

**Table S4. Ti/Tv ratio and mean coverage for exome-sequencing**

<b>ID</b>	<b>111289</b>	<b>111290</b>	<b>111292</b>	<b>111296</b>	<b>111299</b>	<b>111304</b>	<b>111310</b>	<b>111311</b>	<b>111313</b>	<b>111316</b>	<b>111317</b>	<b>133328</b>
<b>Ti/Tv</b>	3.27	3.18	3.15	3.19	3.18	3.13	3.17	3.18	3.21	3.16	3.19	3.18
<b>Cvg</b>	107.95	110.68	115.59	120.55	113.75	111.03	202.3*	106.51	125.08	108.86	123.45	103.55
<b>ID</b>	<b>133341</b>	<b>133344</b>	<b>133346</b>	<b>4899</b>	<b>4999</b>	<b>5144</b>	<b>5302</b>	<b>5308</b>	<b>5403</b>			
<b>Ti/Tv</b>	3.19	3.18	3.19	3.14	3.16	3.14	3.22	3.1	3.22			
<b>Cvg</b>	130.47	97.07	120.41	117.97	113.14	120.11	124.26	112.57	127.27			

Notes: 1. Cvg is the mean coverage for each sample.

2. Every two samples were sequenced in one HiSeq lane, and the sample 111310 were sequenced alone in one lane, which doubled its coverage. Cvg is the mean coverage for each sample.

3. The sample 111311 was not analyzed in this study since this is a non-European individual.