**Virologica Sinica**

**Supplementary Data**

**Characteristics of SARS-CoV-2 transmission in a medium-sized city with traditional communities during the early COVID-19 epidemic in China**

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**Supplementary Table S1** Relationships among patients and family members in families A and B.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Family** | **Case ID** | **Identity** | **Gathering at Hospital (12 days)** | **Gathering at Funeral (4 days)** |
| A | Case 1 | Family A member, took care of her father in the hospital | Yes, frequently | Yes, frequently |
| A | Case 2 | Family A member, case 1’s sister | Yes, frequently | Yes, frequently |
| A | Case 3 | Family A member, case 1’s brother | Yes, frequently | Yes, frequently |
| A | Case 4 | Associated with family A, an old friend of family A | Yes, frequently | Yes, frequently |
| A | Case 5 | Associated with family A, case 1’s aunt | Yes, frequently | Yes, frequently |
| A | Case 6 | Family A member, case 1’s sister-in-law/case 3’s wife | Yes, occasionally | Yes, moderate |
| A | Case 7 | Associated with family A, a close friend of case 1 | no | Yes, moderate |
| A | Case 8 | Family A member, case 1’s niece/the daughter of cases 3 and 6 | Yes, occasionally | Yes, occasionally |
| B | Case 9 | Family B member, a restaurant waiter | / | / |
| A | Case 10 | Associated with family A, case 6’s father, only contacted case 6 | No | No |
| B | Case 11 | Family B member, case 9’s daughter, living with case 9 | / | / |
| A | Case 12 | Family A member, the mother of cases 1, 2, and 3/the mother-in-law of case 6/the grandmother of case 8 | Yes, occasionally | No |
| A | Case 13 | Family A member, case 1’s daughter | Yes, occasionally | Yes, occasionally |
| B | Case 14 | Family B member, case 9’s sister-in-law, close contacted case 9 | / | / |
| A | Case 15 | Associated with family A, a relative of family A | No | Yes, moderate |
| B | Case 16 | Family B member, case 14’s husband | / | / |
| B | Case 17 | Family B member, the mother-in-law of cases 9 and 16/the mother of cases 14 and 18 | / | / |
| B | Case 18 | Family B member, case 9’s husband/case 14’s brother | / | / |
| A | Case 19 | Associated with family A, a friend of family A | No | No |
| B | Case 20 | Family B member, the son of cases 9 and 18 | / | / |
| B | Case 21 | Family B member, the wife of the case 20/the daughter-in-law of cases 9 and 18 | / | / |
| B | Case 22 | Associated with family B, case 9’s neighbour, only contacted case 9 | / | / |
| B | Case 23 | Associated with family B, case 21’s father, only contacted case 21 | / | / |
| Non-family | Case 24 | A case without clear epidemiological linkage | / | / |

IDs in red belonged to family A; IDs in purple belonged to family B.

**Supplementary Table S2** Inter-individual SNPs and iSNVs in families A and B.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Family** | **Case ID** | **Sample ID** | **SNP-Group** | **C8782T** | **T11418C** | **T28144C** | **T5473C** | **C25490T** | **C28926T** | **C241T** | **A10286G** |
| **Counts** | **Coverage** | **Frequency** | **Counts** | **Coverage** | **Frequency** | **Counts** | **Coverage** | **Frequency** | **Counts** | **Coverage** | **Frequency** | **Counts** | **Coverage** | **Frequency** | **Counts** | **Coverage** | **Frequency** | **Counts** | **Coverage** | **Frequency** | **counts** | **coverage** | **frequency** |
| A | Case 01 | AY018 | A | 8912 | 8984 | 99.20% | 1309 | 1314 | 99.62% | 8397 | 8421 | 99.71% | 202 | 7236 | 2.79% | 453 | 28385 | 1.60% | 59 | 39393 | 0.15% | 3 | 1086 | 0.28% | 8 | 3691 | 0.22% |
| A | Case 02 | AY022 | A | 6515 | 6574 | 99.10% | 1156 | 1157 | 99.91% | 8309 | 8332 | 99.72% | 50 | 7193 | 0.70% | 31 | 37293 | 0.08% | 68 | 46756 | 0.15% | 58 | 926 | 6.26% | 8 | 3998 | 0.20% |
| A | Case 03 | AY095 | A | 5318 | 5319 | 99.98% | 6035 | 6062 | 99.55% | 22759 | 22840 | 99.65% | 2 | 8901 | 0.02% | 4 | 8542 | 0.05% | 26 | 35531 | 0.07% | 0 | 14979 | 0.00% | 1 | 9220 | 0.01% |
| A | Case 04 | AY021 | A | 1017 | 1020 | 99.71% | 167 | 168 | 99.40% | 1808 | 1813 | 99.72% | 2 | 742 | 0.27% | 3 | 3554 | 0.08% | 9 | 6949 | 0.13% | 2 | 127 | 1.57% | 1 | 694 | 0.14% |
| A | Case 05 | AY025 | A | 60719 | 61171 | 99.26% | 8595 | 8614 | 99.78% | 74200 | 74400 | 99.73% | 205 | 43309 | 0.47% | 194 | 192002 | 0.10% | 416 | 271763 | 0.15% | 40 | 8204 | 0.49% | 33 | 28979 | 0.11% |
| A | Case 06 | AY029 | A | Sanger | 1 | 100.00% | 10/Sanger | 10 | 100.00% | 425 | 426 | 99.77% | 1 | 83 | 1.20% | 2 | 1199 | 0.17% | 0 | 0 | 0.00% | 115 | 122 | 94.26% | 0 | 0 | 0.00% |
| A | Case 07 | AY034 | B | 33758 | 34013 | 99.25% | 5206 | 5213 | 99.87% | 32878 | 32963 | 99.74% | 13986 | 23903 | 58.51% | 69621 | 69879 | 99.63% | 214 | 130221 | 0.16% | 18 | 3749 | 0.48% | 42 | 14982 | 0.28% |
| A | Case 08 | AY049 | A | 83289 | 83384 | 99.89% | 100937 | 101341 | 99.60% | 189738 | 190332 | 99.69% | 17 | 138864 | 0.01% | 20 | 90843 | 0.02% | 30 | 213292 | 0.01% | 19 | 139847 | 0.01% | 12 | 155403 | 0.01% |
| B | Case 09 | AY124 | B | 7830 | 7900 | 99.11% | 1448 | 1453 | 99.66% | 6557 | 6574 | 99.74% | 3373 | 5872 | 57.44% | 15979 | 16041 | 99.61% | 53 | 28207 | 0.19% | 30 | 835 | 3.52% | 776 | 3385 | 22.92% |
| A | Case 10 | AY131 | A | 704 | 712 | 98.88% | 164 | 171 | 95.91% | 796 | 800 | 99.50% | 2 | 598 | 0.33% | 8 | 4763 | 0.17% | 9 | 5855 | 0.15% | 92 | 220 | 41.82% | 0 | 0 | 0.00% |
| B | Case 11 | AY156 | B | 595 | 599 | 99.33% | 1417 | 1444 | 98.13% | 3506 | 3530 | 99.32% | 1082 | 1129 | 95.84% | 1557 | 1595 | 97.62% | 2 | 5063 | 0.04% | 0 | 0 | 0.00% | 158 | 3096 | 5.10% |
| A | Case 12 | AY385 | A | 2056 | 2225 | 92.40% | 437 | 457 | 95.62% | 2061 | 2111 | 97.63% | 12 | 1895 | 0.63% | 11 | 8650 | 0.13% | 20 | 13657 | 0.15% | 1216 | 2883 | 42.18% | 0 | 0 | 0.00% |
| A | Case 13 | AY159 | A | 289 | 291 | 99.31% | Sanger | 1 | 100.00% | 102 | 104 | 98.08% | 0 | 0 | 0.00% | 0 | 0 | 0.00% | 1 | 280 | 0.36% | 19 | 53 | 35.85% | 0 | 0 | 0.00% |
| B | Case 14 | AY195 | B | 25460 | 25653 | 99.25% | 3717 | 3723 | 99.84% | 26121 | 26215 | 99.64% | 9910 | 17499 | 56.63% | 53773 | 53979 | 99.62% | 27743 | 123816 | 22.41% | 31 | 2484 | 1.25% | 3000 | 11091 | 27.05% |
| A | Case 15 | AY248 | A | 58384 | 58786 | 99.32% | 8985 | 9904 | 99.79% | 67046 | 67188 | 99.79% | 254 | 45560 | 0.56% | 185 | 195992 | 0.09% | 421 | 282311 | 0.15% | 38 | 7445 | 0.51% | 38 | 30042 | 0.13% |
| B | Case 16 | AY288 | C | 11893 | 11960 | 99.44% | 1815 | 1820 | 99.73% | 16965 | 17014 | 99.71% | 6689 | 11825 | 56.57% | 29234 | 29394 | 99.46% | 66806 | 67134 | 99.51% | 16 | 2011 | 0.80% | 11 | 6136 | 0.18% |
| B | Case 17 | AY733 | C | 657 | 659 | 99.70% | 120 | 120 | 100.00% | 797 | 850 | 93.76% | 494 | 816 | 60.54% | 1675 | 2122 | 78.93% | 3206 | 3712 | 86.37% | 0 | 0 | 0.00% | 2 | 695 | 0.29% |
| B | Case 18 | AY316 | C | 25003 | 25233 | 99.09% | 4438 | 4447 | 99.80% | 22053 | 22102 | 99.78% | 10490 | 17411 | 60.25% | 43778 | 43931 | 99.65% | 68769 | 81579 | 84.30% | 11 | 2389 | 0.46% | 23 | 10986 | 0.21% |
| A | Case 19 | AY308 | A | 9486 | 9564 | 99.18% | 1653 | 1656 | 99.82% | 8293 | 8331 | 99.54% | 39 | 7925 | 0.49% | 23 | 25485 | 0.09% | 41 | 32438 | 0.13% | 4 | 1280 | 0.31% | 9 | 5309 | 0.17% |
| B | Case 20 | AY360 | C | 3508 | 3533 | 99.29% | 551 | 551 | 100.00% | 2564 | 2618 | 97.94% | 2327 | 3449 | 67.47% | 6930 | 6948 | 99.74% | 11536 | 12295 | 93.83% | 19 | 496 | 3.83% | 3 | 1406 | 0.21% |
| B | Case 21 | AY361 | C | 3841 | 3873 | 99.17% | 591 | 591 | 100.00% | 8124 | 8133 | 99.89% | 2234 | 3592 | 62.19% | 10456 | 10485 | 99.72% | 29936 | 30102 | 99.45% | 9 | 590 | 1.53% | 5 | 1981 | 0.25% |
| B | Case 22 | AY427 | B | NA | NA | NA | Sanger | 1 | / | 130 | 134 | 97.01% | 171 | 282 | 60.64% | Sanger | 1 | / | 59 | 60180 | 0.10% | 62 | 62 | 100.00% | NA | NA | NA |
| non-family | Case 24 | AY587 | C | 169 | 172 | 98.26% | 86 | 229 | 81.22% | 353 | 356 | 99.16% | 252 | 301 | 83.72% | 207 | 242 | 85.54% | 342 | 423 | 80.85% | 0 | 0 | 0.00% | 0 | 0 | 0.00% |

Inter-individual SNPs are noted in green background.

Inter-individual iSNVs are noted in blue background.

The threshold of minor allele frequency > 1%.

IDs in red belonged to family A; IDs in purple belonged to family B.

Reference: WIV04.

**Supplementary Table S3** Different distribution patterns of significant SNPs and iSNVs in families A and B.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **SNP/iSNV** | **Family A** | **Family B** |  | **non-family** | 　 |
| **Case 1** | **Case 4** | **Case 5** | **Case 2** | **Case 3** | **Case 6** | **Case 8** | **Case 10** | **Case 12** | **Case 13** | **Case 15** | **Case 19** | **Case 7** | **Case 9** | **Case 11** | **Case 14** | **Case 16** | **Case 17** | **Case 18** | **Case 20** | **Case 21** | **Case 22** | **Case 24** | **Count** |
| AY018 | AY021 | AY025 | AY022 | AY095 | AY029 | AY049 | AY131 | AY385 | AY159 | AY248 | AY308 | AY034 | AY124 | AY156 | AY195 | AY288 | AY733 | AY316 | AY360 | AY361 | AY427 | AY587 |
| **C8782T, T11418C and T28144C shared by all individuals** | 　 |
| **T5473C** | 2.79% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 58.51% | 57.44% | 95.84% | 56.63% | 56.57% | 60.54% | 60.25% | 67.47% | 62.19% | 60.64% | 83.72% | 12 |
| **C25490T** | 1.60% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 99.63% | 99.61% | 97.62% | 99.62% | 99.46% | 78.93% | 99.65% | 99.74% | 99.72% | Sanger-T | 85.54% | 12 |
| **C28926T** | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 22.41% | 99.51% | 86.37% | 84.30% | 93.83% | 99.45% | 　 | 80.85% | 7 |
| **A10286G** | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 22.92% | 5.10% | 27.05% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 3 |
| 　 |
| **A361C** | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 87.87% | 1 |
| **C874T** | 　 | 　 | 　 | 　 | 　 | 　 | 99.24% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 1 |
| **C1613T** | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 98.99% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 1 |
| **C9438T** | 　 | 　 | 　 | 　 | 　 | 61.38% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 1 |
| **G15438T** | 　 | 　 | 　 | 　 | 　 | 99.62% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 1 |
| **G17064T** | 　 | 　 | 　 | 　 | 　 | 54.29% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 1 |
| **G17581A** | 　 | 　 | 　 | 　 | 99.17% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 1 |
| **C18555T** | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 93.01% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 1 |
| **T18927C** | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 94.29% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 1 |
| **C21161T** | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 80.69% | 1 |
| **C21646T** | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 |  | 　 | 84.02% | 　 | 　 | 　 | 　 | 1 |
| **C26804T** | 　 | 　 | 　 | 　 | 99.53% | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 　 | 1 |

Inter-individual SNPs are noted in green background.

Inter-individual iSNVs are noted in blue background.

Unique SNPs within individual case are noted in yellow background.

IDs in red belonged to family A; IDs in purple belonged to family B.

**Supplementary Table S4** The Anyang SARS-CoV-2 genomes, with CNCB-NGDC accession numbers.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **No.** | **Accession number** | **Sample ID** | **ORF1\_ab (CT value)** | **N (CT value)** | **NGS strategy** | **Platform** | **Sanger sequencing** |
| 1 | GWHAZQL01000000 | AY009 | 33.77  | 32.12  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 2 | GWHAZQM01000000 | AY012 | 31.24  | 34.12  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 3 | GWHAZQN01000000 | AY013 | 33.72  | 33.43  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 4 | GWHAZQO01000000 | AY018 | 28.97  | 30.03  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 5 | GWHAZQP01000000 | AY021 | 31.34  | 32.05  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 6 | GWHAZQQ01000000 | AY022 | 32.37  | 33.47  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 7 | GWHAZQR01000000 | AY023 | 31.55  | 31.52  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 8 | GWHAZQS01000000 | AY025 | 28.24  | 29.20  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 9 | GWHAZQT01000000 | AY029 | 35.34  | 37.55  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 10 | GWHAZQU01000000 | AY030 | 30.30  | 30.71  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 11 | GWHAZQV01000000 | AY032 | 28.70  | 29.45  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 12 | GWHAZQW01000000 | AY034 | 27.42  | 28.94  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 13 | GWHAZQX01000000 | AY036 | 36.18  | 34.37  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 14 | GWHAZQY01000000 | AY049 | 22.85  | 24.59  | metagenomic | Novaseq | / |
| 15 | GWHAZQZ01000000 | AY077 | 30.22  | 31.59  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 16 | GWHAZRA01000000 | AY082 | 33.12  | 33.17  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 17 | GWHAZRB01000000 | AY095 | 25.42  | 26.29  | metagenomic | Novaseq | / |
| 18 | GWHAZRC01000000 | AY105 | 26.01  | 25.82  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 19 | GWHAZRD01000000 | AY106 | 34.78  | 33.53  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 20 | GWHAZRE01000000 | AY124 | 30.99  | 30.41  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 21 | GWHAZRF01000000 | AY131 | 34.48  | 33.41  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 22 | GWHAZRG01000000 | AY135 | 31.54  | 32.20  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 23 | GWHAZRH01000000 | AY143 | 31.19  | 32.09  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 24 | GWHAZRI01000000 | AY156 | 28.58  | 29.93  | metagenomic | Novaseq | / |
| 25 | GWHAZRJ01000000 | AY159 | 34.21  | 36.03  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 26 | GWHAZRK01000000 | AY195 | 28.62  | 29.20  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 27 | GWHAZRL01000000 | AY207 | 34.31  | 33.72  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 28 | GWHAZRM01000000 | AY248 | 27.57  | 28.01  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 29 | GWHAZRN01000000 | AY255 | 35.20  | 35.98  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 30 | GWHAZRO01000000 | AY276 | 36.40  | 37.14  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 31 | GWHAZRP01000000 | AY288 | 32.17  | 32.82  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 32 | GWHAZRQ01000000 | AY292 | 36.59  | 36.04  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 33 | GWHAZRR01000000 | AY308 | 28.57  | 27.26  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 34 | GWHAZRS01000000 | AY316 | 26.13  | 25.79  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 35 | GWHAZRT01000000 | AY354 | 37.10  | 38.85  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 36 | GWHAZRU01000000 | AY360 | 33.10  | 35.00  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 37 | GWHAZRV01000000 | AY361 | 31.27  | 32.16  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 38 | GWHAZRW01000000 | AY373 | 29.65  | 31.76  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 39 | GWHAZRX01000000 | AY385 | 27.90  | 29.84  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 40 | GWHAZRY01000000 | AY400 | 35.96  | 34.58  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 41 | GWHAZRZ01000000 | AY413 | 34.48  | 34.05  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 42 | GWHAZSA01000000 | AY416 | 32.96  | 34.21  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 43 | GWHAZSB01000000 | AY477 | 35.94  | 33.95  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 44 | GWHAZSC01000000 | AY508 | 38.82  | 36.14  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 45 | GWHAZSD01000000 | AY509 | 25.19  | 26.48  | metagenomic | Novaseq | / |
| 46 | GWHAZSE01000000 | AY538 | 28.74  | 28.75  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 47 | GWHAZSF01000000 | AY571 | 32.31  | 33.45  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 48 | GWHAZSG01000000 | AY587 | 29.21  | 28.41  | metagenomic | Novaseq | / |
| 49 | GWHAZSH01000000 | AY603 | 36.93  | 37.24  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 50 | GWHAZSI01000000 | AY632 | 31.93  | 33.22  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 51 | GWHAZSJ01000000 | AY666 | 30.60  | 30.42  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 52 | GWHAZSK01000000 | AY669 | 29.20  | 29.35  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 53 | GWHAZSL01000000 | AY731 | 28.73  | 30.71  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 54 | GWHAZSM01000000 | AY733 | 28.31  | 30.83  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 55 | GWHAZSN01000000 | AY775 | 34.93  | 34.28  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 56 | GWHAZSO01000000 | AY776 | 36.53  | 35.92  | multiplex PCR amplicon | MGISEQ-2000 | Yes |
| 57 | GWHAZSP01000000 | AY777 | 27.67  | 28.33  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 58 | GWHAZSQ01000000 | AY788 | 31.30  | 31.31  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 59 | GWHAZSR01000000 | AY790 | 24.53  | 26.05  | multiplex PCR amplicon | MGISEQ-2000 | / |
| 60 | GWHAZSS01000000 | AY851 | 24.43  | 25.16  | multiplex PCR amplicon | MGISEQ-2000 | / |

All the Anyang SARS-CoV-2 genomes have been submitted to CNCB-NGDC.

Positive samples were identified using the RT-qPCR targeting two regions of ORF1\_ab and N.

Positive samples were identified using the RT-qPCR targeting two regions of ORF1\_ab and N.

Based on the NGS data, the near full-length genomes of 41 samples were successfully assembled, and the short gaps in the incomplete genomes of the other 19 samples were filled by Sanger sequencing.



**Supplementary Fig S1** Root-to-tip plot. The presence of a temporal signal in the SARS-CoV-2 genomes was examined, and the correlation between sampling date and genetic divergence is shown in the root-to-tip plot. Blue circles represent the Anyang SARS-CoV-2 genomes. The sampling date was shown in decimal years.



**Supplementary Fig. S2** Phylogenetic cluster of communities 1 and 2.Significant SNPs and the divergence time (time to most recent common ancestor) are denoted on the branches.

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**Supplementary Fig. S3** The SNP statistics schematic of the Anyang SARS-CoV-2 genomes. **A** Cumulative distribution of SNPs in the virus genome. SNPs carried by five or more genomes are indicated by colored bars. **B** Counts of different variant types in different genes. Bars in blue, orange, red, and green represent synonymous variants, nonsynonymous variants, other variants, and deletions, respectively.

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**Supplementary Fig. S4** SNP distribution in the 60 Anyang SARS-CoV-2 genomes. Bars in blue, orange, green, and red represent synonymous variants, nonsynonymous variants, variants in non-coding regions, and deletions, respectively. Significant SNPs in the three community transmission events are shown.

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**Supplementary Fig. S5** Infected patients and the corresponding SNPs in communities 2 and 3. Cases in grey are related to community transmission according to the SNP analysis, but lack support of definite epidemiological evidence. Arrows represent the direction of SNP dynamics.