039	0.015	0.010		0.014	0.002	0.002	
Human orthopneumovirus A														0.013	0.006	0.007						0.018	0.008	0.009	
Human coronavirus 229E			24.250	39.976	44.253	43.445							20.632	36.534	40.995	39.913					32.613	49.613	51.458	50.988	
Human coronavirus HKU1														0.012	0.005	0.006						0.014	0.005	0.006	
Human Coronavirus NL63			1.840	3.525	3.366	3.361							1.565	3.214	3.111	3.085					2.460	4.383	3.886	3.911	
Human coronavirus OC43			9.047	8.833	11.176	11.022							7.698	8.087	10.348	10.136					12.239	10.905	12.939	12.858	
FLU B sgm 1			1.760	4.028	2.832	2.952							4.560	5.066	3.844	4.001						0.327	0.125	0.118	
FLU B sgm 2			3.290	3.445	2.803	2.959							5.455	5.192	4.522	4.828						0.465	0.199	0.195	
FLU B sgm 3			4.652	3.432	2.050	2.161							6.825	4.949	3.179	3.490					0.468	0.636	0.173	0.148	
FLU B sgm 4			0.769	2.012	1.331	1.400							1.535	2.430	1.730	1.841					0.348	1.158	0.667	0.660	
FLU B sgm 5			1.946	3.350	2.498	2.558							3.567	3.898	3.197	3.261						0.296	0.163	0.155	
FLU B sgm 6			0.398	1.119	0.816	0.843							0.873	1.769	1.456	1.578						0.063	0.015	0.015	
FLU B sgm 7			1.672	1.543	1.072	1.134							1.836	1.818	1.429	1.506					0.060	0.394	0.115	0.117	
FLU B sgm 8			2.096	2.522	2.158	2.179							2.092	2.511	2.163	2.220					0.168	1.369	1.229	1.183	
{ Human parainfluenza 3					0.182	0.065	0.062							0.005	0.001	0.001						0.008	0.002	0.002	
{ Human parainfluenza 3													0.339	0.166	0.061	0.058					0.528	0.223	0.074	0.073	
Human rubulavirus 2			33.935	22.483	24.501	24.784							29.022	20.565	22.711	22.760					45.272	27.768	28.338	28.961	
Respiratory syncytial virus			0.734	0.148	0.106	0.124							0.632	0.142	0.099	0.114					0.708	0.166	0.116	0.130	
	ZeptoMetrix RP 2.1 Control 1				ZeptoMetrix RP 2.1 Control 2				ZeptoMetrix RP 2.1 Control 1				ZeptoMetrix RP 2.1 Control 2				ZeptoMetrix RP 2.1 Control 1				ZeptoMetrix RP 2.1 Control 2				

Supplementary Result
Figure 5: ZeptoMetrix RP
2.1 sequence analysis
with three different
inStrain options

Three different inStrain options were used to compare the classification of HQ paired-end short reads (min 100bp) from the ZeptoMetrix Respiratory Virus Control 1 and 2. The relative abundances of the identified viral signals are shown in a heat map generated in GraphPad Prism (v 10.0.3). The ZeptoMetrix taxa are shown in boxes and single lines under the heading 'ZeptoMetrix taxa'. The ZeptoMetrix control was sequenced using the same viral bait capture methods used in the Pilot 2 experiment. I.e. veSEQ, RVI-seq = inHouse method, II 3pl and II 8pl = Illumina 3 plex and 8 plex method. The three different inStrain options were: option 1 "with database mode, min genome coverage 1, min read average nucleotide identity (ani) of (0.92) and skip mm profiling", option 2 'no database mode, min genome coverage 0, min read ani of 0.9', option 3 (default) "no database mode, min genome coverage 0, min read ani 0.95".