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| |  |  |  | | --- | --- | --- | | [**Series GSE164805**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) |  | [Query DataSets for GSE164805](https://www.ncbi.nlm.nih.gov/gds/?term=GSE164805%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | The transcriptional profiles of severe COVID-19 |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Experiment type | Expression profiling by array |
| Summary | The study aims at investigating the specifical transcriptional signatures of severe COVID-19 |
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| Overall design | We applied microarray analysis of the whole genome transcriptome to peripheral blood mononuclear cells (PBMCs) taken from severe and mild COVID-19 patients as well as healthy controls. |
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| Contributor(s) | [Zhang Q](https://www.ncbi.nlm.nih.gov/pubmed/?term=Zhang%20Q%5bAuthor%5d), [Diao H](https://www.ncbi.nlm.nih.gov/pubmed/?term=Diao%20H%5bAuthor%5d) |
| Citation missing | *Has this study been published? Please*[*login*](https://www.ncbi.nlm.nih.gov/geo/submitter)*to update or*[*notify GEO*](mailto:geo@ncbi.nlm.nih.gov?subject=Citation%20for%20GSE164805%20[not%20logged%20in]&body=Thank%20you%20very%20much%20for%20helping%20to%20keep%20GEO%20citation%20links%20up-to-date.%20Please%20enter%20the%20PubMed%20ID%20(PMID)%20or%20full%20citation%20for%20GSE164805%20below,%20and%20we%20will%20update%20the%20record%20accordingly%20within%20the%20next%20day%20or%20two.%20The%20PubMed%20ID%20or%20citation%20is:)*.* |
| Submission date | Jan 14, 2021 |
| Last update date | Jan 15, 2021 |
| Contact name | Qiong Zhang |
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| City | Hangzhou |
| ZIP/Postal code | 310058 |
| Country | China |
|  |  |
| Platforms (1) | |  |  | | --- | --- | | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) | Agilent-085982 Arraystar human lncRNA V5 microarray | |
| Samples (15)  [[Less...](javascript:HandleVisibilityChangeL1719327271()) Less...](javascript:HandleVisibilityChangeL1719327271()) | |  |  | | --- | --- | | [GSM5019817](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019817) | PBMC\_healthy\_subject1 | | [GSM5019818](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019818) | PBMC\_healthy\_subject2 | | [GSM5019819](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019819) | PBMC\_healthy\_subject3 |  |  |  | | --- | --- | | [GSM5019820](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019820) | PBMC\_healthy\_subject4 | | [GSM5019821](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019821) | PBMC\_healthy\_subject5 | | [GSM5019822](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019822) | PBMC\_mild\_patient\_subject1 | | [GSM5019823](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019823) | PBMC\_mild\_patient\_subject2 | | [GSM5019824](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019824) | PBMC\_mild\_patient\_subject3 | | [GSM5019825](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019825) | PBMC\_mild\_patient\_subject4 | | [GSM5019826](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019826) | PBMC\_mild\_patient\_subject5 | | [GSM5019827](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019827) | PBMC\_severe patient\_subject1 | | [GSM5019828](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019828) | PBMC\_severe patient\_subject2 | | [GSM5019829](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019829) | PBMC\_severe patient\_subject3 | | [GSM5019830](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019830) | PBMC\_severe patient\_subject4 | | [GSM5019831](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019831) | PBMC\_severe patient\_subject5 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019831**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019831) |  | [Query DataSets for GSM5019831](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019831%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_severe patient\_subject5 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, severe patient |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: COVID-19 group: severe gender: male age: 60 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Last update date | Jan 15, 2021 |
| Contact name | Qiong Zhang |
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| Country | China |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019830**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019830) |  | [Query DataSets for GSM5019830](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019830%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_severe patient\_subject4 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, severe patient |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: COVID-19 group: severe gender: male age: 51 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Last update date | Jan 15, 2021 |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019829**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019829) |  | [Query DataSets for GSM5019829](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019829%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_severe patient\_subject3 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, severe patient |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: COVID-19 group: severe gender: male age: 73 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Last update date | Jan 15, 2021 |
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| City | Hangzhou |
| ZIP/Postal code | 310058 |
| Country | China |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019828**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019828) |  | [Query DataSets for GSM5019828](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019828%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_severe patient\_subject2 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, severe patient |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: COVID-19 group: severe gender: male age: 52 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Last update date | Jan 15, 2021 |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| Status | Public on Jan 15, 2021 |
| Title | PBMC\_severe patient\_subject1 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, severe patient |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: COVID-19 group: severe gender: male age: 54 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Last update date | Jan 15, 2021 |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019826**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019826) |  | [Query DataSets for GSM5019826](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019826%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_mild\_patient\_subject5 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, mild patient |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: COVID-19 group: mild gender: female age: 53 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Country | China |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| Status | Public on Jan 15, 2021 |
| Title | PBMC\_mild\_patient\_subject4 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, mild patient |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: COVID-19 group: mild gender: male age: 54 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
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| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Submission date | Jan 14, 2021 |
| Last update date | Jan 15, 2021 |
| Contact name | Qiong Zhang |
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| ZIP/Postal code | 310058 |
| Country | China |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019824**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019824) |  | [Query DataSets for GSM5019824](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019824%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_mild\_patient\_subject3 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, mild patient |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: COVID-19 group: mild gender: male age: 51 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Last update date | Jan 15, 2021 |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019823**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019823) |  | [Query DataSets for GSM5019823](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019823%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_mild\_patient\_subject2 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, mild patient |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: COVID-19 group: mild gender: male age: 44 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019822**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019822) |  | [Query DataSets for GSM5019822](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019822%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_mild\_patient\_subject1 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, mild patient |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: COVID-19 group: mild gender: male age: 55 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Country | China |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019821**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019821) |  | [Query DataSets for GSM5019821](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019821%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_healthy\_subject5 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, HC |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: healthy gender: female age: 56 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Last update date | Jan 15, 2021 |
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| City | Hangzhou |
| ZIP/Postal code | 310058 |
| Country | China |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| --- | --- |
| **Data table header descriptions** | |
| **ID\_REF** |  |
| **VALUE** | Normalized signal intensity |

|  |  |
| --- | --- |
| **Data table** | |
| **ID\_REF** |  |

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| --- | --- | --- | --- | --- |
| |  |  |  | | --- | --- | --- | | [**Sample GSM5019820**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019820) |  | [Query DataSets for GSM5019820](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019820%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_healthy\_subject4 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, HC |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: healthy gender: male age: 71 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Country | China |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019819**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019819) |  | [Query DataSets for GSM5019819](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019819%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_healthy\_subject3 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, HC |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: healthy gender: male age: 54 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019818**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019818) |  | [Query DataSets for GSM5019818](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019818%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_healthy\_subject2 |
| Sample type | RNA |
|  |  |
| Source name | PBMC, HC |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: healthy gender: male age: 56 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
|  |  |
| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |

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| |  |  |  | | --- | --- | --- | | [**Sample GSM5019817**](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM5019817) |  | [Query DataSets for GSM5019817](https://www.ncbi.nlm.nih.gov/gds/?term=GSM5019817%5bAccession%5d) | | |
| Status | Public on Jan 15, 2021 |
| Title | PBMC\_healthy\_subject1 |
| Sample type | RNA |
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| Source name | PBMC, HC |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Characteristics | cell type: peripheral blood mononuclear cells (PBMCs) disease: healthy gender: male age: 62 |
| Treatment protocol | NA |
| Growth protocol | NA |
| Extracted molecule | total RNA |
| Extraction protocol | NA |
| Label | Cy3 |
| Label protocol | Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3' bias utilizing a random priming method (Arraystar Flash RNA Labeling Kit, Arraystar). The labeled cRNAs were purified by RNeasy Mini Kit (Qiagen). The concentration and specific activity of the labeled cRNAs (pmol Cy3/μg cRNA) were measured by NanoDrop ND-1000. |
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| Hybridization protocol | 1 μg of each labeled cRNA was fragmented by adding 5 μl 10 × Blocking Agent and 1 μl of 25 × Fragmentation Buffer, then heated the mixture at 60°C for 30 min, finally 25 μl 2 × GE Hybridization buffer was added to dilute the labeled cRNA. 50 μl of hybridization solution was dispensed into the gasket slide and assembled to the LncRNA expression microarray slide. The slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. |
| Scan protocol | The hybridized arrays were washed, fixed and scanned with using the Agilent DNA Microarray Scanner (part number G2505C). |
| Description | NA |
| Data processing | Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed with using the GeneSpring GX v12.1 software package (Agilent Technologies). After quantile normalization of the raw data, LncRNAs and mRNAs that at least 5 out of 15 samples have flags in Present or Marginal (“All Targets Value”) were chosen for further data analysis. Differentially expressed LncRNAs and mRNAs with statistical significance between the two groups were identified through P-value/FDR filtering. Differentially expressed LncRNAs and mRNAs between the two samples were identified through Fold Change filtering. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed mRNAs played in these biological pathways or GO terms. Hierarchical Clustering and combined analysis were performed using in-house scripts. |
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| Platform ID | [GPL26963](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL26963) |
| Series (1) | |  |  | | --- | --- | | [GSE164805](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164805) | The transcriptional profiles of severe COVID-19 | |