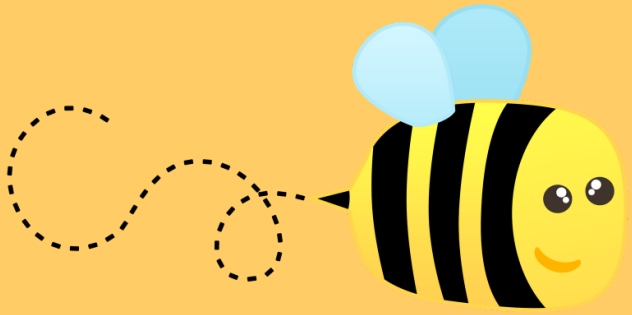
2018 SEVINOMICS
Spring Meeting



Genome adaptations to high altitude in the Eastern Honey bee

9 April 2018

Estación Biológica Doñana CSIC

Santiago Montero-Mendieta

What is adaptation?

- A feature of an organism that has been favored by ***natural selection*** because of that feature's positive effect on relative fitness

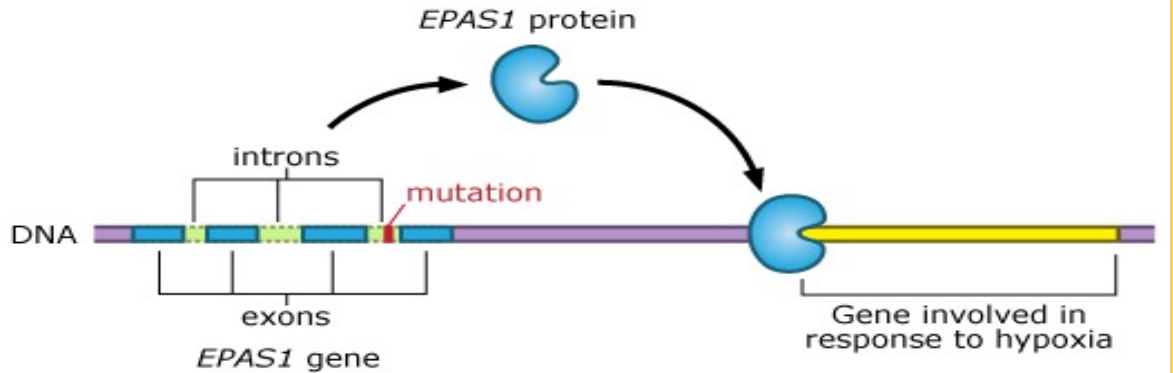
What is *local* adaptation?

- Evolution, through ***divergent*** natural selection, of traits that have high fitness in the environmental conditions specific to a population

These adaptations are local because they are NOT found throughout the whole species, only in certain populations

E.g. Local adaptation to **high altitude habitats**

Local adaptation to altitude

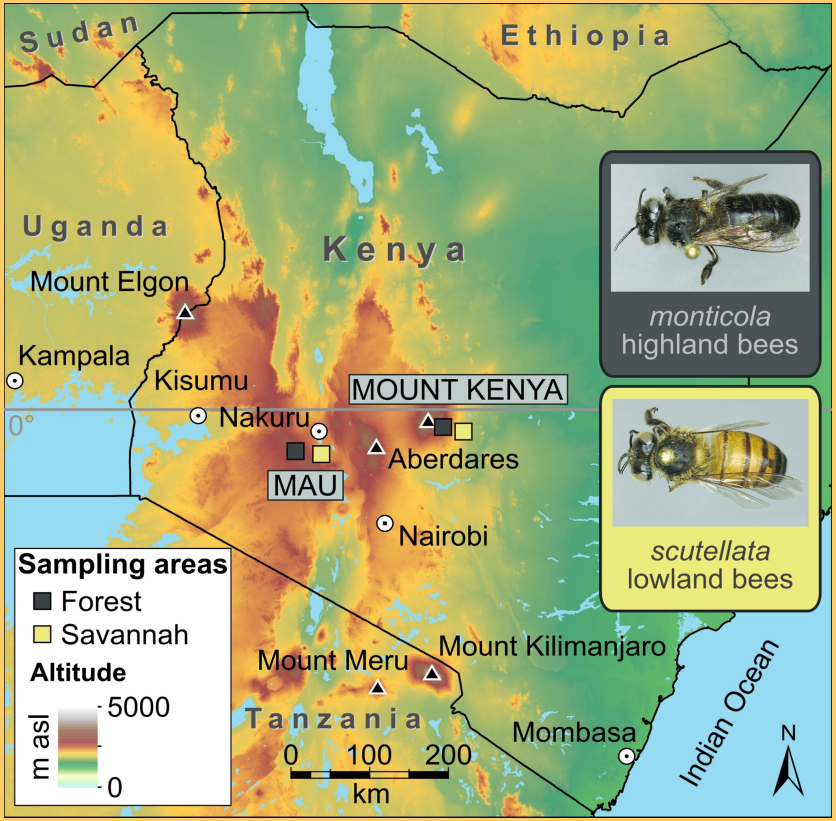


Human populations in Tibet have adapted to survive at extremely high altitudes (>2500m)

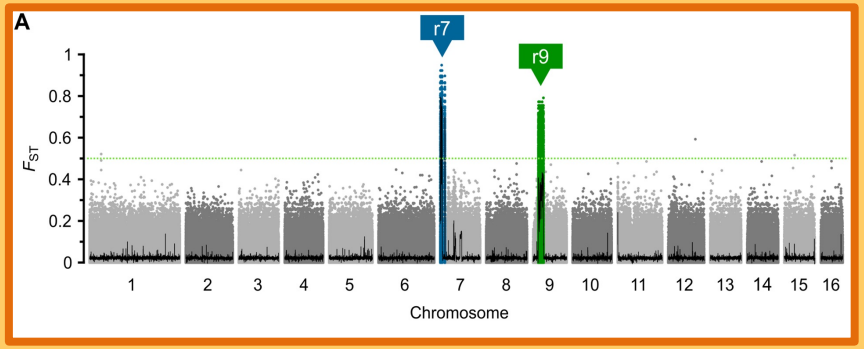
Genes involved in ***decreased hemoglobin*** levels: EPAS1, EGLN1, PPARA

Yi *et al.* (2010). Science

Local adaptation to altitude



Kenyan honeybees inhabiting mountain forests differ in ***behavior and morphology*** from those found in the surrounding lowland savannahs



Octopamine receptor genes: learning and foraging behavior in honeybees

Wallberg *et al.* (2017) PLOS Genetics

Social behavior in bees can change with altitude

Social Sweat Bee (*Halictus rubicundus*) has solitary behavior in high-altitude habitats

Bees are crucial as pollinators

Distribution of *Apis mellifera*

Distribution of *Apis cerana*

Sampling

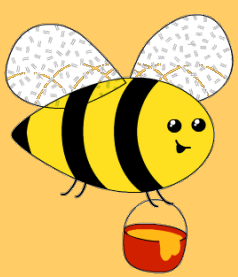

Tianshui (1100 m)
Deqin (2714 m)
Lijiang (2485 m)
Kunming (1800 m)
Hekou (67 m)
Xishuangbanna (570 m)
Thai A (1377 m)
Thai B (299 m)
China
NINGXIA
SHANXI
SHAANXI
SHANDONG
HENAN
JIANGSU
HUBEI
ANHUI
SICHUAN
ZHEJIANG
GUIZHOU
HUNAN
JIANGXI
FUJIAN
YUNNAN
PROVINCIA DE CANTÓN
Taiwán
HAINAN
Myanmar (Birmania)
Tailandia
Vietnam
Luzon
Mar de la China Meridional
ASSAM
NAGALAND
MANIPUR
TRIPURA
MIZORÁN

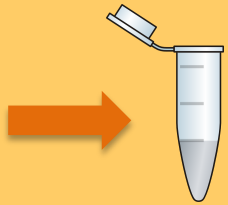
Aims of the study

- Understanding the genetic structure of these populations

- Identifying regions of the genome associated with adaptation to high altitude habitats

Experimental procedure





DNA extraction
& library prep

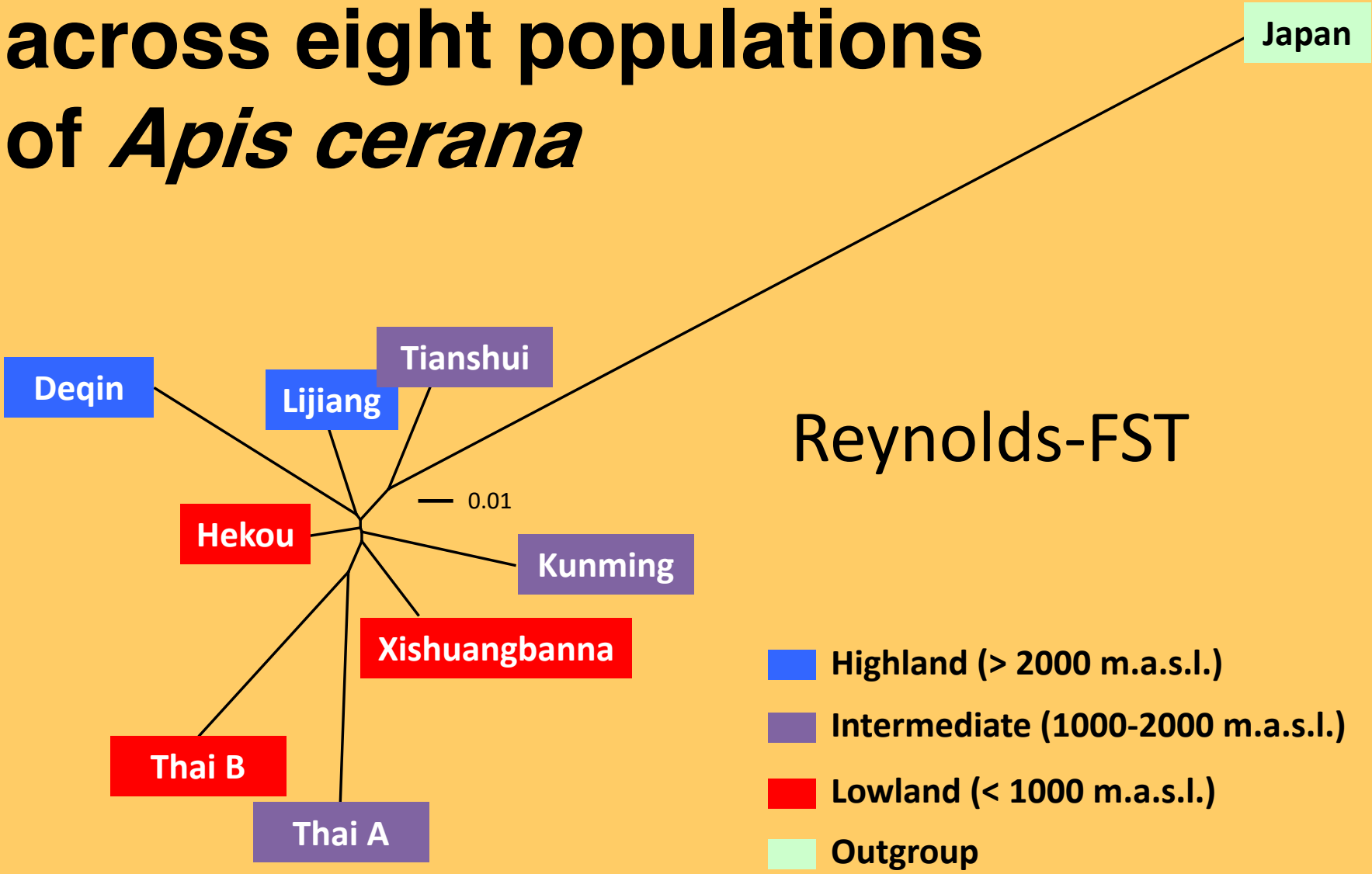
Whole-genome
sequencing

Bioinformatics
analysis

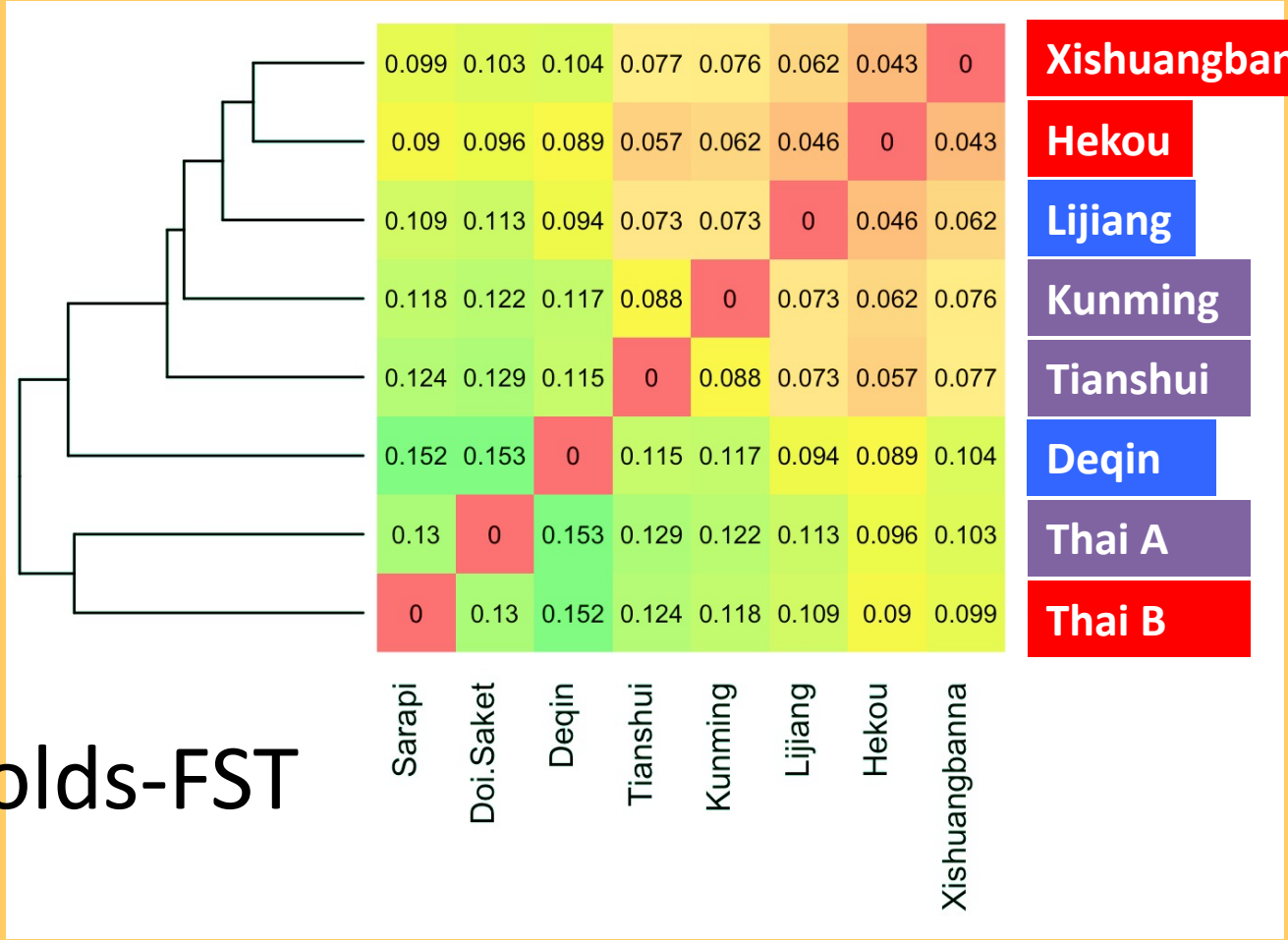
- Reads were mapped against the *Apis cerana* reference genome
- ***5.8 million biallelic SNPs*** were detected using FreeBayes
- We did a series of population genomic analyses: ADXMITURE, FST scans, genetic diversity, environmental association, haplotype homozygosity

Results

Genetic distance across eight populations of *Apis cerana*

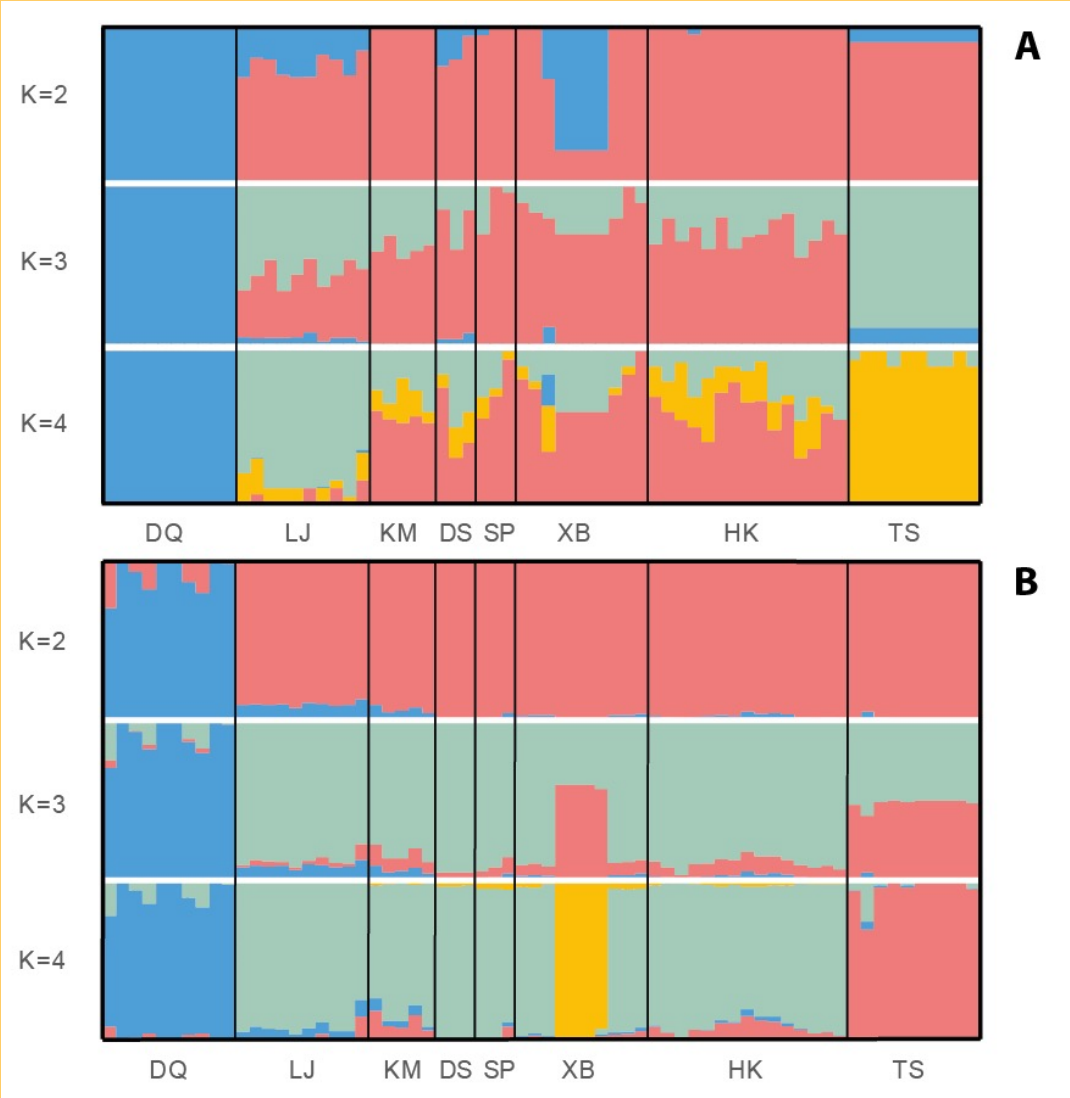


Genetic differentiation



Reynolds-FST

Population structure



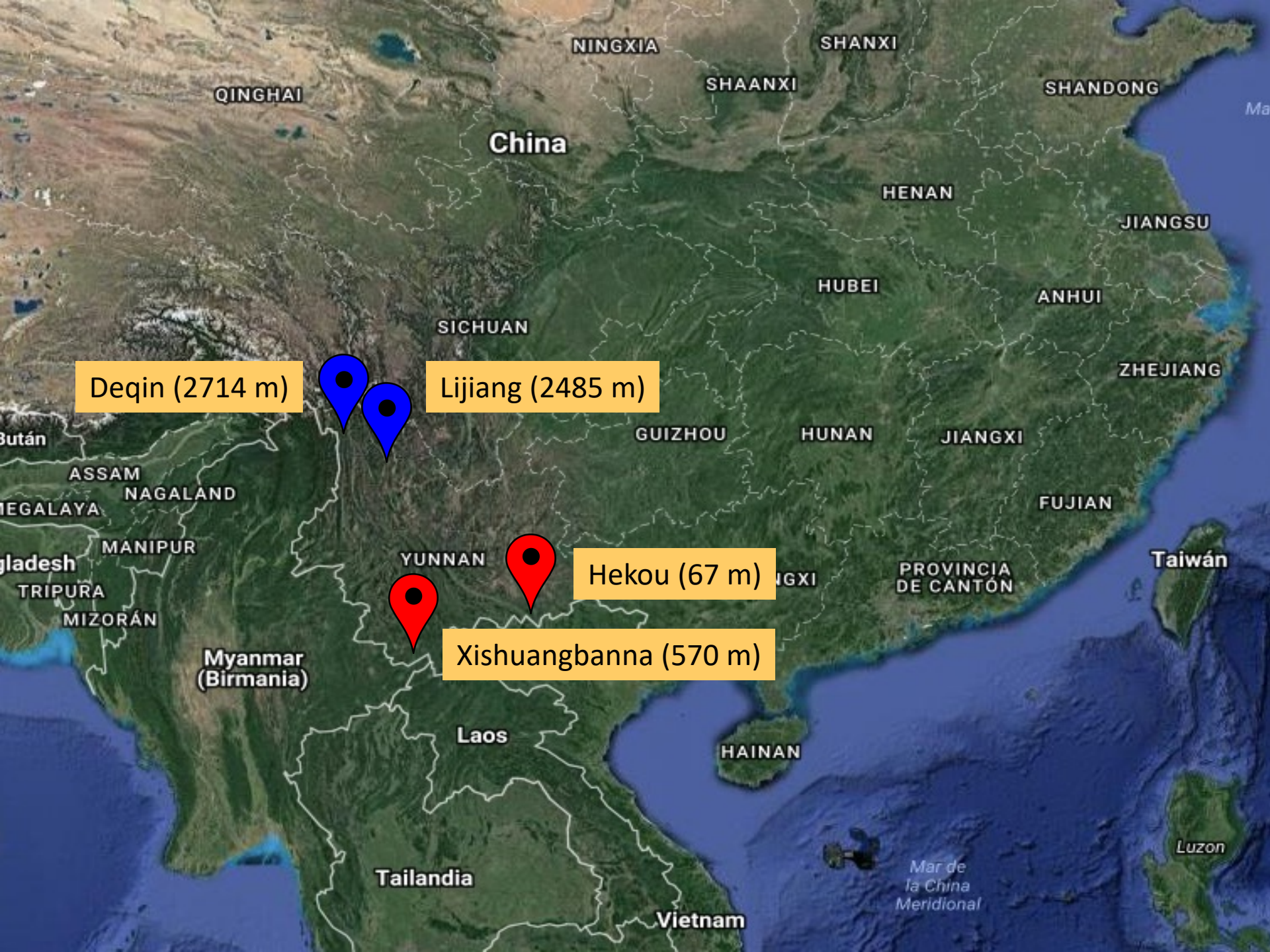
ADMIXTURE

Alexander *et al.* (2009)
Genome Research

sNMF

Frichot *et al.* (2014)
Genetics

HIGHLAND vs LOWLAND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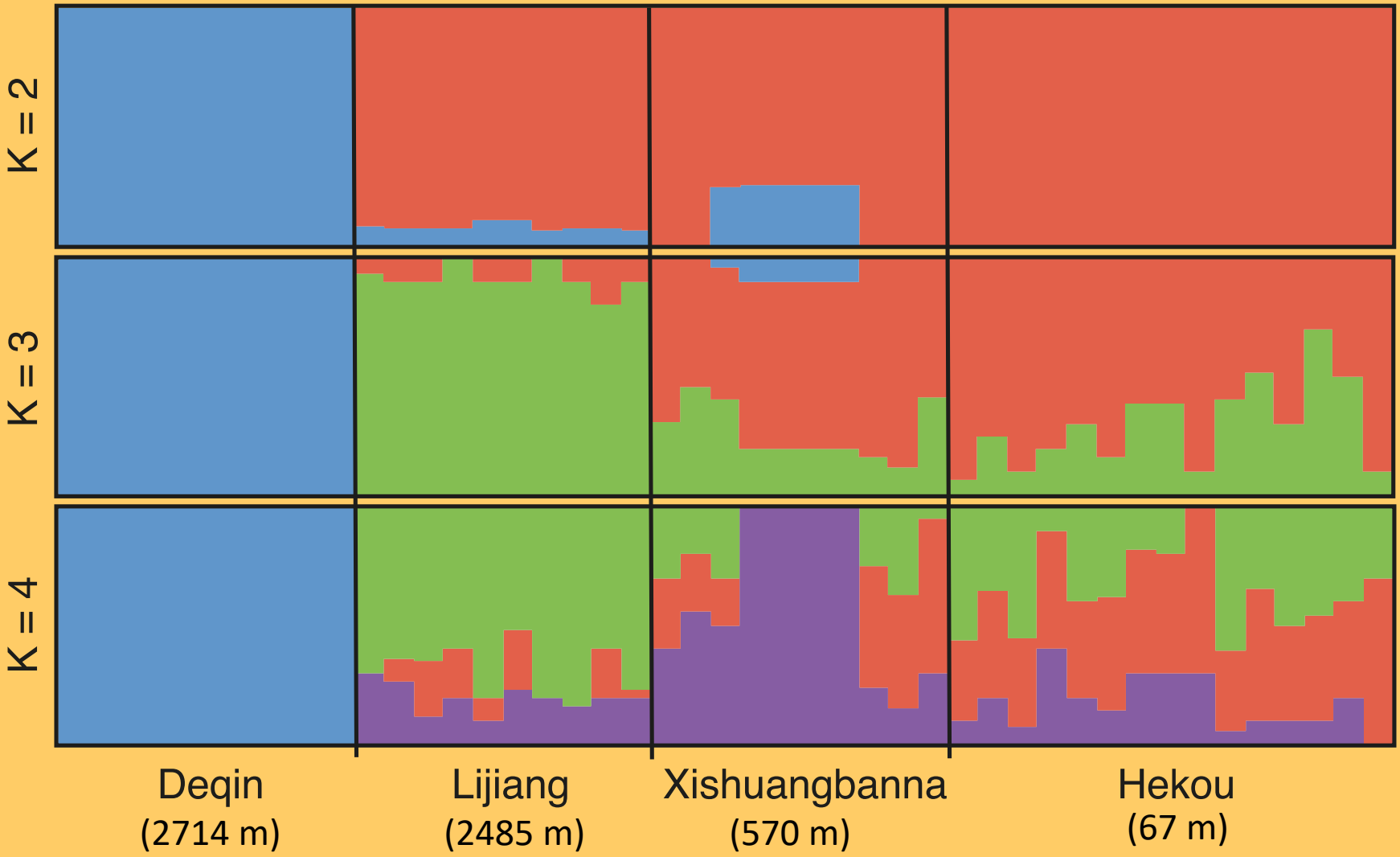
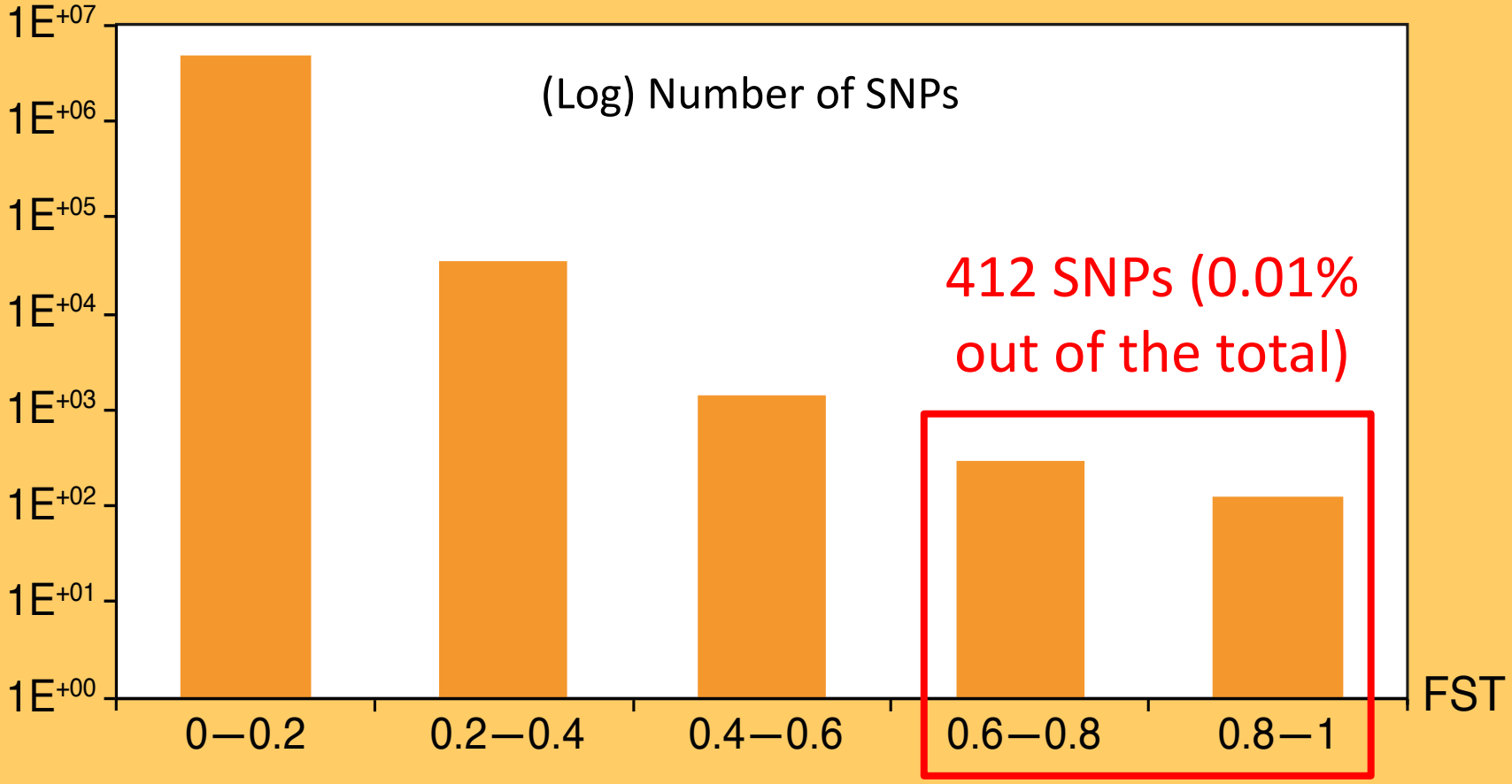
GUIZHOU
HUNAN
JIANGXI
FUJIAN
YUNNAN
PROVINCIA DE CANTÓN
Taiwán
ASSAM
NAGALAND
MANIPUR
TRIPURA
MIZORÁN
Myanmar (Birmania)
Laos
HAINAN
Tailandia
Vietnam
Luzon
Mar de la China Meridional

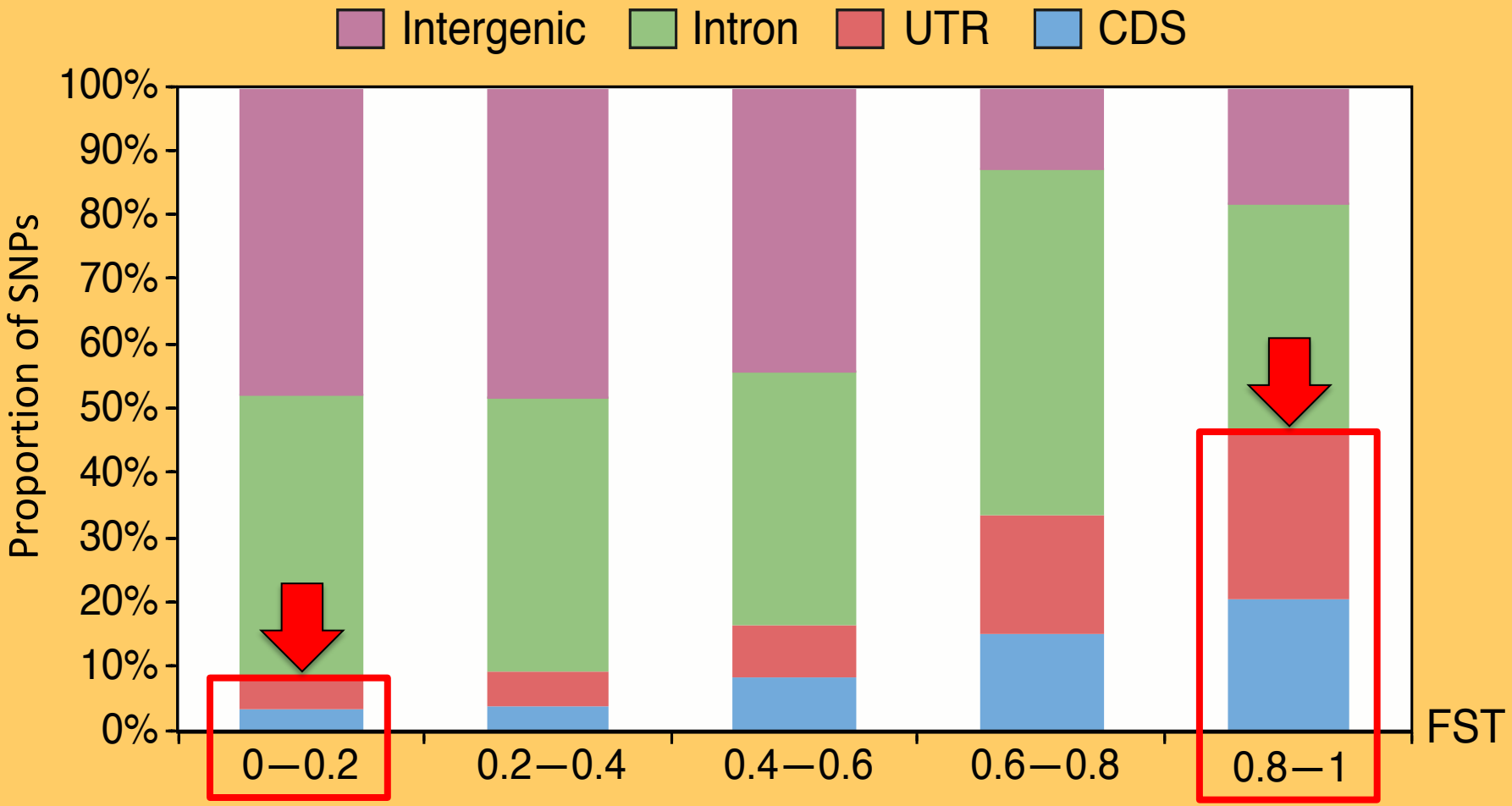
Highland vs Lowland



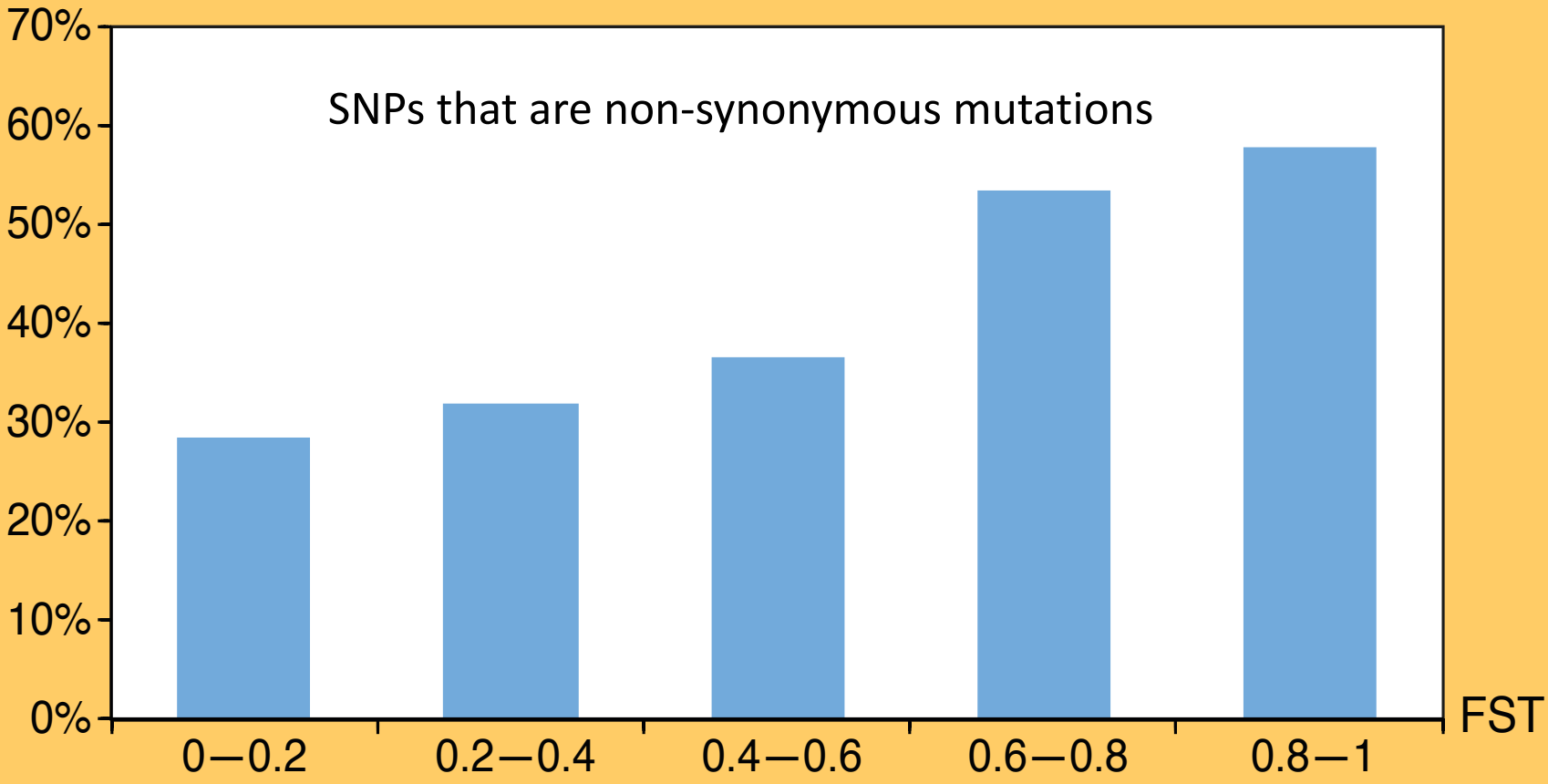
Highly differentiated SNPs are not common between highland and lowland bees



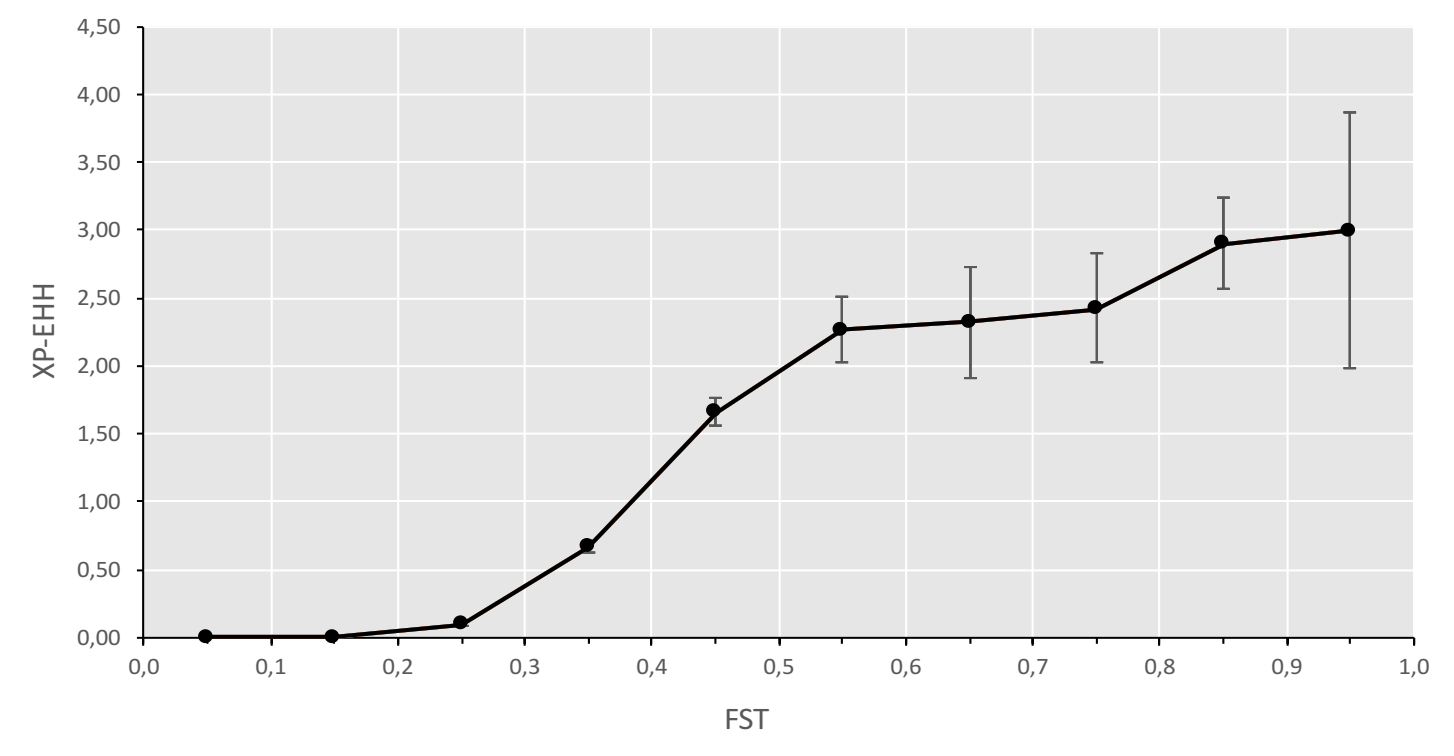
Highly differentiated SNPs are more frequently located in UTRs and CDS



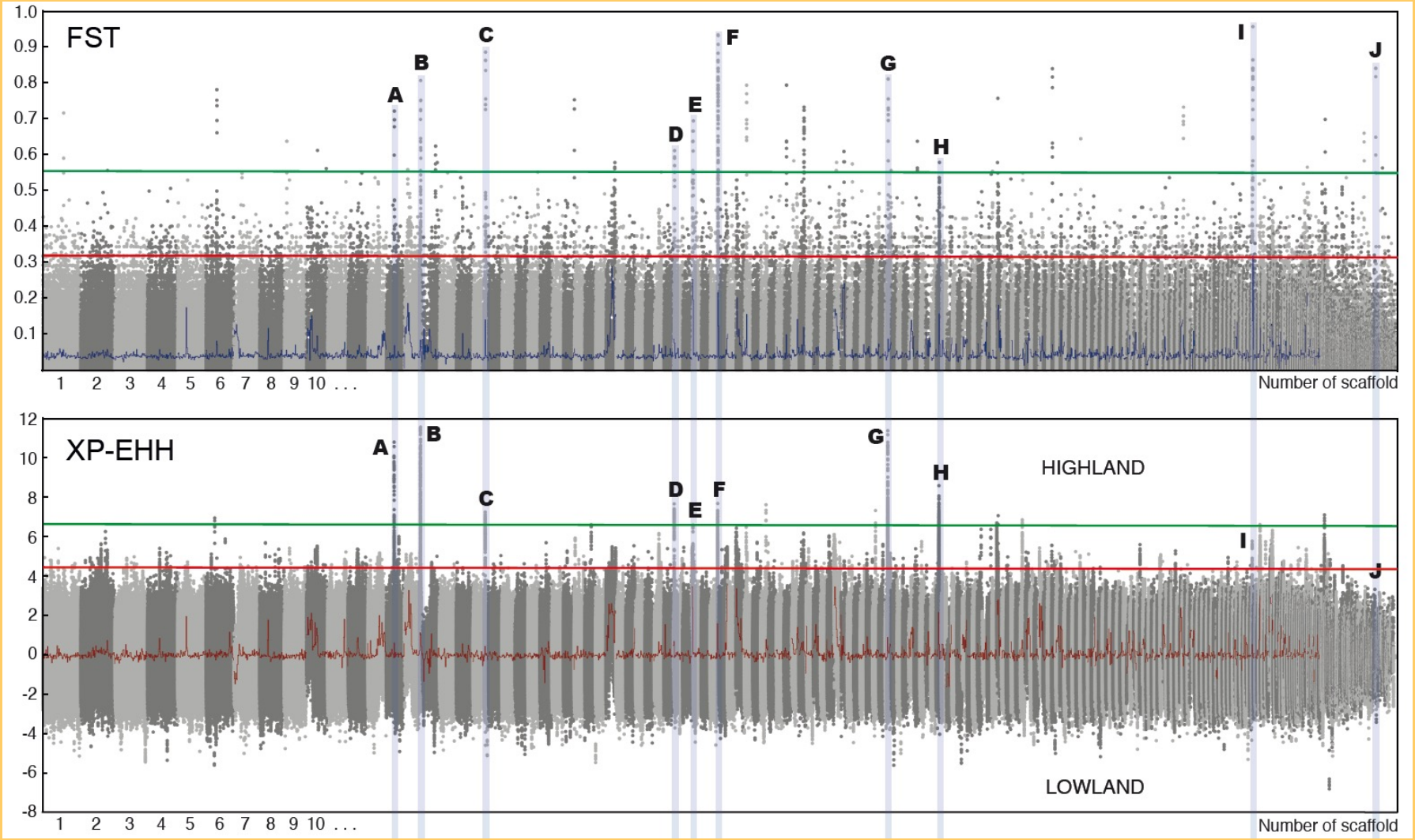
Highly differentiated SNPs found in CDS often cause non-synonymous mutations



XP-EHH scores increase at high F_{ST} regions, implying haplotype homozygosity on highland bees



Selective sweeps in highland bees occur on a restricted set of genes



Genes involved on high altitude adaptation in *Apis cerana*

Sweep	# SNPs	Scaffold	Gene annotation
B	27	0015	esterase FE4-like
F	17	0041	leucokinin receptor
J	22	1417	NMDA receptor
…	…	…	…

- Development
- Reproduction
- Courtship behavior

- Feeding and sucrose responses
- Affect blood pressure
- Enhance memory retention
- Disturb circadian rhythmicity

- Olfactory learning
- Memory formation

SUMMARY

1. Several ***extremely differentiated*** genomic regions between highland and lowland bees

2. These regions are ***biased towards coding sequences*** and contain a higher proportion of non-synonymous mutations

3. These regions show high haplotype homozygosity in the highland bees, indicating ***selective sweeps*** in them

4. Genes associated with these regions have diverse functionality – further investigation is required !

Thank you!