Summary M1 Mediators ADDIS

STAT 550

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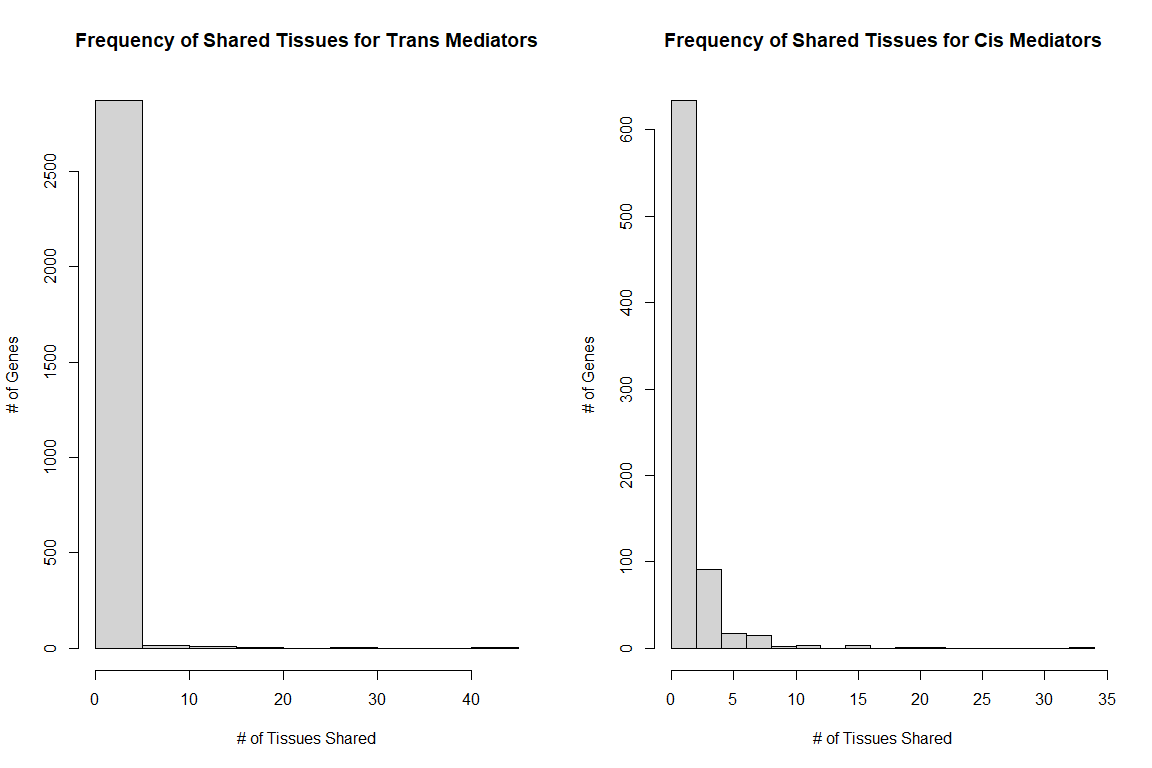
3/28/2021

Total number of Cis and Trans genes identified as Mediators under MRPC-ADDIS

|  |  |  |
| --- | --- | --- |
|  | Total.Num.Genes | Percent.Of.Total |
| Cis Only | 1356 | 0.2652582 |
| Trans Only | 3674 | 0.7187011 |
| Both Cis & Trans | 82 | 0.0160407 |

Total number of Unqiue Cis and Trans genes identified as Mediators under MRPC-ADDIS

|  |  |  |
| --- | --- | --- |
|  | Total.Unique.Genes | Percent.Of.Total |
| Cis Only Unique | 730 | 0.1994536 |
| Trans Only Unique | 2848 | 0.7781421 |
| Both Cis & Trans | 82 | 0.0224044 |



ADDIS Trans Mediator Tissue Counts

|  |  |
| --- | --- |
| Num.of.Genes | Num.of.Shared |
| 2656 | 1 |
| 160 | 2 |
| 34 | 3 |
| 13 | 4 |
| 8 | 5 |
| 3 | 6 |
| 1 | 7 |
| 4 | 8 |
| 2 | 9 |
| 3 | 10 |
| 3 | 11 |
| 2 | 13 |
| 1 | 14 |
| 1 | 15 |
| 1 | 16 |
| 1 | 17 |
| 2 | 20 |
| 1 | 26 |
| 1 | 30 |
| 1 | 44 |

ADDIS Cis Mediator Tissue Counts

|  |  |
| --- | --- |
| Num.of.Genes | Num.of.Shared |
| 514 | 1 |
| 120 | 2 |
| 60 | 3 |
| 31 | 4 |
| 10 | 5 |
| 7 | 6 |
| 7 | 7 |
| 8 | 8 |
| 2 | 10 |
| 2 | 11 |
| 1 | 12 |
| 2 | 15 |
| 1 | 16 |
| 1 | 20 |
| 1 | 21 |
| 1 | 34 |

ADDIS Unique Cis Mediator Gene Types

|  |  |
| --- | --- |
|  | Percentage |
| IG\_V\_gene | 0.00685 |
| IG\_V\_pseudogene | 0.00274 |
| lncRNA | 0.26301 |
| miRNA | 0.00137 |
| polymorphic\_pseudogene | 0.00274 |
| processed\_pseudogene | 0.04658 |
| protein\_coding | 0.50274 |
| TEC | 0.01918 |
| TR\_V\_gene | 0.00137 |
| TR\_V\_pseudogene | 0.00137 |
| transcribed\_processed\_pseudogene | 0.02055 |
| transcribed\_unitary\_pseudogene | 0.00685 |
| transcribed\_unprocessed\_pseudogene | 0.07260 |
| translated\_unprocessed\_pseudogene | 0.00137 |
| unprocessed\_pseudogene | 0.03973 |
| NA’s | 0.01096 |

ADDIS Unique Trans Mediator Gene Types

|  |  |
| --- | --- |
|  | Percentage |
| IG\_C\_gene | 0.00105 |
| IG\_D\_gene | 0.00316 |
| IG\_J\_gene | 0.00070 |
| IG\_V\_gene | 0.00667 |
| IG\_V\_pseudogene | 0.00632 |
| lncRNA | 0.20154 |
| miRNA | 0.06812 |
| misc\_RNA | 0.05969 |
| Mt\_tRNA | 0.00140 |
| polymorphic\_pseudogene | 0.00035 |
| processed\_pseudogene | 0.18645 |
| protein\_coding | 0.24122 |
| pseudogene | 0.00035 |
| ribozyme | 0.00035 |
| rRNA | 0.00211 |
| rRNA\_pseudogene | 0.01369 |
| scaRNA | 0.00035 |
| snoRNA | 0.02669 |
| snRNA | 0.06250 |
| TEC | 0.00808 |
| TR\_C\_gene | 0.00035 |
| TR\_J\_gene | 0.00421 |
| TR\_J\_pseudogene | 0.00070 |
| TR\_V\_gene | 0.00176 |
| TR\_V\_pseudogene | 0.00105 |
| transcribed\_processed\_pseudogene | 0.00772 |
| transcribed\_unitary\_pseudogene | 0.00105 |
| transcribed\_unprocessed\_pseudogene | 0.02247 |
| unitary\_pseudogene | 0.00105 |
| unprocessed\_pseudogene | 0.06742 |
| NA’s | 0.00140 |

ADDIS gene types for genes found as both Cis and Trans Mediators

|  |  |  |  |
| --- | --- | --- | --- |
| Cis.Gene.Type | Percent.Cis | Trans.Gene.Type | Percent.Trans |
| lncRNA | 0.18293 | IG\_V\_gene | 0.01220 |
| processed\_pseudogene | 0.04878 | lncRNA | 0.17073 |
| protein\_coding | 0.59756 | processed\_pseudogene | 0.10976 |
| transcribed\_processed\_pseudogene | 0.03659 | protein\_coding | 0.43902 |
| transcribed\_unprocessed\_pseudogene | 0.08537 | transcribed\_processed\_pseudogene | 0.01220 |
| unprocessed\_pseudogene | 0.03659 | transcribed\_unitary\_pseudogene | 0.01220 |
| NA’s | 0.0122 | transcribed\_unprocessed\_pseudogene | 0.13415 |
| – | – | unprocessed\_pseudogene | 0.10976 |

##   
## Pearson's Chi-squared test with Yates' continuity correction  
##   
## data: as.matrix(cont.table)  
## X-squared = 36.549, df = 1, p-value = 1.489e-09

2X2 contingency table of mediator gene type

|  |  |  |  |
| --- | --- | --- | --- |
|  | cis | trans | margins |
| non-pseudo | 588 | 1969 | 2557 |
| pseudo | 142 | 879 | 1021 |
| margins | 730 | 2848 | 3578 |

##   
## Chi-squared test for given probabilities  
##   
## data: summary(trans.types)  
## X-squared = 43.777, df = 1, p-value = 3.68e-11

Chi-Square GOF observed vs. Expected proportions ADDIS

|  |  |  |
| --- | --- | --- |
|  | non-pseudo | pseudogene |
| observed | 0.6913624 | 0.3086376 |
| expected | 0.7453746 | 0.2546254 |

##   
## Pearson's Chi-squared test with Yates' continuity correction  
##   
## data: as.matrix(Lcont.table)  
## X-squared = 50.456, df = 1, p-value = 1.219e-12

2X2 contingency table of mediator gene type

|  |  |  |  |
| --- | --- | --- | --- |
|  | cis | trans | margins |
| non-pseudo | 819 | 1313 | 2132 |
| pseudo | 186 | 585 | 771 |
| margins | 1005 | 1898 | 2903 |

##   
## Chi-squared test for given probabilities  
##   
## data: summary(L.trans.types)  
## X-squared = 28.724, df = 1, p-value = 8.345e-08

Chi-Square GOF observed vs. Expected proportions LOND

|  |  |  |
| --- | --- | --- |
|  | non-pseudo | pseudogene |
| observed | 0.6917808 | 0.3082192 |
| expected | 0.7453746 | 0.2546254 |