

Supplementary Table-1 - Frequency of selected phage clones with H5N1-VLP vaccinated individuals using H5N1-Indonesia GFPDL					
Seq Region	Peptide Sequence	VLP-NOVA-Indonesia 06			
		Placebo	VLP-15 ug	VLP-45 ug	VLP-90 ug
HA1					
HA-4-20	IVLLLAIVSLVKSDQIC			1	2
HA-12-90	SLVKSDQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDL GVKPLILRDCSVAGWLLGNPMCDEFINVP			3	9
HA-23-145	YHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDLGVKPLILRDC SVAGWLLGNPMCDEFINVPESYIVEKANPTNDLCYPGSFNDEEELKH LLSRINHFEEKIIPKSSWSDHEASS				1
HA-28-148	STEQVDTIMEKNVTVTHAQDILEKTHNGKLCDDLGVKPLILRDCSVAGW LLGNPMCDEFINVPESYIVEKANPTNDLCYPGSFNDEEELKHLISRIN HFEEKIIPKSSWSDHEASSGV	1		2	3
HA-61-96	DGVKPLILRDCSVAGWLLGNPMCDEFINVPESYIV		1	1	1
HA-83-203	CDEFINVPESYIVEKANPTNDLCYPGSFNDEEELKHLISRINHFEEKIIP PKSSWSDHEASSGVSSACPYLGSFRRNVVWLIKKNSTYPTIKKSYN NTNQEDLLVWGIHHPNDAAEQ			4	5
HA-98-199	KANPTNDLCYPGSFNDEEELKHLISRINHFEEKIIPKSSWSDHEASSGV SSACPYLGSFRRNVVWLIKKNSTYPTIKKSYNNTNQEDLLVWGIH PND			1	
HA-100-212	NPTNDLCYPGSFNDEEELKHLISRINHFEEKIIPKSSWSDHEASSGVSS ACPYLGSFRRNVVWLIKKNSTYPTIKKSYNNTNQEDLLVWGIHHPN DAEQTRLYQNPTT				5
HA-109-147	GSFNDEEELKHLISRINHFEEKIIPKSSWSDHEASSGV			1	7
HA-112-189	NDYEELKHLISRINHFEEKIIPKSSWSDHEASSGVSSACPYLGSFRR NVVWLIKKNSTYPTIKKSYNNTNQEDLL				5
HA-116-189	ELKHLISRINHFEEKIIPKSSWSDHEASSGVSSACPYLGSFRRNV WLIKKNSTYPTIKKSYNNTNQEDLL			3	1
HA-120-242	LLSRINHFEEKIIPKSSWSDHEASSGVSSACPYLGSFRRNVVWLIK NSTYPTIKKSYNNTNQEDLLVWGIHHPNDAAEQTRLYQNPTTYISIGTS TLNQRLVPKIATRISKVNGQSGRM	1			
HA-124-159	INHFEKIIPKSSWSDHEASSGVSSACPYLGSF		1	1	1
HA-135-200	KSSWSDHEASSGVSSACPYLGSFRRNVVWLIKKNSTYPTIKKSYNN TNQEDLLVWGIHHPNDA			1	6
HA-136-305	SSWSDHEASSGVSSACPYLGSFRRNVVWLIKKNSTYPTIKKSYNNT NQEDLLVWGIHHPNDAAEQTRLYQNPTTYISIGTSTLNQRLVPKIATR KVNGQSGRMEFFWTILKPNDAINFESNGNFIAPYAYKIVKKGDSAIMKS ELEYGNCNTKCQTPMGAINSSM			1	3
HA-140-200	DHEASSGVSSACPYLGSFRRNVVWLIKKNSTYPTIKKSYNNTNQEDL LVLWGIHHPNDA				1
HA-140-204	DHEASSGVSSACPYLGSFRRNVVWLIKKNSTYPTIKKSYNNTNQEDL LVLWGIHHPNDAAEQT			2	1
HA-145-276	SGVSSACPYLGSFRRNVVWLIKKNSTYPTIKKSYNNTNQEDLLVW GIHHPNDAAEQTRLYQNPTTYISIGTSTLNQRLVPKIATRISKVNGQSGRME FFWTILKPNDAINFESNGNFIAPYAYKIVKKG			1	4

HA-145-302	SGVSSACPYLGSPSFFRNVVWLIKKNSTYPTIKKSYNNTNQEDLLVLWG IHHPNDAAEQTRLYQNPTTYISIGTSTLNQRLVPKIATRISKVNGQSGRME FFWTILKPNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTK CQTPMGAIN				3
HA-167-245	IKKNSTYPTIKKSYNNTNQEDLLVLWGIHHPNDAAEQTRLYQNPTTYISIG TSTLNQRLVPKIATRISKVNGQSGRMEFF			2	7
HA-170-212	NSTYPTIKKSYNNTNQEDLLVLWGIHHPNDAAEQTRLYQNPTT			1	4
HA-173-247	YPTIKKSYNNTNQEDLLVLWGIHHPNDAAEQTRLYQNPTTYISIGTSTLN QRLVPKIATRISKVNGQSGRMEFFWT			14	1
HA-202-210	EQTRLYQNP			1	2
ha-204-301	TRLYQNPTTYISIGTSTLNQRLVPKIATRISKVNGQSGRMEFFWTILKPN DAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMGAI		2		1
HA-207-245	YQNPTTYISIGTSTLNQRLVPKIATRISKVNGQSGRMEFF		1		1
HA-207-301	YQNPTTYISIGTSTLNQRLVPKIATRISKVNGQSGRMEFFWTILKPNDAI NFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMGAI		1	1	1
HA-233-312	SKVNGQSGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKGDSAIMK SELEYGNCNTKCQTPMGAINSSMPFHNIHP			1	6
HA-245-312	PNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMG AINSSMPFHNIHP			1	13
HA-245-313	PNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMG AINSSMPFHNIHPL			1	9
HA-248-335	ILKPNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTP MGAINSSMPFHNIHPLTIGECPKYVKSRLVATGLRN				6
HA-248-337	ILKPNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTP MGAINSSMPFHNIHPLTIGECPKYVKSRLVATGLRNSP			1	5
HA-250-362	KPNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPM GAINSSMPFHNIHPLTIGECPKYVKSRLVATGLRNSPQRESRRKRG LFGAIAGFIEGGWQG			2	1
HA-250-360	KPNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPM GAINSSMPFHNIHPLTIGECPKYVKSRLVATGLRNSPQRESRRKRG LFGAIAGFIEGGW			11	8
HA-256-308	NFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMGAINSS MPFH		1		1
HA-256-341	NFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMGAINSS MPFHNIHPLTIGECPKYVKSRLVATGLRNSPQRES				2
HA-259-312	SNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMGAINSSMPF HNIHP		2	1	1
TOTAL		2	9	58	127
HA2					
HA-345-432	KRGLFGAIAGFIEGGWQGMVDGWYGYHHSNEQGSYAADKESTQKAI DGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMED				5
HA-345-477	KRGLFGAIAGFIEGGWQGMVDGWYGYHHSNEQGSYAADKESTQKAI DGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWT YNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNK				7
HA-356-438	IEGGWQGMVDGWYGYHHSNEQGSYAADKESTQKAI DGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVW	3	5		1

HA-356-445	IEGGWQGMVDGWYGYHHSNEQSGSYAADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELL	1	6		1
HA-360-425	WQGMVDGWYGYHHSNEQSGSYAADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIEN				7
HA-360-402	WQGMVDGWYGYHHSNEQSGSYAADKESTQKAIDGVTNKVNSIID				26
HA-360-403	WQGMVDGWYGYHHSNEQSGSYAADKESTQKAIDGVTNKVNSIID			1	32
HA-365-476	DGWYGYHHSNEQSGSYAADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNA				7
HA-372-494	HSNEQSGSYAADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNEC			5	1
HA-375-380	EQSGSY			37	51
HA-379-416	GYAADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREF	1	89		1
HA-380-416	YAADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREF	1			1
HA-381-452	AADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERT	8			1
HA-381-498	AADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESI			4	1
HA-385-477	STQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAK	5			1
HA-387-451	TQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENE				1
HA-392-450	DGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMEN				3
HA-396-445	NKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELL			1	27
HA-390-501	AIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESIRNG				5
HA-396-476	DNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNA			16	1
HA-395-452	TNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENER				1
HA-398-494	KVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNEC				4
HA-399-501	NSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESIRNG	1			1
HA-413-524	GREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESIRNGTYNYPQYSEEARLKREEISGVKL		1	4	1
HA-415-473	EFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLR				19

HA-415-474	EFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVK NLYDKVRLQLRD			38	1
HA-415-476	EFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVK NLYDKVRLQLRDNA		28	39	59
HA-425-475	NLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL RDN	0	0	0	71
TOTAL		20	129	145	337
NA					
NA-599-722	SIWVIHSIQTNQHQAESISNTNPLTEKAVASVTLAGNSSLCPIRGWAVH SKDNNIRIGSKGDVFIREFPISCHECRTFFLTQGALLNDKHSNGTVK DRSPHRTLMSCPVGGEAPSPYNSRF	1		5	6
NA-607-855	QTGNQHQAESISNTNPLTEKAVASVTLAGNSSLCPIRGWAVH GSKGDVFIREFPISCHECRTFFLTQGALLNDKHSNGTVKDRSPHRT LMSCPVGGEAPSPYNSRFESVAWSASACHDGTSWLTIGISGPDNEAVAV LKYNGIITDTIKSWRNDILRTQESECACVNGSCFTVMTDGPSNGQASYK IFKMEKGKVVKSVELDAPNYHYEECSCYPDAGEITCVCRDNWHGSRN PWVSFN				1
NA-628-668	VASVTLAGNSSLCPIRGWAVH SKDNNIRIGSKGDVFIREFPISCHECRTFFLTQGALLNDKHS NGTVKDRSPHRTLMSCPVGGEAPSPYNSRFESVAWSASACHDGT SW				1
NA-644-738	GWAVH SKDNNIRIGSKGDVFIREFPISCHECRTFFLTQGALLNDKHS NGTVKDRSPHRTLMSCPVGGEAPSPYNSRFESVAWSASACHDGT SW	1			
NA-669-738	IREPFISCHECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMSCPVG EAPSPYNSRFESVAWSASACHDGT		4	25	28
NA-672-722	CSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMSCPVG EAPSPYNSRF	1			
NA-674-744	ISCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMSCPVG EAPSPYNSRFESVAWSASACHDGTSWLT		3		
NA-695-765	KHSNGTVKDRSPHRTLMSCPVG EAPSPYNSRFESVAWSASACHDGT SWLTIGISGPDNEAVLKYNGIIT		2	29	32
NA-697-860	VKDRSPHRTLMSCPVG EAPSPYNSRFESVAWSASACHDGT SWLTIGISGPDNEAVLKYNGIITDTIKSWRNDILRTQESECACVNGSCFTVMTDG PSNGQASYKIFKMEKGKVVKSVELDAPNYHYEECSCYPDAGEITCVCR DNWHGSRNPWVSFNQNLLEY				1
NA-708-849	SCPVG EAPSPYNSRFESVAWSASACHDGT SWLTIGISGPDNEAVLKYNGIITDTIKSWRNDILRTQESECACVNGSCFTVMTDG PSNGQASYKIFKMEKGKVVKSVELDAPNYHYEECSCYPDAGEITCVCRDNWHGSRN				1
NA-710-728	PVG EAPSPYNSRFESVAWS				1
NA-716-767	SPYNSRFESVAWSASACHDGT SWLTIGISGPDNEAVLKYNGIITDTIK SW				1
NA-725-899	VAWSASACHDGT SWLTIGISGPDNEAVLKYNGIITDTIKSWRNDILRTQESECACVNGSCFTVMTDG PSNGQASYKIFKMEKGKVVKSVELDAPNYHYEECSCYPDAGEITCVCRDNWHGSRN PWVSFNQNLLEYQIGYICSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF				1
NA-734-804	DGT SWLTIGISGPDNEAVLKYNGIITDTIKSWRNDILRTQESECACVNGSCFTVMTDG PSNGQASYKIF	3			

NA-749-820	EAVAVLKYNGIITDTIKSWRNDILRTQESECACVNGSCFTVMTDGPSNG QASYKIFKMEKGKVVKSVELDAP	1			
NA-762-851	DTIKSWRNDILRTQESECACVNGSCFTVMTDGPSNGQASYKIFKMEKG KVVKSVELDAPNYHYEECSCYPDAGEITCVCRDNWHGSRNPW				1
NA789-975	VMTDGPSNGQASYKIFKMEKGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGSRNPWVSFNQNLEYQIGYICSGVFGDNPRPNDGTGS CGPMSPNGAYGVKGFsfkyngvwigrtkstnsrsgfemiwdpngw TGTDSFSVKQDIVAITDWSGYSGSFVQHPGLDCIRPCFWVELI	1			
NA-789-948	VMTDGPSNGQASYKIFKMEKGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGSRNPWVSFNQNLEYQIGYICSGVFGDNPRPNDGTGS CGPMSPNGAYGVKGFsfkyngvwigrtkstnsrsgfemiwdpngw TGTDSFSVKQDIVAITDWS				1
NA-792-905	DGPSNGQASYKIFKMEKGKVVKSVELDAPNYHYEECSCYPDAGEITCV CRDNWHGSRNPWVSFNQNLEYQIGYICSGVFGVVKVELDAPNYHGDN PRPNDGTGSCGPMSPNGAYGVKGFsf	1			
NA-792-939	DGPSNGQASYKIFKMEKGKVVKSVELDAPNYHYEECSCYPDAGEITCV CRDNWHGSRNPWVSFNQNLEYQIGYICSGVFGDNPRPNDGTGSCGP MSPNGAYGVKGFsfkyngvwigrtkstnsrsgfemiwdpngwtgt DSSFSVKQ				1
NA-811-864	YEECSCYPDAGEITCVCRDNWHGSRNPWVSFNQNLEYQIG	1	5	17	21
NA-832-919	DAGEITCVCRDNWHGSRNPWVSFNQNLEYQIGYICSGVFGDNPRPND GTGSCGPMSPNGAYGVKGFsfkyngvwigrtkstnsrsgf				1
NA-832-958	DAGEITCVCRDNWHGSRNPWVSFNQNLEYQIGYICSGVFGDNPRPND GTGSCGPMSPNGAYGVKGFsfkyngvwigrtkstnsrsgfemiwdp NGWTGTDSSFSVKQDIVAITDWSGYSGSFVQHP			5	2
NA-850-899	PWVSFNQNLEYQIGYICSGVFGDNPRPNDGTGSCGPMSPNGAYGVKG FSF	1			
NA-865-930	ICSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFsfkyngvwigrtk STNSRSGFEMIWDPNGWTG	3	5	44	46
NA-886-939	MSPNGAYGVKGFsfkyngvwigrtkstnsrsgfemiwdpngwtgt DSSFSVKQ				1
NA-920-929	EMIWDPNGWT			13	17
NA-920-955	EMIWDPNGWTGTDSSFSVKQDIVAITDWSGYSGSFV				1
NA-920-957	EMIWDPNGWTGTDSSFSVKQDIVAITDWSGYSGSFVQH			6	1
NA-920-956	EMIWDPNGWTGTDSSFSVKQDIVAITDWSGYSGSFVQ				1
NA-948-1004	SGYSGSFVQHPGLDCIRPCFWVELIRGRPKESTIWTSGSSISFCGV NSDTVSW			1	
NA-978-1004	RPKESTIWTSGSSISFCGVNSDTVSW		2	46	47
TOTAL		14	21	191	214