

March 15, 2022

SUMMARY ON OCE-specific SNP dataset. (the data are in Moscow BIO Linux workstation in /home/afedorov/NOV2021)

- 1) Start from Simons' dataset. The program `OceaniaSimonStep1.pl` counts number of Alt-allele SNPs in OCE: /Aus|Bou|Pap/, which should be 7 or more alleles (among 19 people) The program also counts this allele in OCE-flanking populations: /Dus|Mao|Igo|Hav/. In the rest of Simons' populations this allele must be absent. It creates the phase-1 OCE-specific SNPs (`OCE_SNPs_$(chr)`), where `$(chr)` means the number of chromosome (from 1 to 22)
- 2) Comparison with 1000G dataset. The second program `Oceania1000gStep2.pl` compares phase-1 OCE-specific SNPs with all 2504 individuals from 1000G. The number of "OCE-specific phase-1" alleles in all 1000G should be less or equal to the number of these alleles among 19 OCE people. Thus, the frequency of OCE-specific SNPs at this second step must be >100 times frequent than in the rest of the world. This computation creates phase-2 OCE-specific SNPs, which are stored in the `OceaniaSpecificSNPs_$(chr)` files. After application of V3 (OCE freq in 1000G unknown!!, yet total freq is <150x than in Oceania) in `OceaniaSpecificV3_$(chr)` files I got **71,848** SNPs.
- 3) Final comparison with Estonian dataset using `OceanEstoniaStep3.pl` program. The number of OCE-specific alleles among all Estonian DB people must be 4 or less. This is the final phase-3 purification (very weak with main purpose to print populations that have Region-specific alleles in the final table). The main results are in the files specific for each chromosome: `OceaniaSpecificSNPsEstonia2_$(chr)` and also the combined file for all chromosomes: `OceaniaSpecificSNPsEstonia2_ALL`. This file contains the number of OCE-specific alleles in all datasets (Simons, 1000G, and Estonian) and also the name of populations, where they present. See this table below,

Col-1	Col-2.	Col-3.	Col-4	Col-5.	Col-6	Col-7	Col-8	Col9.	Col10.	Col11.	Col12.	Col13	Col14	Col15	Col16	Col-17+
rs373000721	9	0	0	0	CHR1	833529	rs373000721	G	A	0	0	0	0	0	NOT	Koi_OCE Kos_OCE Koi_OCE
rs367861531	10	0	0	0	CHR1	835831	rs367861531	G	A	0	0	0	1	0	YRI	Koi_OCE Kos_OCE Koi_OCE
rs369581566	10	0	0	0	CHR1	837238	rs369581566	G	A	0	0	0	0	0	NOT	Koi_OCE Kos_OCE Koi_OCE
rs377052638	8	0	0	0	CHR1	837992	rs377052638	C	G	0	0	0	0	0	NOT	Koi_OCE Kos_OCE Koi_OCE
rs373451994	10	0	0	0	CHR1	839636	rs373451994	G	A	0	0	0	0	0	NOT	Koi_OCE Kos_OCE Koi_OCE
rs146441147	9	0	0	0	CHR1	979559	rs146441147	C	T	0	0	0	0	0	NOT	Kos_OCE Koi_OCE
rs372205897	12	0	0	0	CHR1	1029701	rs372205897	C	T	0	0	0	0	0	NOT	Kos_OCE Koi_OCE
rs373322116	12	0	0	0	CHR1	1047802	rs373322116	G	A	0	0	0	0	0	NOT	Kos_OCE Koi_OCE
rs375647989	8	0	0	0	CHR1	1107859	rs375647989	A	G	0	0	0	0	0	NOT	Kos_OCE Kos_OCE
rs371814109	8	0	0	0	CHR1	1109872	rs371814109	A	G	0	0	0	0	0	NOT	Kos_OCE Kos_OCE
rs373310048	8	0	0	0	CHR1	1110271	rs373310048	G	A	0	0	0	0	0	NOT	Kos_OCE Kos_OCE
rs11811026	8	0	0	0	CHR1	1112124	rs11811026	C	A	0	0	0	0	0	ASW	Kos_OCE Kos_OCE
rs11811377	8	0	0	0	CHR1	1112318	rs11811377	C	A	1	0	0	1	0	CLM	YRI ASW Kos_OCE Kos_OCE
rs377508467	8	0	0	0	CHR1	1112457	rs377508467	T	G	0	0	0	0	0	NOT	Kos_OCE Kos_OCE
rs375453018	8	0	0	0	CHR1	1114523	rs375453018	C	T	0	0	0	1	0	GWD	ASW Kos_OCE Kos_OCE
rs374835744	8	0	0	0	CHR1	1114552	rs374835744	C	T	0	0	0	1	0	GWD	ASW Kos_OCE Kos_OCE
rs368714026	7	0	0	0	CHR1	1116266	rs368714026	C	T	0	0	0	0	0	NOT	Kos_OCE Kos_OCE
slx1118971	7	0	0	0	CHR1	1118971	slx1118971	C	G	0	0	0	0	0	NOT	Baj_OCE Koi_OCE Kos_OCE Koi_OCE
rs551036611	12	0	0	0	CHR1	1302130	slx1302130	G	A	0	0	2	0	0	KHV	Baj_OCE Agt_OCE
slx1344958	7	0	0	0	CHR1	1344958	slx1344958	A	G	0	0	0	0	0	NOT	Baj_OCE Agt_OCE
rs369955862	7	0	0	0	CHR1	1381934	rs369955862	A	G	0	0	0	0	0	NOT	Leb_OCE Baj_OCE Agt_OCE
slx1385293	7	0	0	0	CHR1	1385293	slx1385293	G	A	0	0	0	0	0	NOT	Baj_OCE Agt_OCE
rs367639744	10	0	0	0	CHR1	1471892	rs367639744	C	T	0	0	0	0	0	NOT	Koi_OCE Koi_OCE
slx1503254	7	0	0	0	CHR1	1503254	slx1503254	T	C	0	0	0	0	0	NOT	Agt_OCE

Col-1 (rs-ID if existed in 1000G, if not then our ID: slx1503254, where first "s" means Simons project, following the chr number, then 'x' separator and position on chr)
Col-2 Number of OCE-specific alleles counts in phase-1 in 19 OCE people from /Aus|Bou|Pap/

Col-3 Number of OCE-specific alleles counts in phase-1 in 19 neighboring OCE people from /Dus|Mao|Igo|Hav/
 Col-4 Always 0, because this item was skipped from AMR-specific SNPs
 Col-5 Always 0, because this item was skipped from AMR-specific SNPs
 Col-6 Chromosome number
 Col-7 Position on chr
 Col-8 repetition of column-1
 Col-9 Reference allele
 Col-10 Alternative allele
 Col-11 Number of OCE-specific alleles in all AMR from 1000G
 Col-12 Number of OCE-specific alleles in all EUR from 1000G
 Col-13 Number of OCE-specific alleles in all EAS from 1000G
 Col-14 Number of OCE-specific alleles in all AFR from 1000G
 Col-15 Number of OCE-specific alleles in all SAS from 1000G
 Col-16 All populations from 1000G where the OCE-specific allele was observed. If not observed the NOT will appear
 Col-17+ All populations from ESTONIAN DB where the OCE-specific allele was observed. For example, Kos_OCE

SUMMARY ON AMR-specific SNP dataset. (the data are in Moscow BIO Linux workstation in /home/afedorov/NOV2021)

- 1) Start from Simons' dataset. The program `AmericanSNPs2020.pl` counts number of Alt-allele SNPs in AMR pure tribes: /Cha|Kar|Sur|Pia/, which should be 3 or more alleles (among 8 people) [COLUMN-2]. The program also counts this allele in AMR more diverse populations, that have admixture: /May|Mix|Pim|Que|Zap/ 14 people (admixed with 30% Europeans and Africans genes) [COLUMN-3]. In order to qualify as AMR-specific SNP I created an additional requirement for the counts: $Col2 + Col3 \geq 7$ (program `purgeNativeAmericanSNPs.pl`). Finally, I also counted the number of alleles in the AMR-flanking populations from Arctic (ARC), that little intersect with AMR: /Ale|Chu|Esk|Ite|Tli|Ulc/ [COLUMN-4] and also Siberia (SIB): /Eve|Man|Yak|Tub/ [COLUMN-5]. In the rest of Simons' populations this allele must be absent. It creates the phase-1 AMR-specific SNPs (`AMR_SNPs_`*\$chr*), where *\$chr* means the number of chromosome (from 1 to 22)
- 2) Comparison with 1000G dataset. The second program `America1000gStep2_v2.pl` compares phase-1 AMR-specific SNPs with all 2504 individuals from 1000G. The number of "AMR-specific phase-1" alleles in all 1000G dataset is divided by 5 regions (EAS, SAS, EUR, AFR, AMR). The number of AMR-specific alleles in AMR populations should be more than the number of these alleles in the rest four regions multiplied by 10 [e.g. $(AFR+EAS+SAS+EUR)*10$]. Thus, the frequency of AMR-specific SNPs at this second step in AMR must be >40 times frequent than in the rest of the world. Since AMR populations from 1000G are very admixed with European and African genomes, this requirement equivalents that in pure AMR-populations the frequency of these alleles should be >100x than their frequency in the rest of the World. This computation creates phase-2 AMR-specific SNPs, which are stored in the `AmericaSpecificSNPs_`*\$chr* files. After application of V3 (AMR freq in 1000G $\geq 9\%$ and $>18\%$ which is taking into account admixture AMR with other continents) in `AmericaSpecificV3_`*\$chr* files I got **4,133** SNPs.
- 3) Final comparison with Estonian dataset using `AmericanSNPsESTONIA.pl` program. The number of AMR-specific alleles among all Estonian DB people must be 4 or less. [A vast majority of Estonian DB are not American populations. They will be listed in the final table]. This is the final phase-3 purification (very weak with main purpose to print populations that have Region-specific alleles in the final table). The main results are in the files specific for each chromosome: `AmericaSpecificSNPsEstonia2_`*\$chr* and also the combined file for all chromosomes: `AmericaSpecificSNPsEstonia2_ALL`. This file contains the number of AMR-specific alleles in all datasets (Simons, 1000G, and Estonian) and also the name of populations, where they present. See example of this table for OCE-specific alleles above.

SUMMARY ON EAS-specific (China-Specific) SNP dataset. (the data are in Moscow BIO Linux workstation in /home/afedorov/NOV2021)

- 4) Start from Simons' dataset. The program `ChinaSimonStep1.pl` counts number of Alt-allele SNPs in EAS pure populations: /Dai|Han|Jap|Kor|Mia|Nax|She|Tuj|YiX/, which should be 8 or more alleles (among 22 people) [COLUMN-2]. The program also counts this allele in EAS more diverse populations, that have admixture: /Cam|TuX|Lah|Xib|Hez|Oro|Mon|Dau|Bur|Ami|Ata|Kin/ [COLUMN-3]. Finally, I also counted the number of alleles in the EAS-flanking populations from the south, that little intersect with EAS: /Kus|BUm|Tam|Leb|Luz|Ulc|Mur|Igo|Haw|Dus/ [COLUMN-4] and also Central Asia: /Eve|EVk|Yak|Tub|Sho|Sak|Alt|Kal|Kaz|Kyr|Uyg/ [COLUMN-5]. In the rest of Simons' populations this allele must have 4 or less counts. It creates the phase-1 China-specific SNPs (`CHI_SNPs_$chr`), where *\$chr* means the number of chromosome (from 1 to 22)
- 5) Comparison with 1000G dataset. The second program `China1000gStep2_v2.pl` compares phase-1 EAS-specific SNPs with all 2504 individuals from 1000G. The number of "EAS-specific phase-1" alleles in all 1000G dataset is divided by 5 regions (EAS, SAS, EUR, AFR, AMR). The number of EAS-specific alleles in EAS populations should be more than the number of these alleles in the rest four regions multiplied by 10 [e.g. (AFR+AMR+SAS+EUR)*10]. Thus, the frequency of AMR-specific SNPs at this second step in AMR must be >40 times frequent than in the rest of the world. This restriction is the lower than for AMR and OCE, because we have 10 times less EAS-specific SNPs. This computation creates phase-2 EAS-specific SNPs, which are stored in the `ChinaSpecificSNPs_$chr` files. After application of V3 (EAS freq in 1000G >=18%) in `ChinaSpecificV3_$chr` files I got **441** SNPs.
- 6) Final comparison with Estonian dataset using `ChinaEstoniaStep3.pl` program. The number of EAS-specific alleles among all Estonian DB people must be 4 or less. [A vast majority of Estonian DB are not EAS populations. They will be listed in the final table]. This is the final phase-3 purification (very weak with main purpose to print populations that have Region-specific alleles in the final table). The main results are in the files specific for each chromosome: `ChinaSpecificSNPsEstonia2_$chr` and also the combined file for all chromosomes: `ChinaSpecificSNPsEstonia2_ALL`. This file contains the number of EAS-specific alleles in all datasets (Simons, 1000G, and Estonian) and also the name of populations, where they present. See example of this table for OCE-specific alleles above.

SUMMARY ON AFR-specific SNP dataset. (the data are in Moscow BIO Linux workstation in /home/afedorov/NOV2021)

- 1) Start from Simons' dataset. The program `AfricaSimonStep1.pl` counts number of Alt-allele SNPs in AFR pure populations: /Moz|Ban|Bia|Mbu|Gam|Luo|Mas|Luh|Som|JuX|Yor|Esa|Man|Men|Kho|Din|Sah/, which should be 17 or more alleles (among 47 people) [COLUMN-2]. The program DOES NOT count this allele in AFR diverse populations, thus, [COLUMN-3, 4, and 5] are empty (0). In the rest of Simons'

populations this allele must have 2 or less counts. It creates the phase-1 AFR-specific SNPs (CHI_SNP_s_*\$chr*), where *\$chr* means the number of chromosome (from 1 to 22)

- 2) Comparison with 1000G dataset. The second program `Africa1000gStep2_v2.pl` compares phase-1 AFR-specific SNPs with all 2504 individuals from 1000G. The number of “AFR-specific phase-1” alleles in all 1000G dataset is divided by 5 regions (EAS, SAS, EUR, AFR, AMR). The number of AFR-specific alleles in AFR populations should be more than the number of these alleles in the rest four regions multiplied by 10 [e.g. (EAS+AMR+SAS+EUR)*10]. Thus, the frequency of AFR-specific SNPs at this second step in AFR must be >40 times frequent than in the rest of the world. This restriction is the lower than for AMR and OCE, because we have strong African admixture in AMR and Southern Europe. This computation creates phase-2 AFR-specific SNPs, which are stored in the `AfricanSpecificSNPs_$chr` files. After application of V3 (AFR freq in 1000G >=18%) in `AfricaSpecificV3_$chr` files I got **112,658** SNPs.
- 3) Final comparison with Estonian dataset using `AfricanSNPsESTONIA.pl` program. The number of AFR-specific alleles among all Estonian DB people must be 4 or less. [A vast majority of Estonian DB are not AFR populations. They will be listed in the final table]. This is the final phase-3 purification (very weak with main purpose to print populations that have Region-specific alleles in the final table). The main results are in the files specific for each chromosome: `AfricanSpecificSNPsEstonia2_$chr` and also the combined file for all chromosomes: `AfricanSpecificSNPsEstonia2_ALL`. This file contains the number of AFR-specific alleles in all datasets (Simons, 1000G, and Estonian) and also the name of populations, where they present. See example of this table for OCE-specific alleles above.

SUMMARY ON EUR-specific SNP dataset. (the data are in Moscow BIO Linux workstation in /home/afedorov/NOV2021)

- 1) Start from Simons’ dataset. The program `EuropeSimonStep1.pl` counts number of Alt-allele SNPs in EUR pure populations: /Alb|Bas|Ber|Bul|Cre|Eng|Est|Fin|Fre|Gre|Hun|Ice|Nor|Orc|Pol|Rus|Saa|Sar|Spa|Tus/, which should be 15 or more alleles (among 41 people) [COLUMN-2]. The program counts these alleles in NON-EUR diverse populations, which should be less than two counts in total. These NON-EUR include the following: /Dai|Han|Jap|Kor|Mia|Nax|She|Tuj|YiX|Moz|Ban|Bia|Mbu|Gam|Luo|Mas|Luh|Som|JuX|Yor|Esa|Man|Men|Kho|Din|Sah/, which are EAS and AFR-populations [COLUMN- 5]. And also /Cam|TuX|Lah|Xib|Hez|Oro|Mon|Dau|Bur|Ami|Ata|Kin/and /Kus|BUM|Tam|Leb|Luz|Ulc|Mur|Igo|Haw|Dus/ which are neighboring to EAS populations. In the rest of Simons’ populations this allele must have only one or zero counts. It creates the phase-1 EUR-specific SNPs (EUR_SNP_s_*\$chr*), where *\$chr* means the number of chromosome (from 1 to 22). **ALTOGETHER I GOT 6585** SNPs.
- 2) Comparison with 1000G dataset. The second program `Europe1000gStep2_v2.pl` compares phase-1 EUR-specific SNPs with all 2504 individuals from 1000G. The number of “EUR-specific phase-1” alleles in all 1000G dataset is divided by 5 regions (EAS, SAS, EUR, AFR, AMR). The number of EUR-specific alleles in EUR populations should be more than the number of these alleles in AFR plus EAS multiplied by 20 plus number of this allele in SAS population ($\$afr + \$asia$)*20 + $\$ind$ *1. In other words, this EUR-specific allele must be 40x less frequent in AFR and EAS and also less frequent than in SAS. Thus, the frequency of AFR-specific SNPs at this second step in AFR must be >40 times frequent than in the rest of the world. This restriction is chosen

because we have strong European admixture in AMR and India (SAS). This computation creates phase-2 EUR-specific SNPs, which are stored in the EuropeSpecificSNPs_\$.chr files. ALTOGETHER I GOT **3925** SNPs.

After application of V3 (EUR freq in 1000G $\geq 18\%$) in EuroSpecificV3_\$.chr files I got **1539** SNPs.

After application of V3 (EUR freq in 1000G $\geq 15\%$) in EuroSpecificV3_\$.chr files I got **2484** SNPs.

3)

March 25, 2022

New thresholds for Region-Specific SNPs.

Table S1. Distribution the numbers of common region-specific SNPs, which MAF > 18%.

Region	Step-1. Number of region-specific SNPs in Simons' Database	Step-2. Number of region-specific SNPs purged on 1000 Genomes	Step-3. Number of region-specific SNPs purged on EGDP DB	Step-4. Number of clusters of Region-specific SNPs
Africa	204,983	112,658	77,820	28,774
Americas	46,994	4,133	3,348	3,222
East Asia	7,789	441	362	272
Europe	6,585	2,484	1,911	1,394
Oceania	77,437	71,848 *	1,358	453

Step-1: Processing SNPs from Simons' Project. Characterization and counting the number of common region-specific SNPs (MAF >18%), which frequency in other regions (those without noticeable admixture).

Step-2. Characterization the number of common region-specific SNPs from Step-1, which MAF in the same region is also >18% in the 1000 Genomes DB. Verification that the frequencies of these region-specific SNP alleles in 1000 Genomes are also reduced at least 40 times in other regions.

*Note that Oceania populations are absent in 1000 Genomes, thus, the requirement for MAF $\geq 18\%$ is omitted for OCE at Step-2. However, this requirement (MAF $>18\%$) is enforced in the next Step-3 for the EGPD Database, which has 51 individuals from OCE populations.

Step-3. Characterization the number of common region-specific SNPs from Step-2, which MAF is also significant ($>16\%$) in EGPD Database in the same region. Confirmation that frequencies of these region-specific SNP alleles in EGPD are drastically reduced in other regions.

Step-4. Grouping of neighboring region-specific SNPs from Step-3 into clusters when the distance between neighboring SNPs is less than 5 Kb.

Final results are in the files for each autosome (1..22): **FinalRegion_chr**

```
afedorov@bio:~/NOV2021$ ls -l Final*
-rw-rw-r-- 1 afedorov afedorov 618734 map 28 04:59 FinalAfrica_1
-rw-rw-r-- 1 afedorov afedorov 280705 map 28 04:59 FinalAfrica_10
-rw-rw-r-- 1 afedorov afedorov 305577 map 28 04:59 FinalAfrica_11
-rw-rw-r-- 1 afedorov afedorov 314769 map 28 04:59 FinalAfrica_12
-rw-rw-r-- 1 afedorov afedorov 175959 map 28 04:59 FinalAfrica_13
-rw-rw-r-- 1 afedorov afedorov 194772 map 28 04:59 FinalAfrica_14
-rw-rw-r-- 1 afedorov afedorov 210933 map 28 04:59 FinalAfrica_15
-rw-rw-r-- 1 afedorov afedorov 281346 map 28 04:59 FinalAfrica_16
-rw-rw-r-- 1 afedorov afedorov 254607 map 28 04:59 FinalAfrica_17
-rw-rw-r-- 1 afedorov afedorov 168675 map 28 04:59 FinalAfrica_18
-rw-rw-r-- 1 afedorov afedorov 162444 map 28 04:59 FinalAfrica_19
-rw-rw-r-- 1 afedorov afedorov 537349 map 28 04:59 FinalAfrica_2
-rw-rw-r-- 1 afedorov afedorov 172259 map 28 04:59 FinalAfrica_20
-rw-rw-r-- 1 afedorov afedorov 120987 map 28 04:59 FinalAfrica_21
-rw-rw-r-- 1 afedorov afedorov 120806 map 28 04:59 FinalAfrica_22
-rw-rw-r-- 1 afedorov afedorov 486291 map 28 04:59 FinalAfrica_3
-rw-rw-r-- 1 afedorov afedorov 444500 map 28 04:59 FinalAfrica_4
-rw-rw-r-- 1 afedorov afedorov 465854 map 28 04:59 FinalAfrica_5
-rw-rw-r-- 1 afedorov afedorov 331425 map 28 04:59 FinalAfrica_6
-rw-rw-r-- 1 afedorov afedorov 356565 map 28 04:59 FinalAfrica_7
-rw-rw-r-- 1 afedorov afedorov 383661 map 28 04:59 FinalAfrica_8
-rw-rw-r-- 1 afedorov afedorov 295573 map 28 04:59 FinalAfrica_9
-rw-rw-r-- 1 afedorov afedorov 36855 map 28 04:57 FinalAmerica_1
-rw-rw-r-- 1 afedorov afedorov 25332 map 28 04:57 FinalAmerica_10
-rw-rw-r-- 1 afedorov afedorov 27948 map 28 04:57 FinalAmerica_11
-rw-rw-r-- 1 afedorov afedorov 33204 map 28 04:57 FinalAmerica_12
-rw-rw-r-- 1 afedorov afedorov 8401 map 28 04:57 FinalAmerica_13
-rw-rw-r-- 1 afedorov afedorov 22686 map 28 04:57 FinalAmerica_14
```

-rw-rw-r--	1	afedorov	afedorov	16685	map	28	04:57	FinalAmerica_15
-rw-rw-r--	1	afedorov	afedorov	17109	map	28	04:57	FinalAmerica_16
-rw-rw-r--	1	afedorov	afedorov	10189	map	28	04:57	FinalAmerica_17
-rw-rw-r--	1	afedorov	afedorov	10505	map	28	04:57	FinalAmerica_18
-rw-rw-r--	1	afedorov	afedorov	7742	map	28	04:57	FinalAmerica_19
-rw-rw-r--	1	afedorov	afedorov	40863	map	28	04:57	FinalAmerica_2
-rw-rw-r--	1	afedorov	afedorov	9631	map	28	04:57	FinalAmerica_20
-rw-rw-r--	1	afedorov	afedorov	7370	map	28	04:57	FinalAmerica_21
-rw-rw-r--	1	afedorov	afedorov	9881	map	28	04:57	FinalAmerica_22
-rw-rw-r--	1	afedorov	afedorov	29183	map	28	04:57	FinalAmerica_3
-rw-rw-r--	1	afedorov	afedorov	31140	map	28	04:57	FinalAmerica_4
-rw-rw-r--	1	afedorov	afedorov	33882	map	28	04:57	FinalAmerica_5
-rw-rw-r--	1	afedorov	afedorov	25600	map	28	04:57	FinalAmerica_6
-rw-rw-r--	1	afedorov	afedorov	29343	map	28	04:57	FinalAmerica_7
-rw-rw-r--	1	afedorov	afedorov	22123	map	28	04:57	FinalAmerica_8
-rw-rw-r--	1	afedorov	afedorov	15800	map	28	04:57	FinalAmerica_9
-rw-rw-r--	1	afedorov	afedorov	6425	map	28	04:58	FinalEastAsia_1
-rw-rw-r--	1	afedorov	afedorov	6466	map	28	04:58	FinalEastAsia_10
-rw-rw-r--	1	afedorov	afedorov	13188	map	28	04:58	FinalEastAsia_11
-rw-rw-r--	1	afedorov	afedorov	6214	map	28	04:58	FinalEastAsia_12
-rw-rw-r--	1	afedorov	afedorov	2395	map	28	04:58	FinalEastAsia_13
-rw-rw-r--	1	afedorov	afedorov	5673	map	28	04:58	FinalEastAsia_14
-rw-rw-r--	1	afedorov	afedorov	25633	map	28	04:58	FinalEastAsia_15
-rw-rw-r--	1	afedorov	afedorov	15854	map	28	04:58	FinalEastAsia_16
-rw-rw-r--	1	afedorov	afedorov	1960	map	28	04:58	FinalEastAsia_17
-rw-rw-r--	1	afedorov	afedorov	2094	map	28	04:58	FinalEastAsia_18
-rw-rw-r--	1	afedorov	afedorov	1286	map	28	04:58	FinalEastAsia_19
-rw-rw-r--	1	afedorov	afedorov	8058	map	28	04:58	FinalEastAsia_2
-rw-rw-r--	1	afedorov	afedorov	432	map	28	04:58	FinalEastAsia_20
-rw-rw-r--	1	afedorov	afedorov	377	map	28	04:58	FinalEastAsia_21
-rw-rw-r--	1	afedorov	afedorov	848	map	28	04:58	FinalEastAsia_22
-rw-rw-r--	1	afedorov	afedorov	20405	map	28	04:58	FinalEastAsia_3
-rw-rw-r--	1	afedorov	afedorov	11617	map	28	04:58	FinalEastAsia_4
-rw-rw-r--	1	afedorov	afedorov	4678	map	28	04:58	FinalEastAsia_5
-rw-rw-r--	1	afedorov	afedorov	3745	map	28	04:58	FinalEastAsia_6
-rw-rw-r--	1	afedorov	afedorov	2299	map	28	04:58	FinalEastAsia_7
-rw-rw-r--	1	afedorov	afedorov	4046	map	28	04:58	FinalEastAsia_8
-rw-rw-r--	1	afedorov	afedorov	2029	map	28	04:58	FinalEastAsia_9
-rw-rw-r--	1	afedorov	afedorov	60356	map	28	04:58	FinalEurope_1
-rw-rw-r--	1	afedorov	afedorov	109950	map	28	04:58	FinalEurope_10
-rw-rw-r--	1	afedorov	afedorov	68216	map	28	04:58	FinalEurope_11

-rw-rw-r--	1	afedorov	afedorov	44735	map	28	04:58	FinalEurope_12
-rw-rw-r--	1	afedorov	afedorov	58988	map	28	04:58	FinalEurope_13
-rw-rw-r--	1	afedorov	afedorov	43285	map	28	04:58	FinalEurope_14
-rw-rw-r--	1	afedorov	afedorov	47169	map	28	04:58	FinalEurope_15
-rw-rw-r--	1	afedorov	afedorov	22366	map	28	04:58	FinalEurope_16
-rw-rw-r--	1	afedorov	afedorov	46130	map	28	04:58	FinalEurope_17
-rw-rw-r--	1	afedorov	afedorov	54384	map	28	04:58	FinalEurope_18
-rw-rw-r--	1	afedorov	afedorov	9280	map	28	04:58	FinalEurope_19
-rw-rw-r--	1	afedorov	afedorov	68573	map	28	04:58	FinalEurope_2
-rw-rw-r--	1	afedorov	afedorov	32177	map	28	04:58	FinalEurope_20
-rw-rw-r--	1	afedorov	afedorov	9570	map	28	04:58	FinalEurope_21
-rw-rw-r--	1	afedorov	afedorov	16612	map	28	04:58	FinalEurope_22
-rw-rw-r--	1	afedorov	afedorov	76950	map	28	04:58	FinalEurope_3
-rw-rw-r--	1	afedorov	afedorov	58887	map	28	04:58	FinalEurope_4
-rw-rw-r--	1	afedorov	afedorov	51787	map	28	04:58	FinalEurope_5
-rw-rw-r--	1	afedorov	afedorov	64694	map	28	04:58	FinalEurope_6
-rw-rw-r--	1	afedorov	afedorov	37134	map	28	04:58	FinalEurope_7
-rw-rw-r--	1	afedorov	afedorov	56939	map	28	04:58	FinalEurope_8
-rw-rw-r--	1	afedorov	afedorov	48349	map	28	04:58	FinalEurope_9
-rw-rw-r--	1	afedorov	afedorov	35976	map	28	04:57	FinalOceania_1
-rw-rw-r--	1	afedorov	afedorov	552	map	28	04:57	FinalOceania_10
-rw-rw-r--	1	afedorov	afedorov	262	map	28	04:57	FinalOceania_11
-rw-rw-r--	1	afedorov	afedorov	15325	map	28	04:57	FinalOceania_12
-rw-rw-r--	1	afedorov	afedorov	890	map	28	04:57	FinalOceania_13
-rw-rw-r--	1	afedorov	afedorov	2977	map	28	04:57	FinalOceania_14
-rw-rw-r--	1	afedorov	afedorov	7703	map	28	04:57	FinalOceania_15
-rw-rw-r--	1	afedorov	afedorov	16842	map	28	04:57	FinalOceania_16
-rw-rw-r--	1	afedorov	afedorov	6375	map	28	04:57	FinalOceania_17
-rw-rw-r--	1	afedorov	afedorov	7439	map	28	04:57	FinalOceania_18
-rw-rw-r--	1	afedorov	afedorov	13609	map	28	04:57	FinalOceania_19
-rw-rw-r--	1	afedorov	afedorov	1726	map	28	04:57	FinalOceania_2
-rw-rw-r--	1	afedorov	afedorov	1782	map	28	04:57	FinalOceania_20
-rw-rw-r--	1	afedorov	afedorov	1391	map	28	04:57	FinalOceania_21
-rw-rw-r--	1	afedorov	afedorov	384	map	28	04:57	FinalOceania_22
-rw-rw-r--	1	afedorov	afedorov	44722	map	28	04:57	FinalOceania_3
-rw-rw-r--	1	afedorov	afedorov	10243	map	28	04:57	FinalOceania_4
-rw-rw-r--	1	afedorov	afedorov	5241	map	28	04:57	FinalOceania_5
-rw-rw-r--	1	afedorov	afedorov	17898	map	28	04:57	FinalOceania_6
-rw-rw-r--	1	afedorov	afedorov	426	map	28	04:57	FinalOceania_7
-rw-rw-r--	1	afedorov	afedorov	4457	map	28	04:57	FinalOceania_8
-rw-rw-r--	1	afedorov	afedorov	522	map	28	04:57	FinalOceania_9