Vgenes Mutation Correlation

Guannan Shen

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Contents

```
## [1] "/home/guanshim/Documents/gitlab/Cario_RNASeq_Microbiom_Inte/DataProcessed/Vgenes"

## # A tibble: 6 x 47
##    IGHV1.18 IGHV1.2 IGHV1.24 IGHV1.3 IGHV3.15 IGHV3.21 IGHV3.23 IGHV3.30
##       <dbl>   <dbl>    <dbl>   <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1     1.13    1.37     2.91    2.50     5.17     1.19     3.38     4.20
## 2    0.856    1.56     3.18    2.64     4.74     1.38     3.61     4.46
## 3    0.729    1.94     3.17    2.55     5.17     1.14     4.14     3.79
## 4    0.848    1.16     3.46    2.09     4.73     1.52     2.84     3.74
## 5    0.832    2.09     3.01    2.39     5.15    0.985     4.26     4.12
## 6     1.11    1.75     3.65    2.34     5.38     1.02     3.89     3.05
##    IGHV3.33 IGHV3.48 IGHV3.49 IGHV3.53 IGHV3.7 IGHV3.72 IGHV3.73 IGHV3.74
##       <dbl>   <dbl>    <dbl>   <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1     4.90    1.13     2.10    2.02     6.23     3.12     1.26     3.54
## 2     5.50    1.52     2.20    1.74     6.38     3.17     1.23     3.27
## 3     5.30    1.49     1.87    1.64     6.20     3.87     1.61     2.75
## 4     5.07   0.947     1.75    1.50     5.58     2.40     1.06     2.61
## 5     5.37    1.05     1.62    1.99     6.47     2.80     1.47     3.64
## 6     5.53    1.75     2.16    1.58     6.89     3.40     1.31     3.69
##    IGHV4.34 IGHV4.39 IGHV4.59 IGHV7.81 IGKV1.39 IGKV1.5 IGKV1D.39 IGKV2.28
##       <dbl>   <dbl>    <dbl>   <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1     1.08   0.906     1.37    4.80    0.796     1.65     1.22     1.79
## 2     1.05   0.881     1.34    4.28    0.773     2.01     1.19     1.52
## 3     1.26   0.750     2.01    4.52     1.01     1.86     1.05     1.94
## 4     1.14   0.742     1.40    4.40    0.886     1.64     1.26     1.66
## 5     1.38   0.854     1.15    4.06    0.641     2.26     1.14     1.54
## 6    0.943   0.936     1.59    4.59     1.14     1.87     1.21     1.74
##    IGKV2D.28 IGKV3.11 IGKV3.15 IGKV3.20 IGKV4.1 IGLV1.40 IGLV1.44 IGLV1.47
##       <dbl>   <dbl>    <dbl>   <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1     3.16    1.22     1.60    1.92     5.20     1.03     2.00     1.82
## 2     1.58    1.19     1.54    2.43     4.61     1.00     1.95    0.970
## 3     1.38    1.05     1.11    1.78     5.11     1.31     2.32    0.836
## 4     1.49    1.45     1.21    1.87     4.68    0.867     2.28     1.07
## 5     2.20    1.42     1.37    2.10     5.01    0.972     1.79    0.937
## 6     1.45    1.39     1.40    2.61     5.22     1.18     2.20    0.772
##    IGLV2.11 IGLV2.14 IGLV2.23 IGLV2.8 IGLV3.1 IGLV3.10 IGLV3.19 IGLV3.21
##       <dbl>   <dbl>    <dbl>   <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1     1.52    2.87     1.01    1.41     3.42     2.64     1.04     3.35
## 2     1.49    2.22    0.989    2.10     3.86     2.77     1.02     2.74
## 3     1.44    2.69     1.54    1.64     3.41     3.10    0.870     3.22
## 4     1.42    2.65     1.08    1.53     3.82     2.44    0.990     3.05
## 5     1.68    2.22    0.839    1.40     3.31     3.30    0.851     2.72
## 6     1.53    2.36    0.960    1.29     4.02     3.51     1.12     3.06
##    IGLV3.25 IGLV3.9 IGLV4.69 IGLV5.48 IGLV6.57 HIV    ID
##       <dbl>   <dbl>    <dbl>   <dbl>    <dbl> <chr> <chr>
```

```
## 1     1.32     1.63     0.744     1.30     6.20 no     MIHIV138
## 2     1.28     1.59     1.15      1.04     5.95 no     MIHIV178
## 3     1.80     1.74     0.608     1.14     6.69 no     MIHIV255
## 4     1.45     1.81     0.601     1.40     5.92 no     MIHIV278
## 5     1.59     1.78     1.16      1.29     6.60 no     MIHIV361
## 6     1.54     1.60     0.641     1.21     6.50 no     MIHIV404

## [1] 32 47

## # A tibble: 6 x 5
##   ID       HIV    iga_smu igk_smu igl_smu
##   <chr>    <chr>    <dbl>   <dbl>   <dbl>
## 1 MIHIV138 no        24.3    10.9    18.1
## 2 MIHIV178 no        24.9    11.2    13.6
## 3 MIHIV255 no        23.2    11.3    15
## 4 MIHIV278 no        24.7    15.5    NA
## 5 MIHIV361 no        22.3     9.22   NA
## 6 MIHIV404 no        18.8    14.2    NA

## # A tibble: 6 x 36
##   Vsymbols   Num Type  Gene_ID          MIHIV138 MIHIV178 MIHIV255
##   <chr>    <dbl> <chr> <chr>               <dbl>    <dbl>    <dbl>
## 1 IGHV1-18     1 heavy ENSG00000211945.2    1.13    0.856    0.729
## 2 IGHV1-2      2 heavy ENSG00000211934.3    1.37    1.56     1.94
## 3 IGHV1-24     3 heavy ENSG00000211950.2    2.91    3.18     3.17
## 4 IGHV1-3      4 heavy ENSG00000211935.3    2.50    2.64     2.55
## 5 IGHV3-15    19 heavy ENSG00000211943.2    5.17    4.74     5.17
## 6 IGHV3-21    22 heavy ENSG00000211947.2    1.19    1.38     1.14
##   MIHIV278 MIHIV361 MIHIV404 MIHIV493 MIHIV582 MIHIV708 MIHIV716 MIHIV914
##      <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1    0.848    0.832    1.11     1.33    0.685    0.875    1.01    0.954
## 2    1.16     2.09     1.75     1.39    1.38     1.44     1.42    1.38
## 3    3.46     3.01     3.65     3.86    3.69     3.46     3.34    2.72
## 4    2.09     2.39     2.34     3.19    2.55     2.91     3.09    2.48
## 5    4.73     5.15     5.38     5.75    4.79     5.34     5.92    4.72
## 6    1.52     0.985    1.02     1.50    1.23     1.15     1.89    1.22
##   MIHIV947 MIHIV972 MIHIV124 MIHIV132 MIHIV154 MIHIV188 MIHIV217 MIHIV286
##      <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1    0.794    0.909    0.767    1.44     1.21     1.05    0.913    0.824
## 2    1.43     1.33     1.22     2.26     1.31     1.88     1.83    1.67
## 3    3.27     2.95     2.94     3.97     4.36     3.27     3.10    3.05
## 4    3.38     2.39     2.21     2.36     2.49     2.30     3.57    3.30
## 5    5.15     5.11     4.88     6.19     6.35     5.63     5.33    5.71
## 6    1.26     1.48     1.35     1.26     1.02     1.11     1.57    1.12
##   MIHIV307 MIHIV323 MIHIV391 MIHIV428 MIHIV594 MIHIV622 MIHIV648 MIHIV683
##      <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1    0.870    1.41     0.954    0.850    0.750    1.18     1.58    0.858
## 2    1.17     2.26     1.56     1.91     1.21     1.62     1.17    1.34
## 3    3.77     4.66     3.55     4.12     3.71     3.27     5.02    3.03
## 4    3.15     4.49     2.99     2.79     2.73     3.43     3.99    3.50
## 5    5.64     6.55     5.55     5.79     4.62     5.98     6.45    6.64
## 6    1.48     2.50     1.24     1.37     1.01     1.57     1.93    1.16
##   MIHIV819 MIHIV825 MIHIV839 MIHIV965 MIHIV998
##      <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1    0.929    0.802    2.28     0.908    1.29
```

```
## 2    1.64    1.27    2.63    1.66    1.35
## 3    3.05    3.21    4.00    3.19    3.56
## 4    3.36    3.09    3.92    3.36    3.05
## 5    5.27    4.89    6.68    6.27    6.31
## 6    1.21    1.10    2.52    1.22    1.33

## [1] 45 36

## # A tibble: 6 x 4
##   ID        Gender   Age HIV
##   <chr>     <chr>  <dbl> <chr>
## 1 MIHIV138 M         29 no
## 2 MIHIV178 M         33 no
## 3 MIHIV255 M         34 no
## 4 MIHIV278 M         23 no
## 5 MIHIV361 F         33 no
## 6 MIHIV404 F         29 no

##  [1] "CD4 count (cells/ul)"
##  [2] "IL-6 (pg/ml)"
##  [3] "CRP (mg/ml)"
##  [4] "iFABP (pg/ml)"
##  [5] "sCD27 (U/ml)"
##  [6] "CD14 (ng/ml)"
##  [7] "LPS (pg/ml)"
##  [8] "LTA\n(OD)"
##  [9] "CD38+ HLA-DR+ CD4 T cells (% of CD4 T cells)"
## [10] "CD38+ HLA-DR+ CD8 T cells (% of CD8 T cells)"
## [11] "CD4 T cells (% viable)"
## [12] "CD8 T cells (% viable)"
## [13] "Tissue HIV RNA (per CD4 T cell)"
## [14] "Plasma VL"
```

Table 1: Vgenes RNAseq

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
CD4 T cells (% viable)	All Participants	IGKV4.1	0.03217	0.0007148	-2.563e-02	32
CD4 T cells (% viable)	All Participants	IGLV1.44	0.04966	0.0022069	-1.793e-02	32
CD8 T cells (% viable)	All Participants	IGKV4.1	0.03568	0.0007929	1.901e-02	32

Table 2: Vgenes RNAseq HIV Infected

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Plasma VL	HIV Infected	IGLV2.8	0.04342	0.000965	4.445e-06	19

Table 3: Vgenes RNAseq Health

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope
CD38+ HLA-DR+ CD4 T cells (% of CD4 T cells)	Healthy Controls	IGHV7.81	0.02084	0.000463	6.496e-01

Table 4: Vgenes MiSeq

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sa
CD4 count (cells/ul)	All Participants	iga_smu	0.03359	0.03359	4.928e-03	3
CD4 count (cells/ul)	All Participants	igl_smu	0.03720	0.03720	6.823e-03	3
sCD27 (U/ml)	All Participants	iga_smu	0.001858	0.001858	-9.638e-02	3
CD14 (ng/ml)	All Participants	igl_smu	0.01366	0.01366	-4.469e-03	3
LPS (pg/ml)	All Participants	iga_smu	0.01513	0.01513	-2.757e-01	3
CD38+ HLA-DR+ CD4 T cells (% of CD4 T cells)	All Participants	iga_smu	0.02222	0.02222	-5.492e-01	3
CD38+ HLA-DR+ CD8 T cells (% of CD8 T cells)	All Participants	iga_smu	0.0433	0.0433	-1.044e-01	3
CD4 T cells (% viable)	All Participants	iga_smu	0.001763	0.001763	1.453e-01	3
CD8 T cells (% viable)	All Participants	iga_smu	0.001005	0.001005	-1.131e-01	3
CD8 T cells (% viable)	All Participants	igl_smu	0.000425	0.000425	-1.511e-01	3

Table 5: Vgenes MiSeq HIV Infected

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
CD8 T cells (% viable)	HIV Infected	igl_smu	0.04793	0.04793	-1.402e-01	19

Table 6: Vgenes MiSeq Health

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
CD4 T cells (% viable)	Healthy Controls	igk_smu	0.02005	0.02005	-1.972e-01	13

Table: Vgenes RNAseq phylum

Table 7: Vgenes RNAseq family

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Prevotellaceae	All Participants	IGKV1.39	0.01111	0.0002468	8.729e-01	27
Brucellaceae	All Participants	IGLV1.40	0.043832	0.0019481	3.825e+02	27
Brucellaceae	All Participants	IGLV3.19	0.007625	0.0001694	5.264e+02	27

Table 8: Vgenes RNAseq genus

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Prevotella	All Participants	IGKV1.39	0.01966	0.0004368	8.722e-01	27

Table 9: Vgenes RNAseq species

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
P. stercorea	All Participants	IGHV3.30	0.01746	0.0010978	9.537e+00	27
P. stercorea	All Participants	IGKV1.39	0.01746	0.0006984	3.173e+00	27
P. stercorea	All Participants	IGLV3.21	0.01746	0.0011640	5.723e+00	27
P. oris	All Participants	IGHV3.73	0.008818	0.000196	8.854e+00	27

Table 10: Vgenes RNAseq phylum

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Tenericutes	HIV Infected	IGLV2.14	0.017094	0.0007597	1.826e+02	14
Tenericutes	HIV Infected	IGLV3.19	0.005291	0.0001176	1.144e+02	14

Table 11: Vgenes RNAseq family

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Christensenellaceae	HIV Infected	IGHV1.18	0.03251	0.0021671	8.254e+01	14
Christensenellaceae	HIV Infected	IGHV1.2	0.04791	0.0056043	8.742e+01	14
Christensenellaceae	HIV Infected	IGHV3.21	0.03087	0.0008225	1.060e+02	14
Christensenellaceae	HIV Infected	IGHV3.23	0.04791	0.0085175	1.051e+02	14
Christensenellaceae	HIV Infected	IGHV3.74	0.04791	0.0070997	1.072e+02	14
Christensenellaceae	HIV Infected	IGHV4.34	0.03087	0.0013718	3.598e+01	14
Christensenellaceae	HIV Infected	IGLV3.25	0.04791	0.0076494	4.774e+01	14
Christensenellaceae	HIV Infected	IGLV3.9	0.03867	0.0034371	1.155e+02	14
Brucellaceae	HIV Infected	IGLV3.19	0.008736	0.0001941	5.286e+02	14

Table: Vgenes RNAseq genus

Table: Vgenes RNAseq species

Table 12: Vgenes RNAseq phylum

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Bacteroidetes	Healthy Controls	IGKV3.20	0.04994	0.00111	2.528e+00	13
Firmicutes	Healthy Controls	IGKV3.20	0.01173	0.0002608	-1.702e+00	13
Verrucomicrobia	Healthy Controls	IGLV3.1	0.02686	0.0005968	1.39e+01	13

Table 13: Vgenes RNAseq family

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Ruminococcaceae	Healthy Controls	IGHV3.7	0.02533	0.0005628	-4.687e+00	13

Table: Vgenes RNAseq genus

Table 14: Vgenes RNAseq species

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
P. oris	Healthy Controls	IGHV3.73	0.004916	0.0001092	9.376e+00	13
P. oris	Healthy Controls	IGLV2.23	0.045937	0.0020417	6.885e+00	13

Table 15: Vgenes miseq phylum

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Cyanobacteria	All Participants	iga_smu	0.00970	0.00970	1.568e+02	27
Cyanobacteria	All Participants	igl_smu	0.01856	0.01856	1.580e+02	27
Firmicutes	All Participants	iga_smu	0.008763	0.008763	8.954e+00	27
Proteobacteria	All Participants	iga_smu	0.03297	0.03297	-8.501e+00	27

Table 16: Vgenes miseq family

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Lachnospiraceae	All Participants	iga_smu	0.04007	0.04007	1.007e+01	27

Table 17: Vgenes RNAseq genus

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Blautia	All Participants	iga_smu	0.03105	0.03105	7.152e+01	27
Blautia	All Participants	igl_smu	0.03470	0.03470	1.236e+02	27

Table 18: Vgenes RNAseq species

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Bacteroides_dorei	All Participants	iga_smu	0.02683	0.02683	1.283e+02	27
Bacteroides_dorei	All Participants	igk_smu	0.04955	0.04955	9.830e+01	27
Bacteroides_dorei	All Participants	igl_smu	0.03370	0.03370	1.368e+02	27
Blautia_luti	All Participants	iga_smu	0.03813	0.03813	1.417e+02	27
Blautia_luti	All Participants	igl_smu	0.03847	0.03847	2.128e+02	27
Blautia_schinkii	All Participants	iga_smu	0.001614	0.001614	3.064e+02	27
Ruminococcus_bromii	All Participants	iga_smu	0.01074	0.01074	6.471e+01	27

Table 19: Vgenes MiSeq phylum

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Tenericutes	HIV Infected	igl_smu	0.01974	0.01974	-6.59e+02	14

Table 20: Vgenes MiSeq family

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Rhodospirillaceae	HIV Infected	igl_smu	0.03986	0.03986	-2.048e+04	14

Table 21: Vgenes MiSeq genus

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Coprococcus	HIV Infected	iga_smu	0.041544	0.041544	-3.157e+02	14
Coprococcus	HIV Infected	igk_smu	0.004191	0.004191	-3.492e+02	14
Thalassospira	HIV Infected	igl_smu	0.02448	0.02448	-2.737e+05	14

Table 22: Vgenes MiSeq species

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Acidaminococcus_intestini	HIV Infected	igk_smu	0.007274	0.007274	-2.086e+02	14
Blautia_glucerasei	HIV Infected	iga_smu	0.01136	0.01136	-1.046e+03	14
Blautia_glucerasei	HIV Infected	igl_smu	0.03358	0.03358	-8.168e+02	14

Table 23: Vgenes MiSeq phylum

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Bacteroidetes	Healthy Controls	iga_smu	0.03153	0.03153	-1.272e+01	13
Cyanobacteria	Healthy Controls	iga_smu	0.01004	0.01004	1.189e+02	13
Firmicutes	Healthy Controls	iga_smu	0.04295	0.04295	7.761e+00	13
Proteobacteria	Healthy Controls	iga_smu	0.01878	0.01878	-2.186e+01	13
Tenericutes	Healthy Controls	iga_smu	0.02769	0.02769	1.692e+02	13

Table 24: Vgenes MiSeq family

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Lachnospiraceae	Healthy Controls	igk_smu	0.04028	0.04028	-1.149e+01	13
Christensenellaceae	Healthy Controls	igk_smu	0.022	0.022	3.691e+01	13
Ruminococcaceae	Healthy Controls	igl_smu	0.03989	0.03989	5.568e+01	13
Moraxellaceae	Healthy Controls	iga_smu	0.04008	0.04008	-1.314e+02	13

Table 25: Vgenes MiSeq genus

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Coprococcus	Healthy Controls	iga_smu	0.03209	0.03209	1.653e+02	13
Acinetobacter	Healthy Controls	iga_smu	0.04353	0.04353	-1.394e+02	13

Table 26: Vgenes MiSeq species

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
P. stercorea	Healthy Controls	iga_smu	0.04835	0.04835	2.89e+02	13
Schlegelella_thermodepolymerans	Healthy Controls	iga_smu	0.03001	0.03001	-4.341e+04	13
Bacteroides_thetaiotaomicron	Healthy Controls	iga_smu	0.007971	0.007971	-1.028e+02	13
Bacteroides_acidifaciens	Healthy Controls	igk_smu	0.02178	0.02178	-3.409e+03	13
Blautia_glucerasei	Healthy Controls	igk_smu	0.04666	0.04666	-1.933e+02	13

Parameter	HIV Status	Gene	Adjusted P	Raw P	Slope	Sample Size
Blautia_schinkii	Healthy Controls	iga_smu	0.001257	0.001257	2.28e+02	13
Ruminococcus_bromii	Healthy Controls	iga_smu	0.02005	0.02005	4.574e+01	13