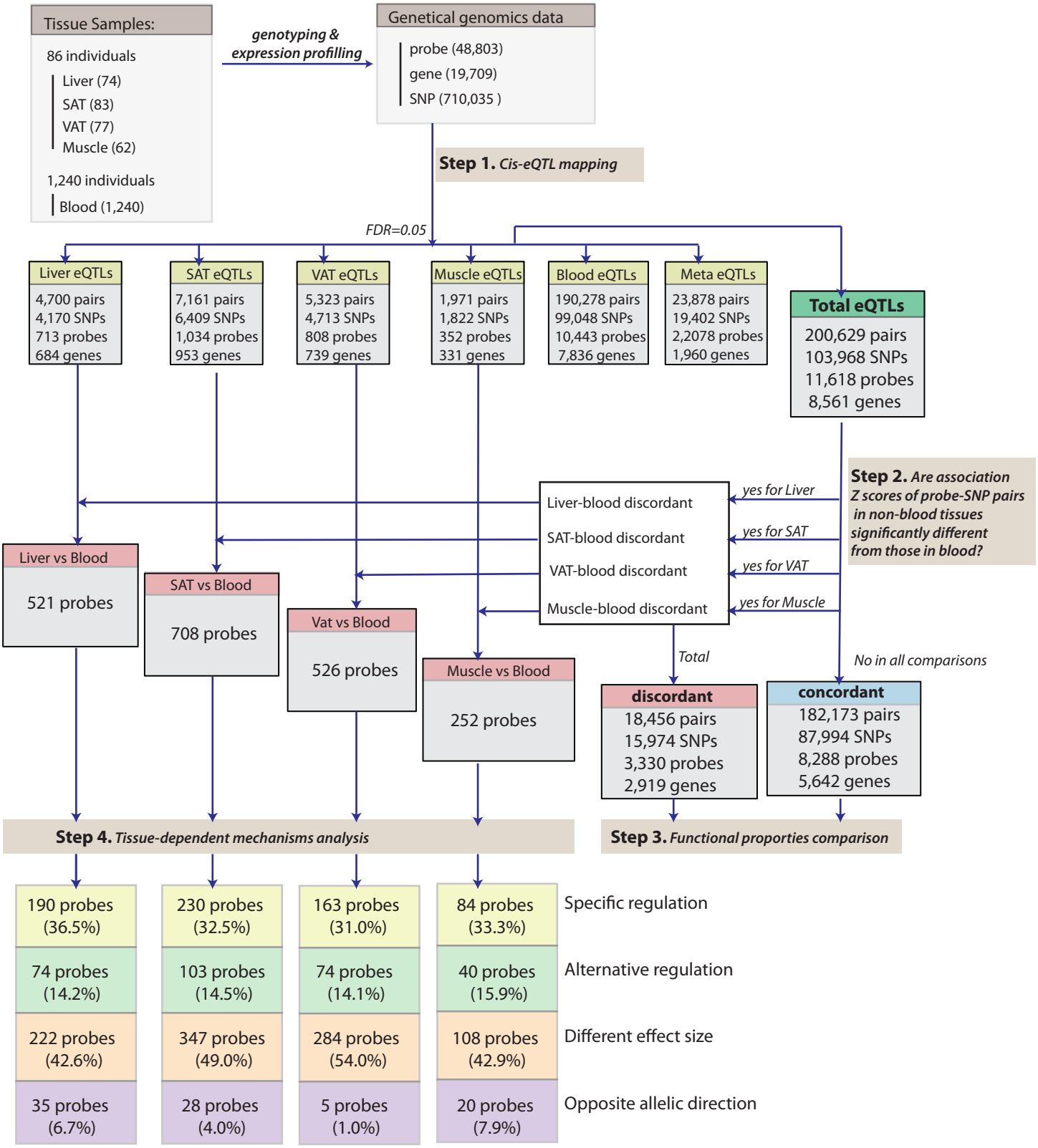
Tissue Samples:
86 individuals
Liver (74)
SAT (83)
VAT (77)
Muscle (62)
1,240 individuals
Blood (1,240)
genotyping & expression profilling
Genetical genomics data
probe (48,803)
gene (19,709)
SNP (710,035)
Step 1. Cis-eQTL mapping
FDR=0.05
Liver eQTLs
4,700 pairs
4,170 SNPs
713 probes
684 genes
SAT eQTLs
7,161 pairs
6,409 SNPs
1,034 probes
953 genes
VAT eQTLs
5,323 pairs
4,713 SNPs
808 probes
739 genes
Muscle eQTLs
1,971 pairs
1,822 SNPs
352 probes
331 genes
Blood eQTLs
190,278 pairs
99,048 SNPs
10,443 probes
7,836 genes
Meta eQTLs
23,878 pairs
19,402 SNPs
2,2078 probes
1,960 genes
Total eQTLs
200,629 pairs
103,968 SNPs
11,618 probes
8,561 genes
Step 2. Are association Z scores of probe-SNP pairs in non-blood tissues significantly different from those in blood?
Liver-blood discordant
SAT-blood discordant
VAT-blood discordant
Muscle-blood discordant
yes for Liver
yes for SAT
yes for VAT
yes for Muscle
Total
No in all comparisons
Liver vs Blood
521 probes
SAT vs Blood
708 probes
Vat vs Blood
526 probes
Muscle vs Blood
252 probes
discordant
18,456 pairs
15,974 SNPs
3,330 probes
2,919 genes
concordant
182,173 pairs
87,994 SNPs
8,288 probes
5,642 genes
Step 4. Tissue-dependent mechanisms analysis
Step 3. Functional proporties comparison
190 probes (36.5%)
230 probes (32.5%)
163 probes (31.0%)
84 probes (33.3%)
Specific regulation
74 probes (14.2%)
103 probes (14.5%)
74 probes (14.1%)
40 probes (15.9%)
Alternative regulation
222 probes (42.6%)
347 probes (49.0%)
284 probes (54.0%)
108 probes (42.9%)
Different effect size
35 probes (6.7%)
28 probes (4.0%)
5 probes (1.0%)
20 probes (7.9%)
Opposite allelic direction