
Supplementary information

Author Correction: Isolation of SARS-CoV-2-related coronavirus from Malayan pangolins

In the format provided by the
authors and unedited

Supplementary Table 1 | PCR primers used to amplify fragments of the Pangolin-CoV genome

	Primer ID	Primer sequences	Length (bp)	Tm (°C)
S gene	Pair 2	CATGGTGGACAGCYTTTGTAC AGNACARWRTAATCAGCAACAC	1505	53
	Pair 3	ACAAATCCWATYCARTTGTCTTCATTTC AGNACARWRTAATCAGCAACAC	1368	55
	Pair 4	TGTGTTGCTGATTAYWYTGNTCT TCCAATRCCATTAACTTATAWGCCAT	1696	54
	Pair 6	TGGCWATATAGGTTAAATGGYATTGGAG CCGTCGATTGTGTGWATTGTSACAT	1882	56
RdRp gene	Pair 7	TGTTGGAAGTGAAGTACCTTACT TCRACAATTTTCAGCAGGACAAC	1750	53
	Pair 10	CGGTGACATGGTACCACATATATC AGTAAGGTCAGTCTCAGTCCAACAT	2106	56
	Pair 54	CAGGCTGTWGTAAATGGTGATTCT TGACGTGATATATGTGGTACCATG	1630	55
M gene	Pair 13	CGACTACTAGCGTGCCTTTG TCTCTGCTATWGTAACCTGRAAGTCAAC	1151	56
	Pair 14	ACTAGCCATCCTTACTGCGCTTC AGAGGRTGAAATGGTGAATTGC	1243	55
Other locations	Pair 15	CGCTGTGAYATHAAGGACCTGC GTCCACCAAAYGTAATGCGG	1459	55
	Pair 16	GGAGCKTCGCAGCGTGTAG ACTGCCAGTTGAATCTGAGG	1406	54
	Pair 17	TCGGCTGCATGCTTAGTG GCACTCAAGAGGGTAGCCAT	768	52
	Pair 18	CTTGATGGCTTTATGGGTAGRATT CTCCWGCACACCTCCTCCAT	2355	55
	Pair 19	CTGAATTACTTACACCACTRGGCAT TAGCACCATAATCAACCACACC	1628	54
	Pair 20	GGTGTGGTTGATTATGGTGCT GCAGGTGGATTAACTTCAACTC	844	53
	Pair 21	AGAGTTGAAGTTTAACTCCACCTGCT ACAACATGCACATAACTTTTCCATAC	2225	54
	Pair 22	TGTATGGAAAAGTTATGTGCATGTTG CTACCACCACGCTGRCTAAACC	1355	55
	Pair 23	TGGTTTAGYCAGCGTGGTGGTAG GCAGAAAGAGGTCTAGTATGTCAAC	2071	58
	Pair 24	AGCTGCTTGTGTCATCTCG ATAGGGCAATACTCAACACACAT	1619	52
	Pair 25	CTGGTAAGAGTCATTTTGCTATTGG TAATAGCTTTAGGGTTACCAATGTCG	1961	55
	Pair 26	CTTCACGACATTGGTAACCCTAAAG CTGCTTCTCCAATTAATGTGACTCC	1110	56
	Pair 27	CTTTGATGGACAACAGGGTGAAG TGCGAAGTGTCCCATGAGC	1560	54
	Pair 28	GTTGCTGCTGGCCTTGAAG TAGTAACCTGAAAGTCAACGAGATG	1558	54
	Pair 31	CACCTGCWACTGTTTGTGGACC TGTGTAACCTCAATACCATTAAACC	1179	55
	Pair 32	CAGGAGTTGTTGGAGAAGGTC CCTAGTGGTGAAGTAATTCAGATACTGG	1375	56
	Pair 33	GAGTTGAAGTTTAACTCCACCTGC CAACATGCACATAACTTTTCCATACAT	2145	53
	Pair 34	TTTTATAAGCTCATGGGACACTTCGC CCTGGAGCRATTTGTCTGACTTC	1644	56
	Pair 35	CAGGTTGTGATGGTGGYAGTT AATTTCCATTTGACTCCTGGGTTT	980	53
	Pair 38	GGTGATGCTGCTCTTGCTTTG AAAATCACATGGGGATAGCACTAC	1000	54
	Pair 39	CAACTTGTGCTAATGACCCTGTG AACWCCTAGCTCTCTGAAGTGG	1173	55
	Pair 40	GGTGACGCATACAAAACATTCCC AGGCTCTCCATCTTACCTTTTCG	290	55
	Pair 41	GGTGACGCATACAAAACATTCCC ACACATAGGGCTGTCAAGTTG	487	54
	Pair 42	GGTGATGCTGCTCTTGCTTTG TTTACAAAAGATGCCATAGCCCTT	1513	54
	Pair 43	GGTGATGCTGCTCTTGCTTTG CTTGAAATAATGGAAGACAGAGAAGC	1459	54
	Pair 44	GGACGCTGTGACATCAAGGAC CAGCCTCATCCACGCACAG	1098	56
	Pair 45	TTGTGATCAACTCCGCGAACC AACWCCTAGCTCTCTGAAGTGG	1089	54
	Pair 47	ATTAAAGGTTTATACCTTCCCAGGTAAC GATGTTGACGTGCCTCTGATAAG	401	55
	Pair 48	ACCTTCCCAGGTAACAAACCAAC GATGTTGACGTGCCTCTGATAAG	388	55
	Pair 51	ACCGCAGAGACAGAAGAAACAG GTCATTCTCCTAAGAAGCTATTAAATC	452	54