

Table 2: Direct deep sequencing results of RNA extracted from AIV-infected tissues

Virus	Gene and length in base pairs (percentage of length)								Genome total:	Total number of reads in library (average read length)
	PB2	PB1	PA	HA	NP	NA	M	NS		
A/ostrich/South Africa/ C42 DKF/2012 (LPAI H5N2)	1179rm ^a 2341bp (87.95%)	939rm 2341bp (99.36%)	548rm 2233bp (88.76%)	652rm 1778bp (90.72%)	332rm 1565bp (90.48%)	233rm 1413bp (78.84%)	129rm 1027bp (82.88%)	221rm 890bp (71.24%)	13 588bp (88.23%)	3 033 358 (58bp, paired-end reads 58bp)
A/ostrich/South Africa/GWA/2012 (LPAI H5N2)	461rm 1835bp (78.39%)	222rm 869bp (37.12%)	76rm 713bp (31.93%)	383rm 1410bp (79.30%)	550rm 809bp (51.69%)	178rm 953bp (67.45%)	119rm 574bp (55.89%)	26rm 330bp (37.08%)	7493bp (55.14%)	618 634 (50bp, paired- end reads)
A/Sacred ibis/ South Africa/IZN/2012 (LPAI H7N1)	27rm 768bp (32.81%)	20rm 742bp (31.70%)	2rm 107bp (4.79%)	93rm 801bp (45.05%)	6rm 147bp (9.39%)	4rm 364bp (25.76%)	0rm - -	3rm 207bp (23.26%)	3136bp (23.08%)	2 638 870 (121bp, paired-end reads)
A/ostrich/South Africa/AI1915/2010 (H1N2)	97rm 1546bp (66.04%)	87rm 1613bp (68.90%)	43rm 1035bp (46.35%)	41rm 857bp (48.20%)	45rm 811bp (51.82%)	152rm 1021bp (72.26%)	38rm 502bp (48.88%)	13rm 302bp (33.93%)	7687bp (56.57%)	3 512 516 (67bp, Single end reads)
A/ostrich/South Africa/AI3246 DWG/2013 (H6N1)	187rm 1624bp (69.37%)	114rm 1737bp (74.20%)	75rm 1584bp (70.98%)	98rm 964bp (54.22%)	52rm 806bp (51.50%)	120rm 1125bp (79.62%)	34rm 707bp (68.84%)	84rm 608bp (68.31%)	9155bp (67.37%)	8 924 671 (63bp, single end reads) single

^a reads mapped