

















Figure ############# Prevalence of deleterious mutations in the ExAC database, for select kidney cancer associated genes.













|  |  |  |  |
| --- | --- | --- | --- |
|   *Overall*  |   *African American*    *(AFR)*  |   *Non-Finnish European (NFE)*  |   *Finnish*  *European*  *(FIN)*  |
|   1/23 indiv.  |   1/17\* indiv  |   1/20 indiv  |   1/54 indiv.  |
|   \*Highest rate among all races in the ExAC database  |

|  |  |  |  |
| --- | --- | --- | --- |
| Derived allele frequency | AFR | EUR | Overall |
| Potentially deleterious mutations  | ExAC |  |  |  |
| 1000G | 4.7% | 3.6% | 4.5% |
| Potentially LoF mutations (1000G) | 1.1% | 0.4% | 0.5% |
| ClinVAR (1000G) | 0.3% | 1.2% | 0.6% |







