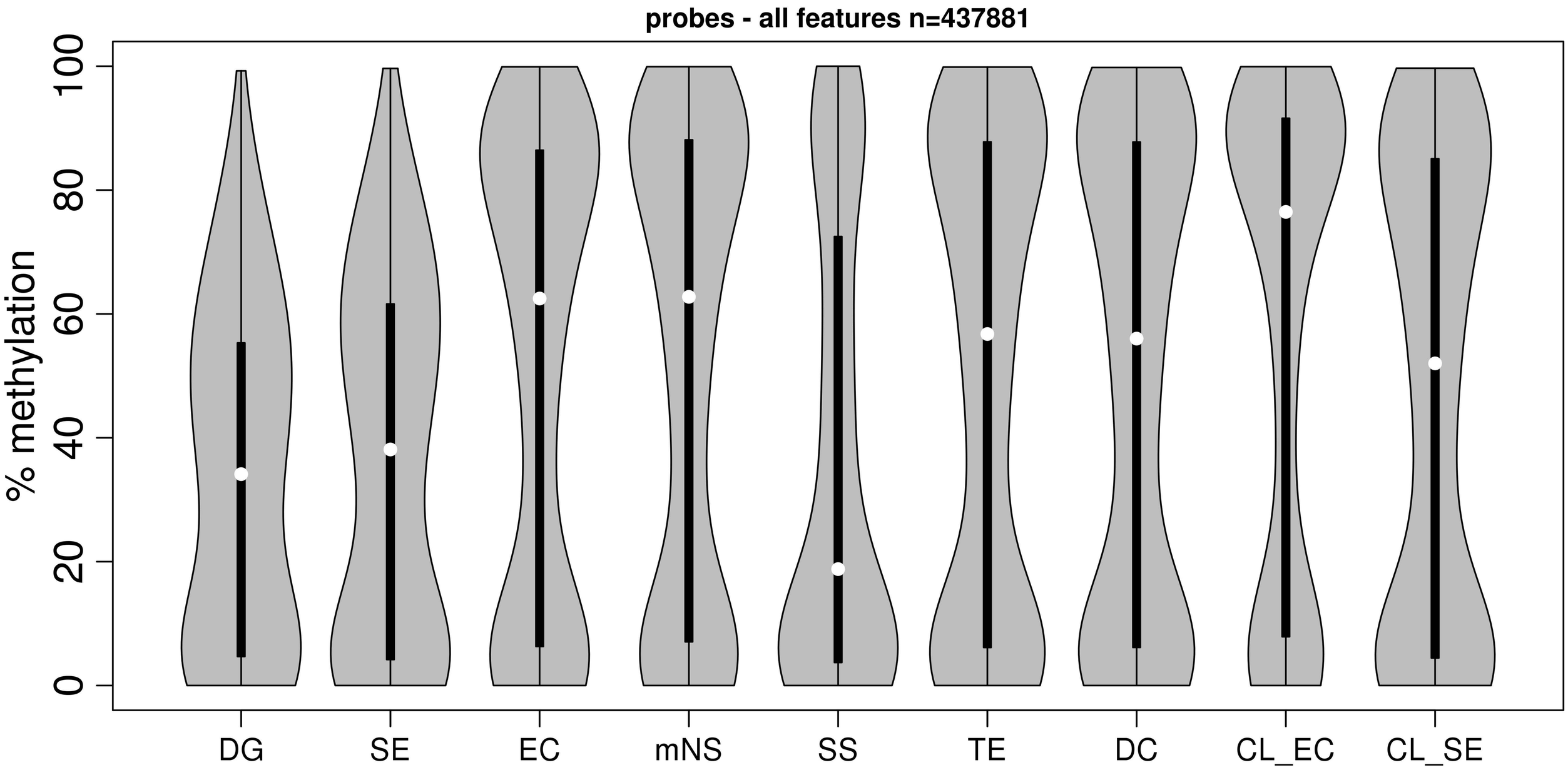
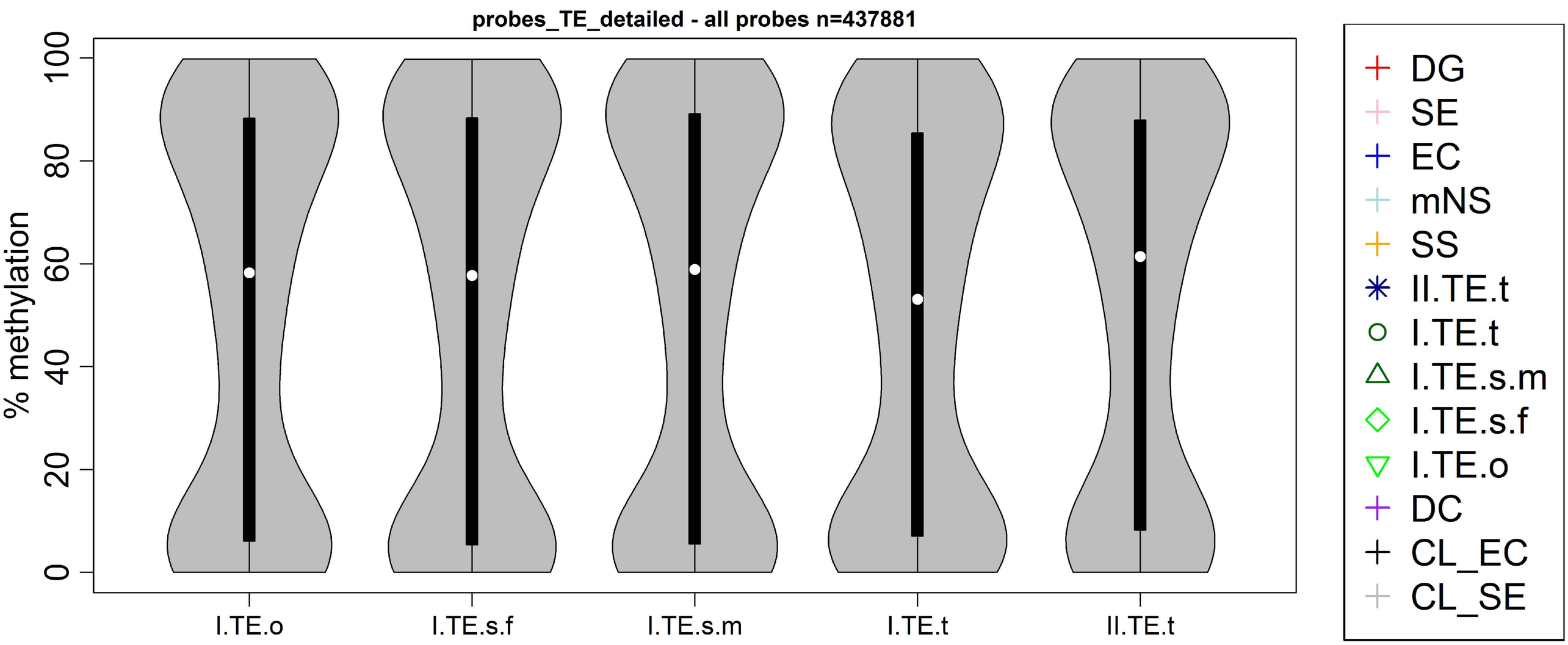
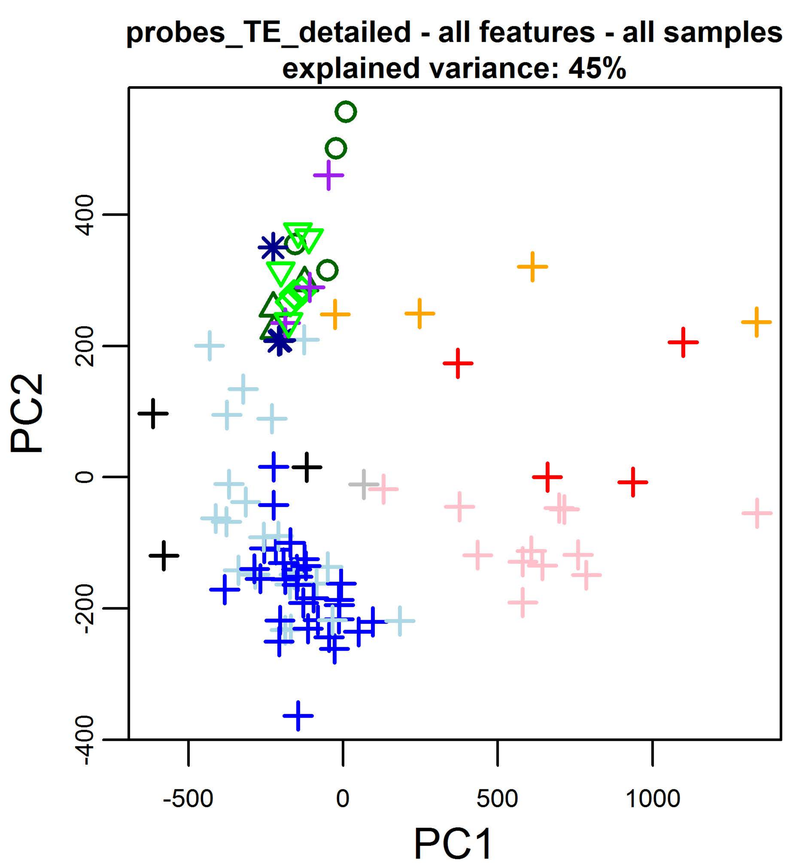
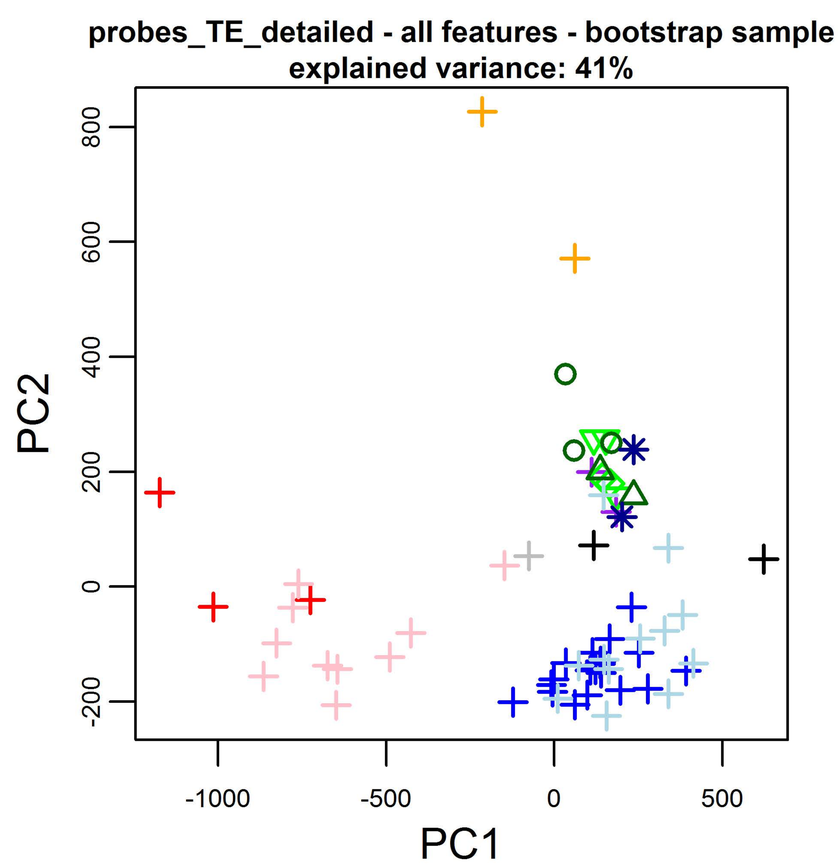
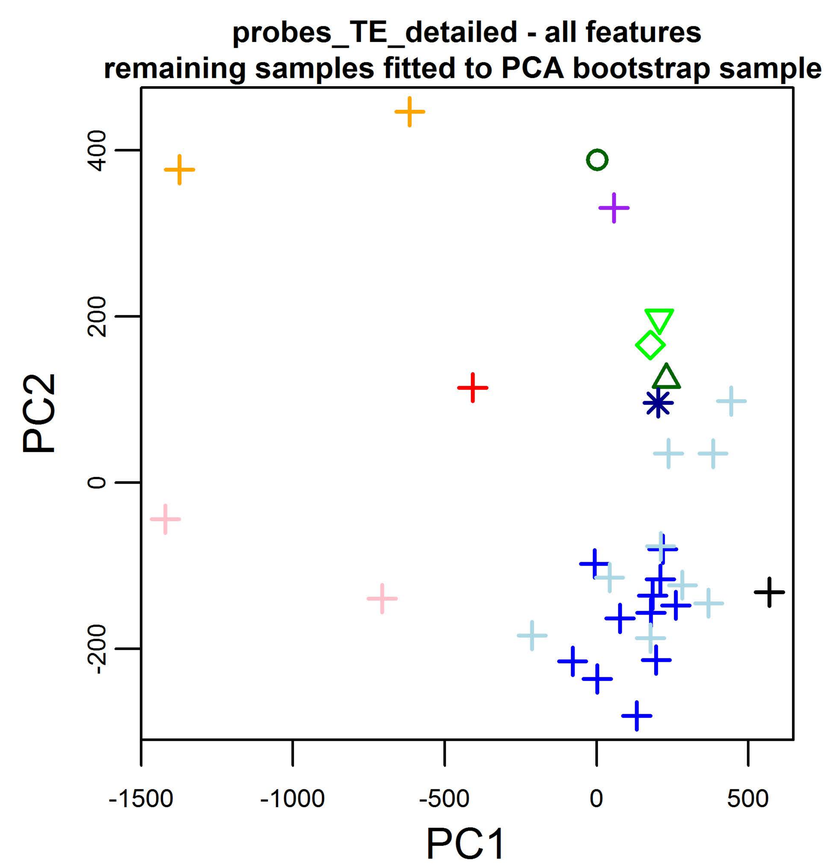
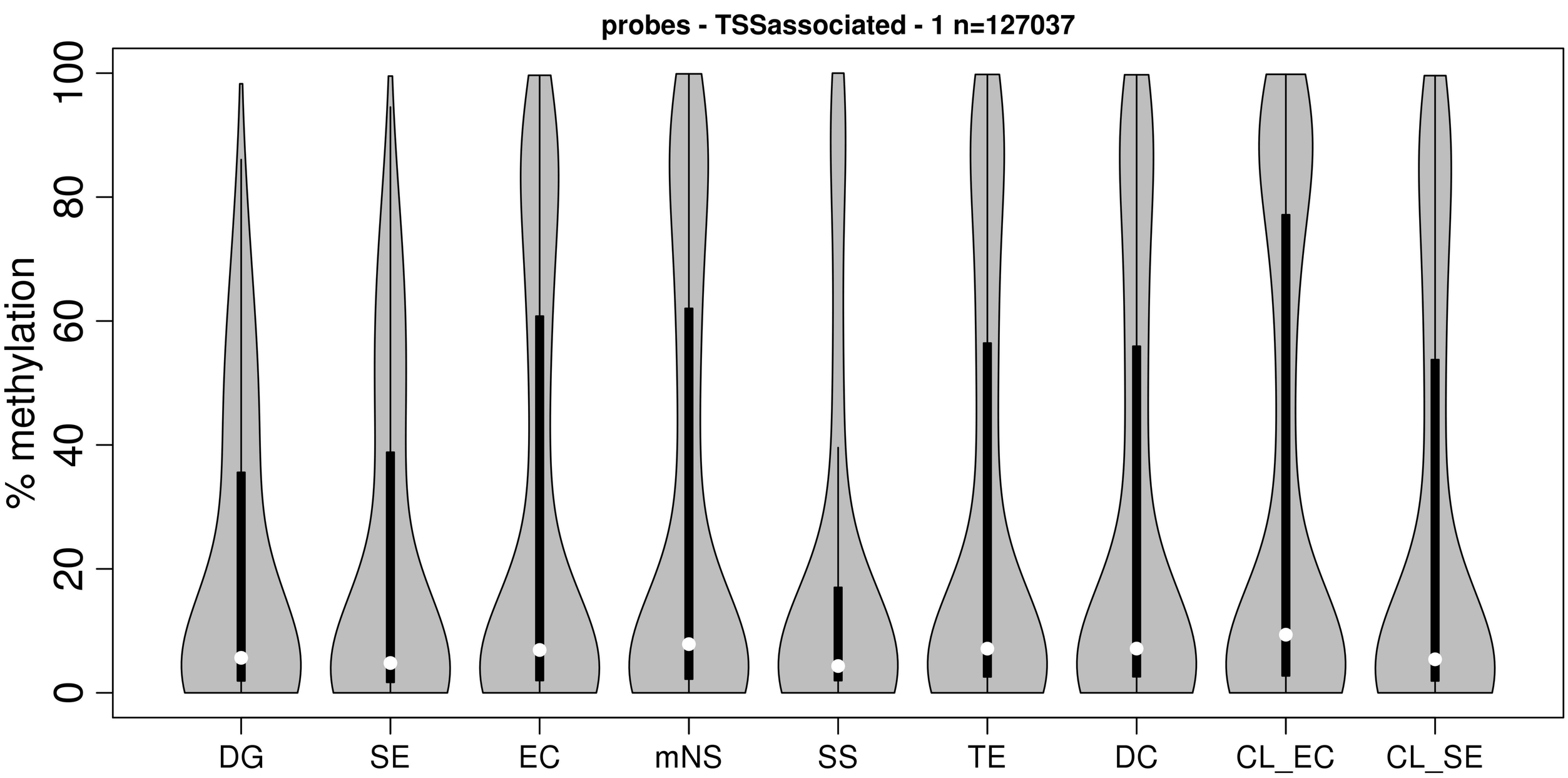

probes - all features n=437881
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

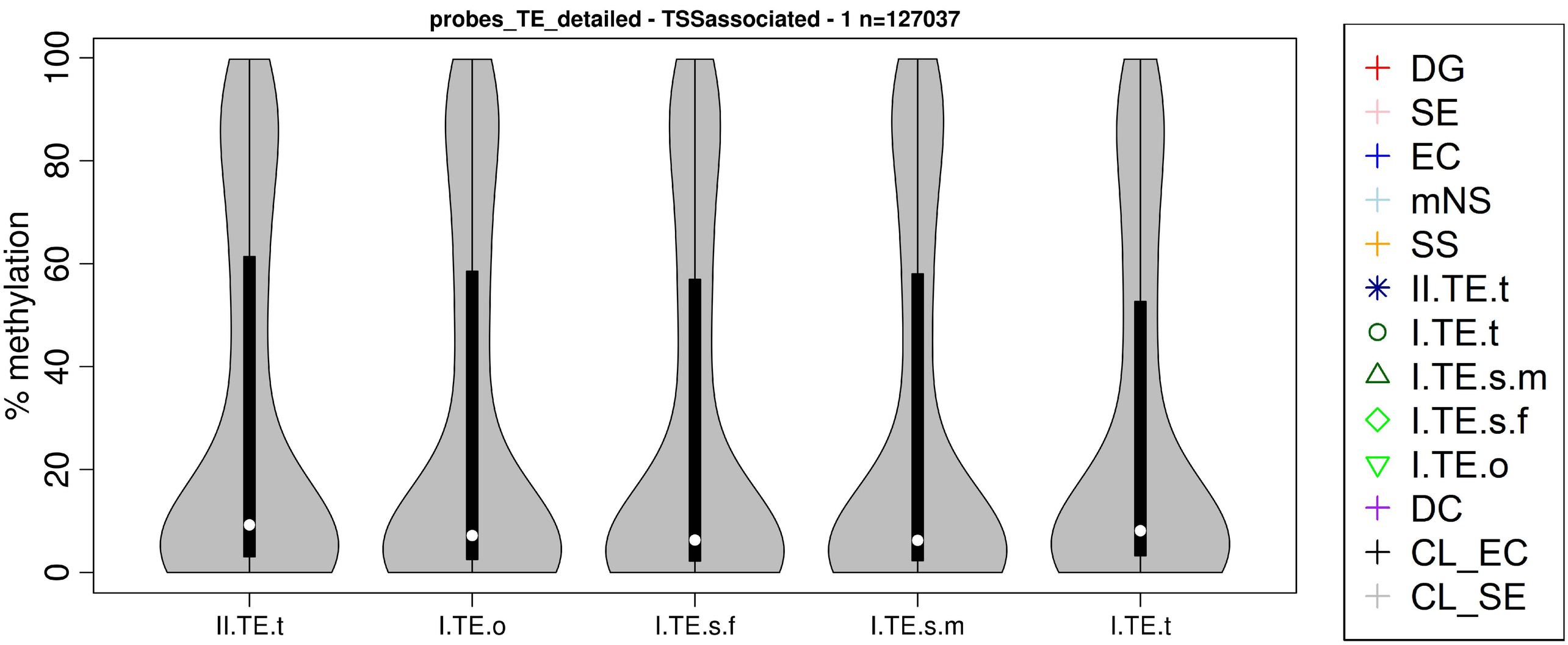

probes_TE_detailed - all probes n=437881
% methylation
0
20
40
60
80
100
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
II.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

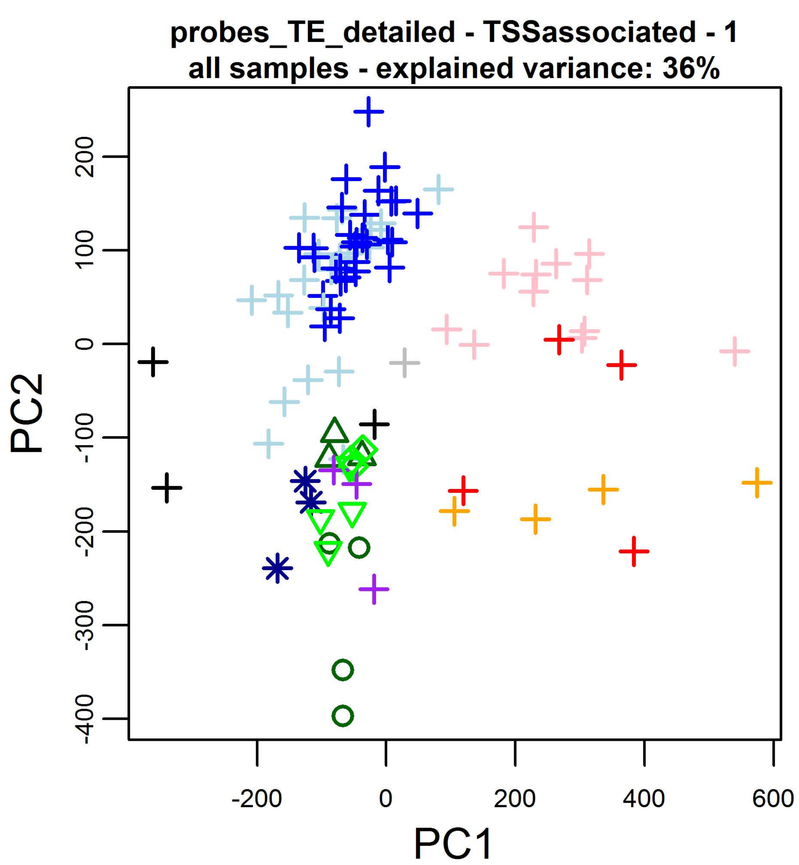

probes_TE_detailed - all features - all samples
explained variance: 45%
PC2
PC1
-400
-200
0
200
400
-500
0
500
1000

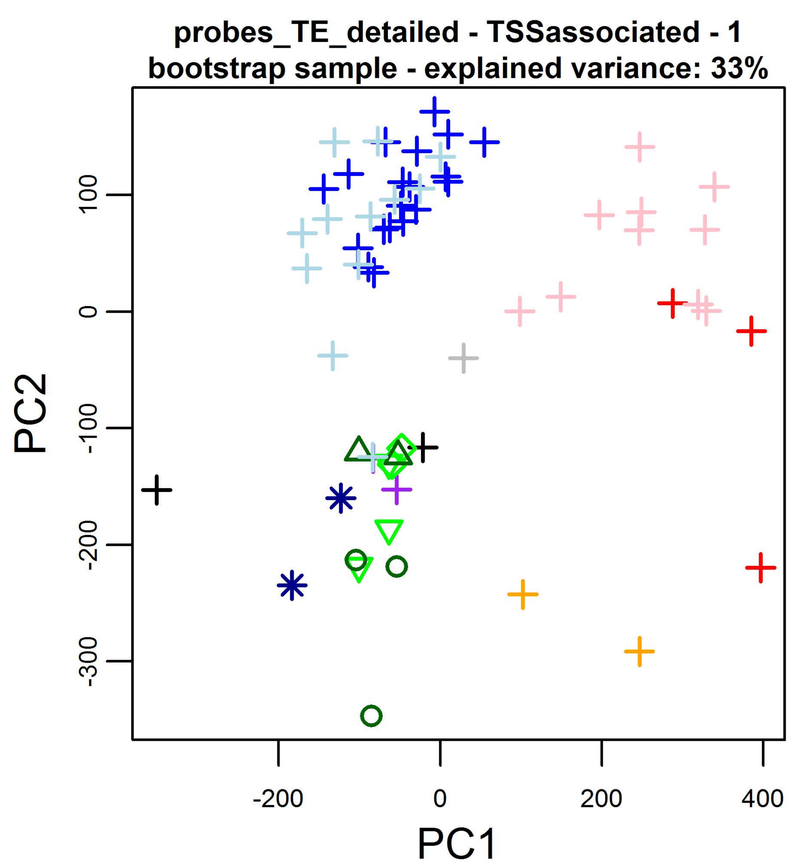

probes_TE_detailed - all features - bootstrap sample
explained variance: 41%
PC2
PC1
-200
0
200
400
600
800
-1000
-500
0
500

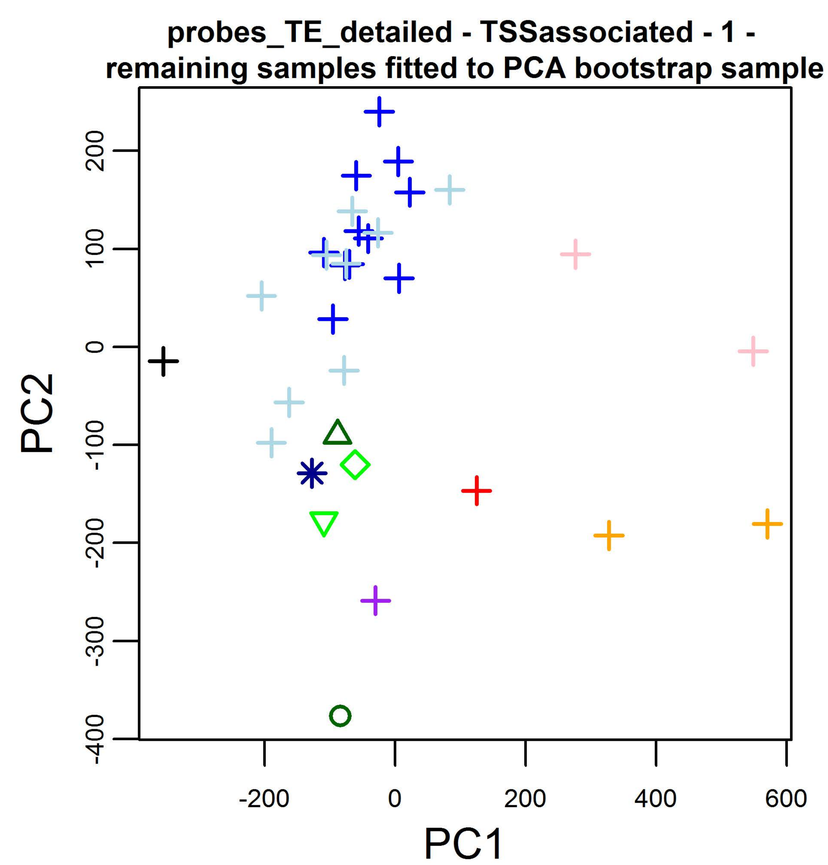

probes_TE_detailed - all features
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-200
0
200
400
-1500
-1000
-500
0
500

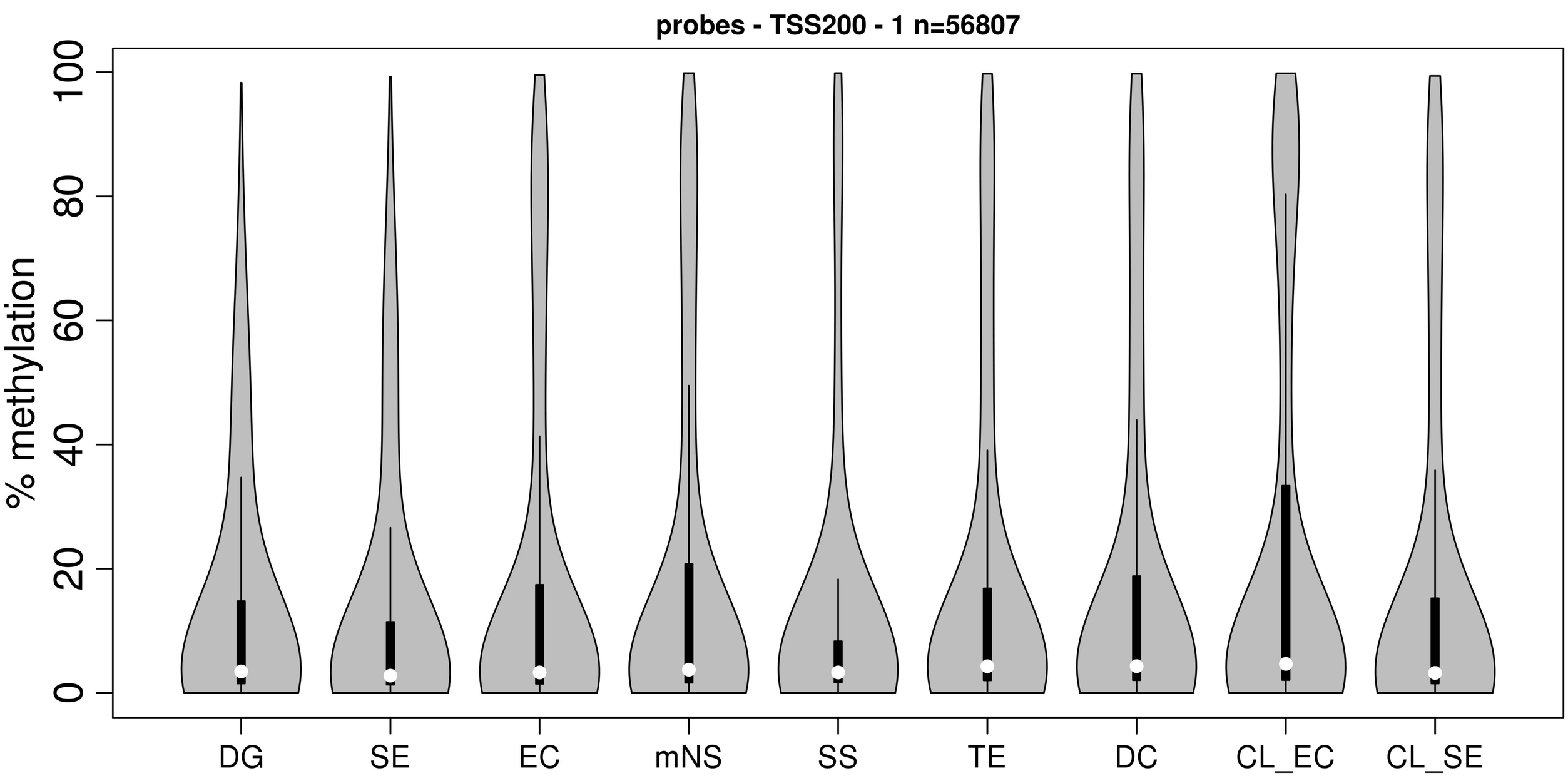

probes - TSSassociated - 1 n=127037
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

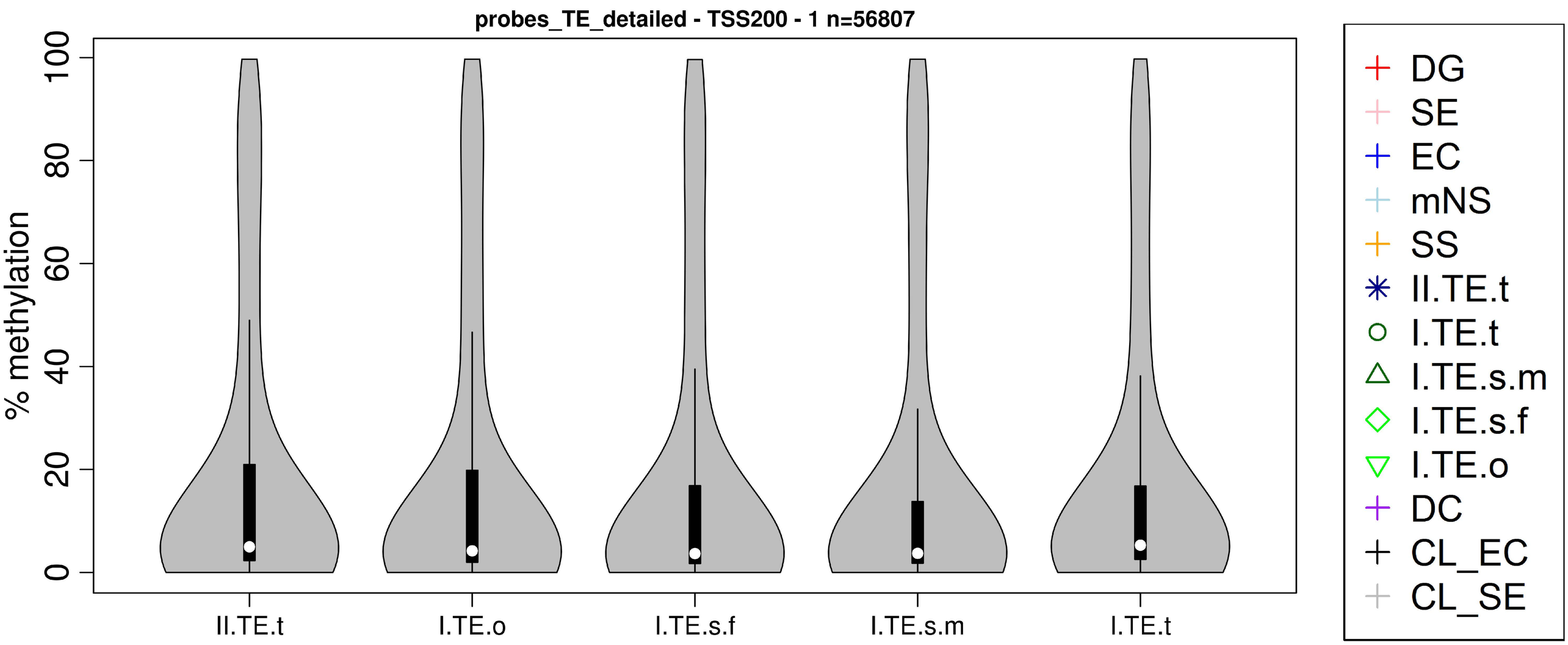

probes_TE_detailed - TSSassociated - 1 n=127037
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

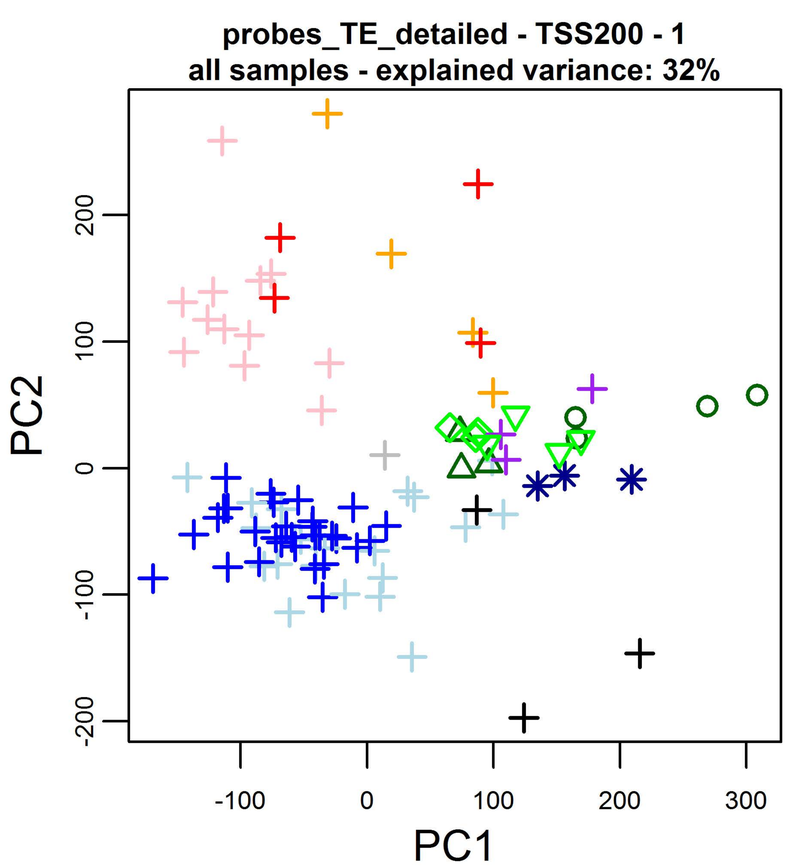

probes_TE_detailed - TSSassociated - 1
all samples - explained variance: 36%
PC2
PC1
-400
-300
-200
-100
0
100
200
-200
0
200
400
600

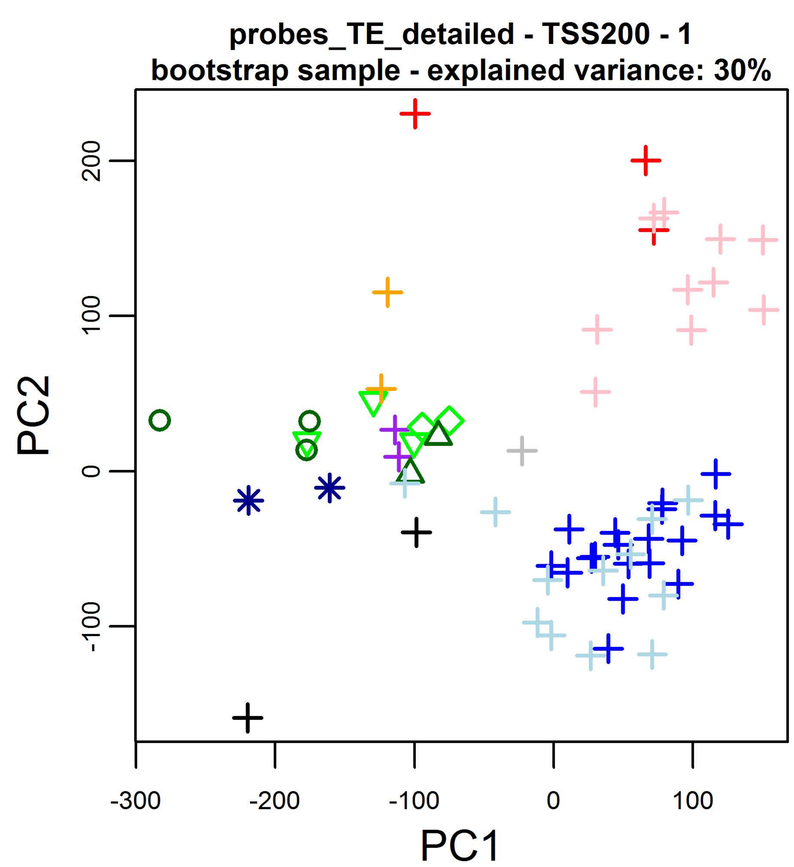

probes_TE_detailed - TSSassociated - 1
bootstrap sample - explained variance: 33%
PC2
PC1
-300
-200
-100
0
100
-200
0
200
400

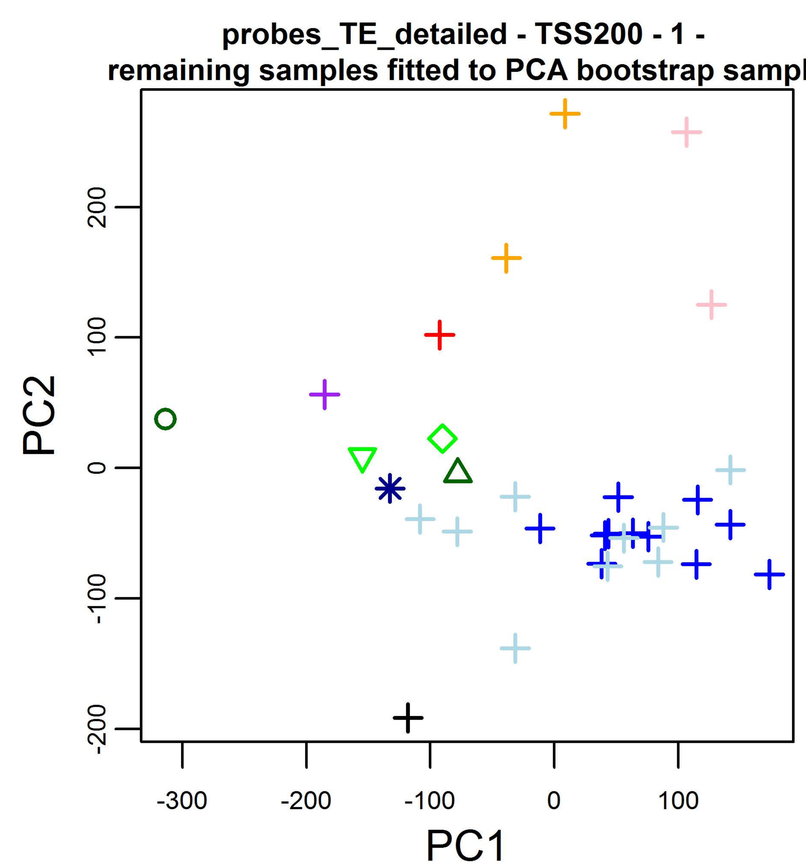

probes_TE_detailed - TSSassociated - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-400
-300
-200
-100
0
100
200
-200
0
200
400
600

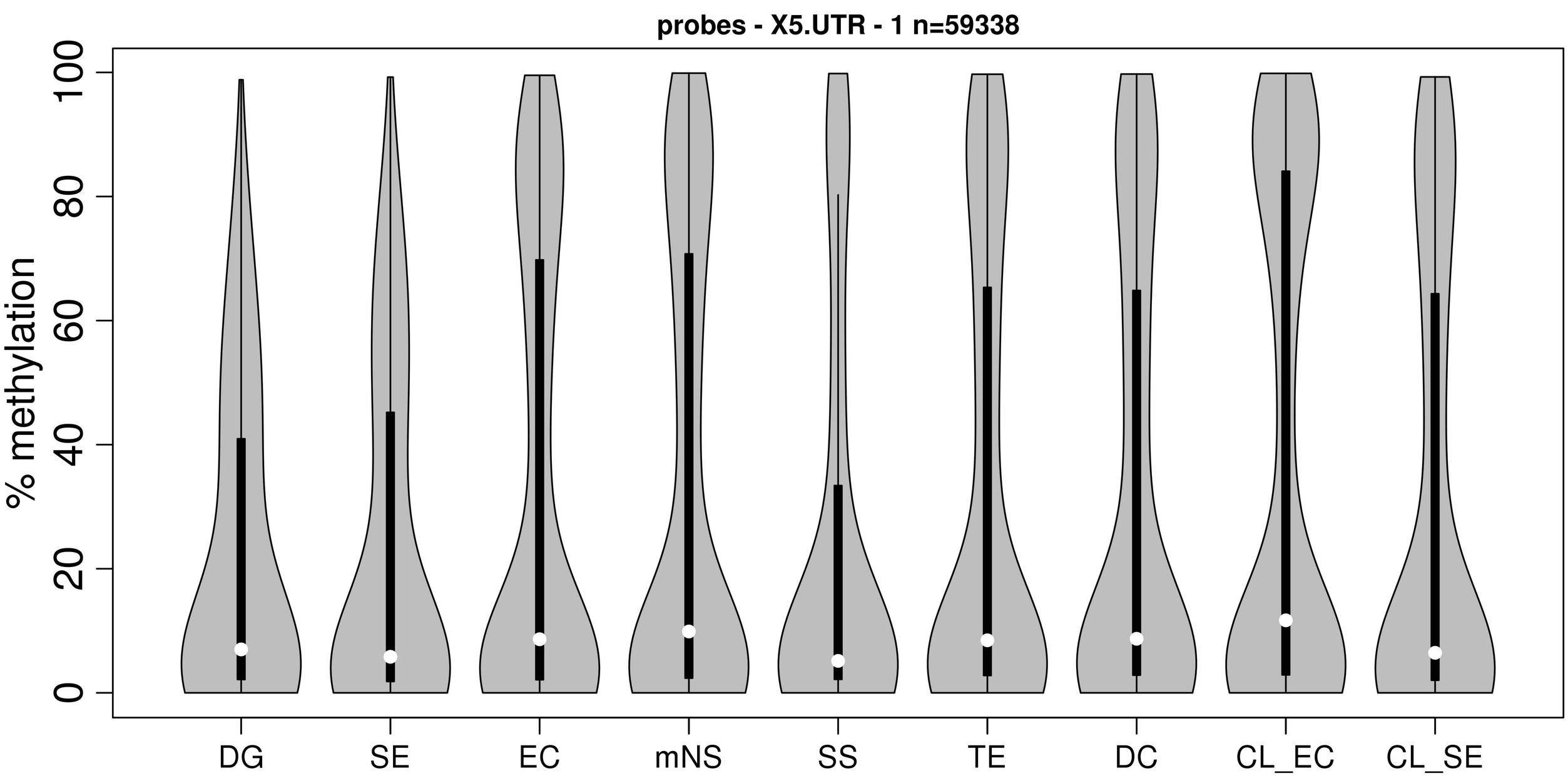

probes - TSS200 - 1 n=56807
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

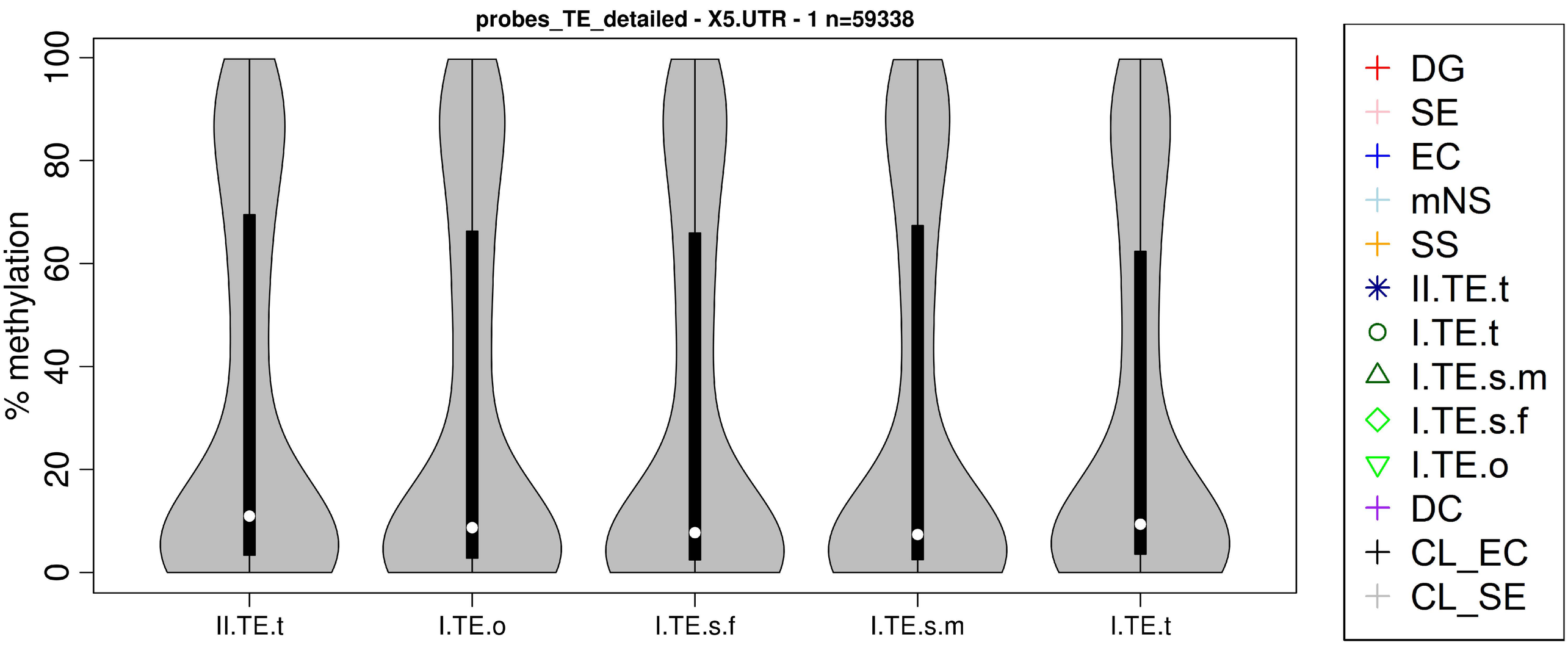

probes_TE_detailed - TSS200 - 1 n=56807
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

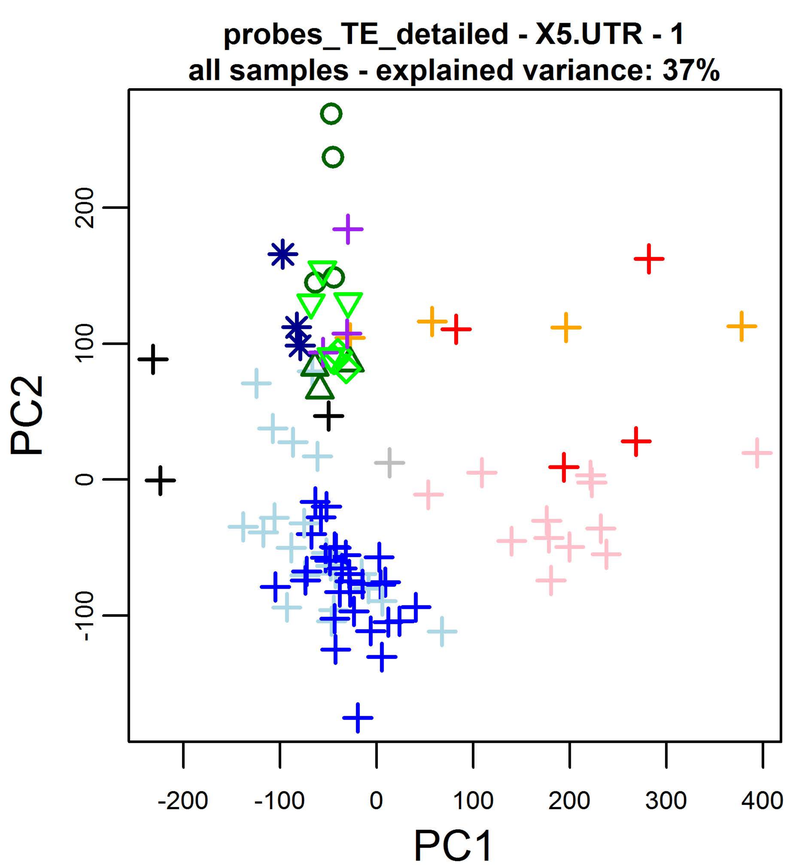

probes_TE_detailed - TSS200 - 1
all samples - explained variance: 32%
PC2
PC1
-200
-100
0
100
200
-100
0
100
200
300

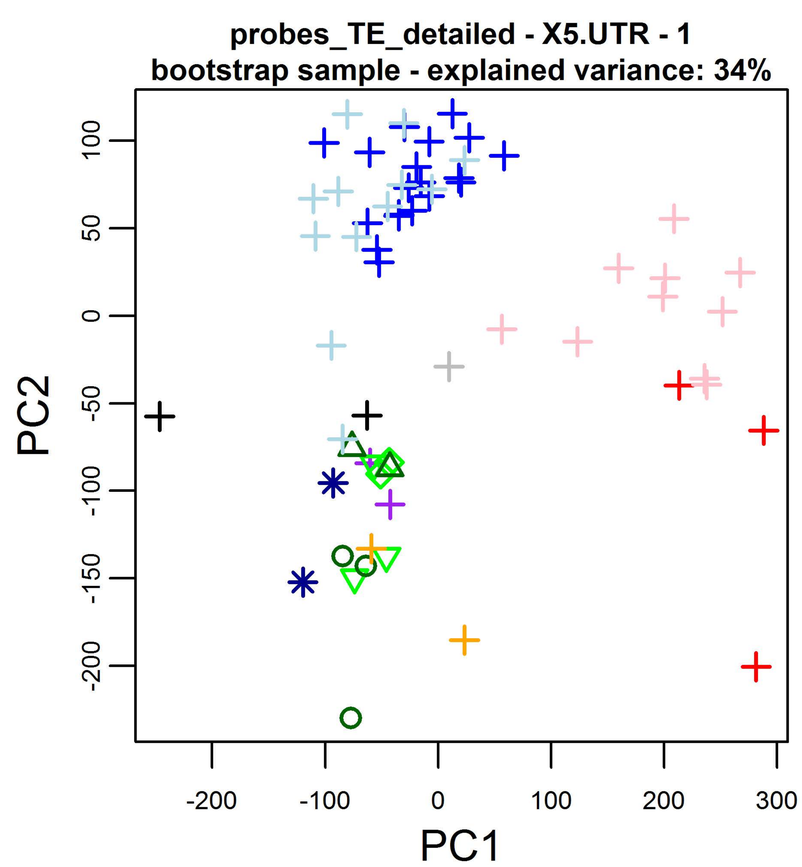

probes_TE_detailed - TSS200 - 1
bootstrap sample - explained variance: 30%
PC2
PC1
-100
0
100
200
-300
-200
-100
0
100

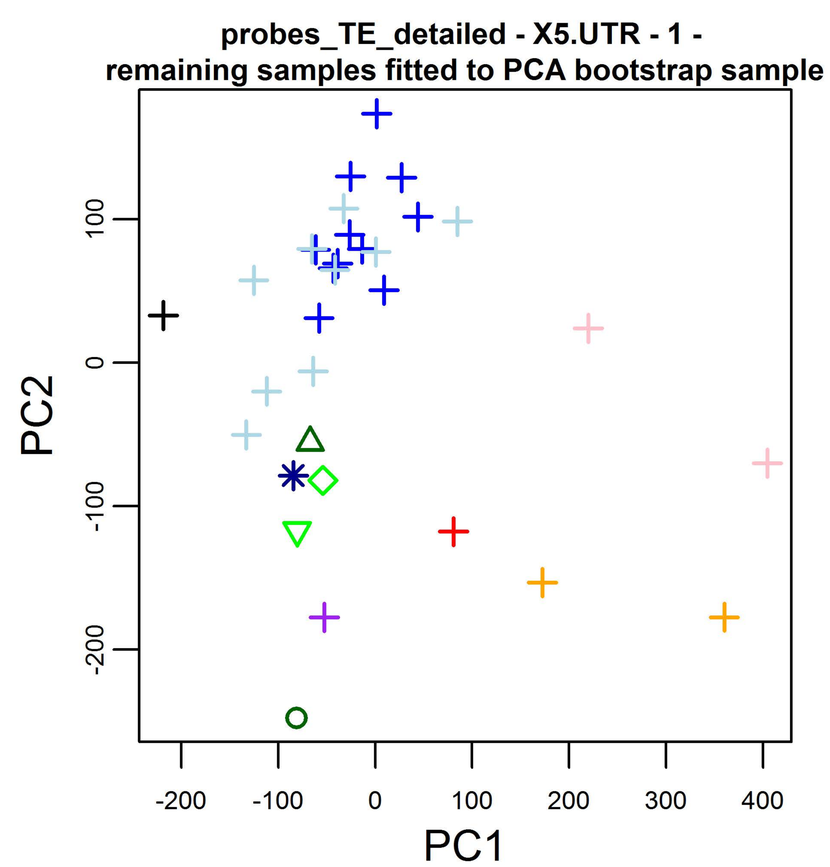

probes_TE_detailed - TSS200 - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-200
-100
0
100
200
-300
-200
-100
0
100

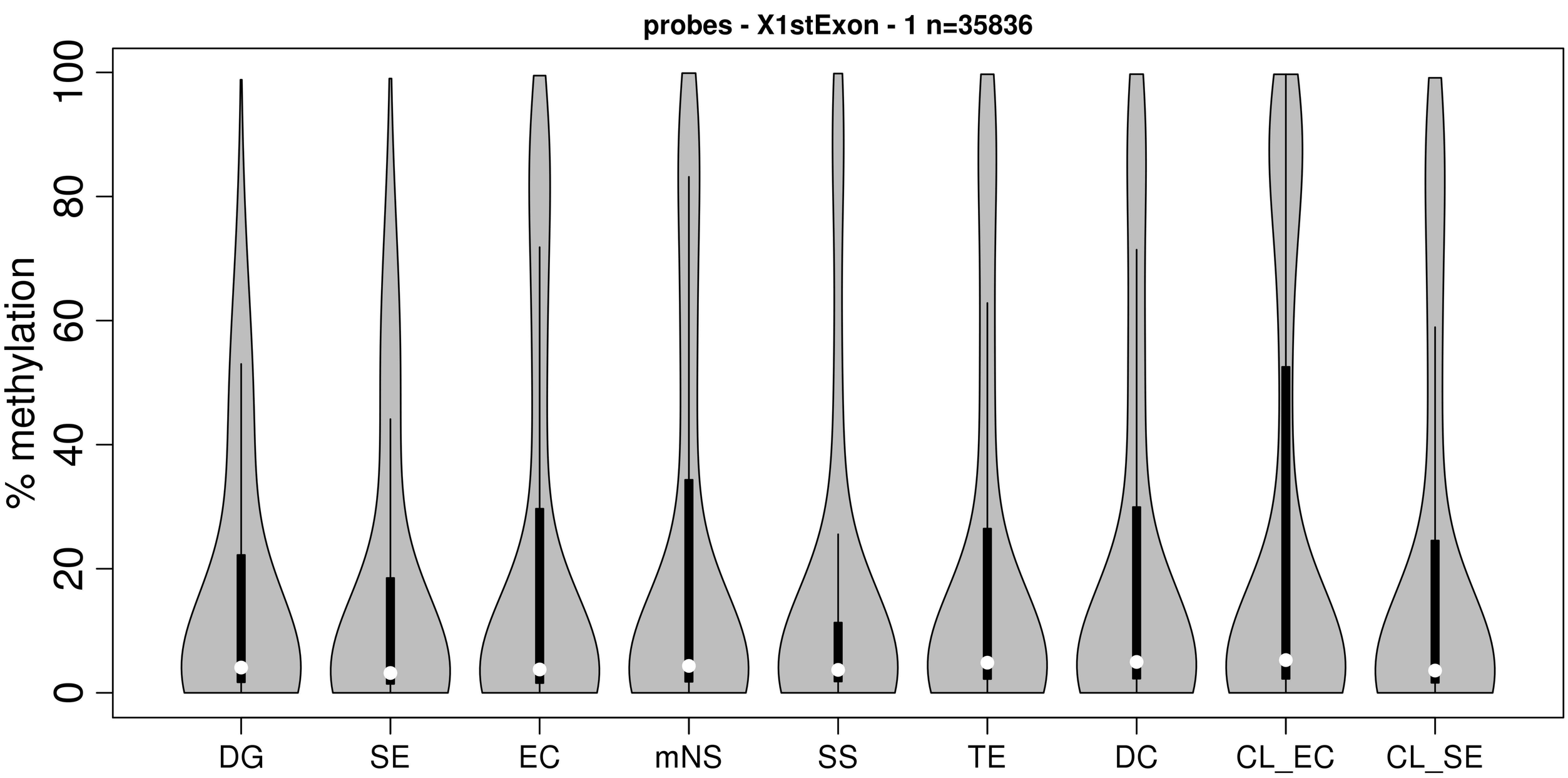

probes - X5.UTR - 1 n=59338
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

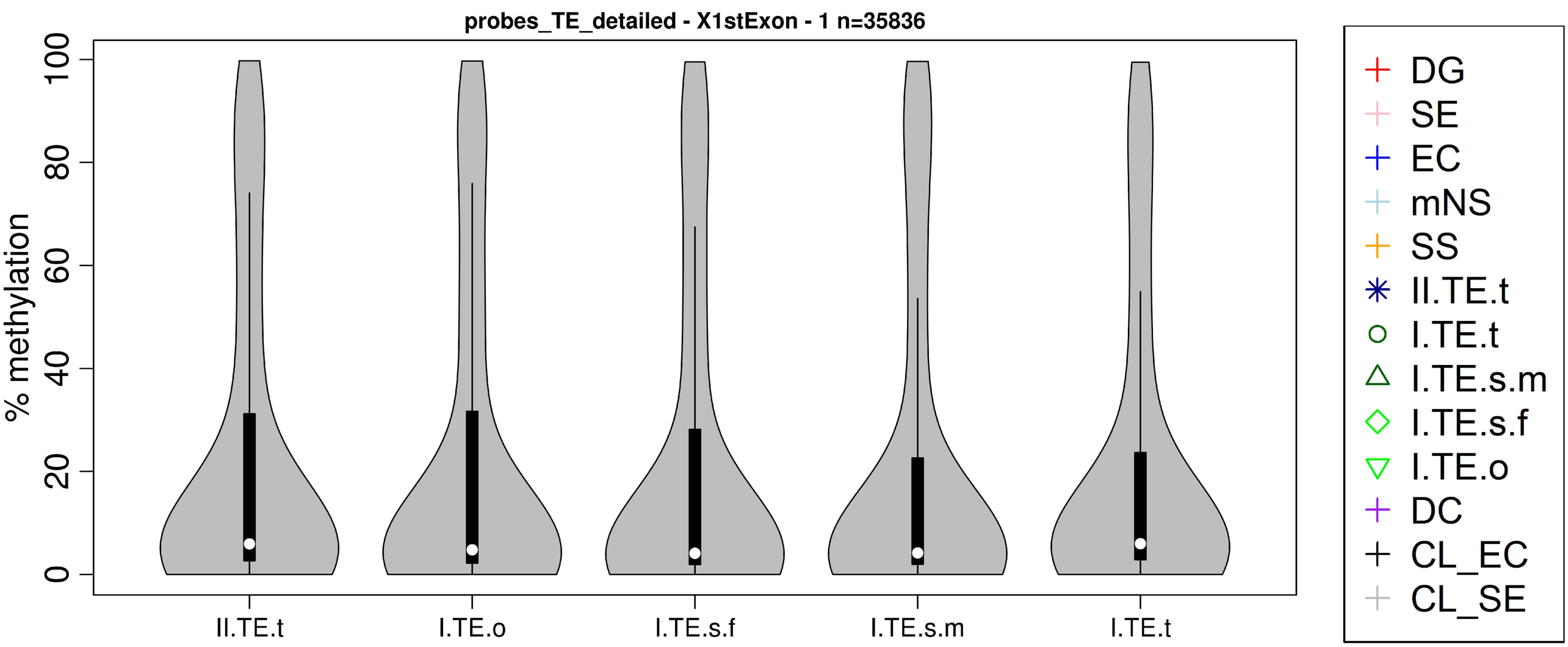

probes_TE_detailed - X5.UTR - 1 n=59338
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

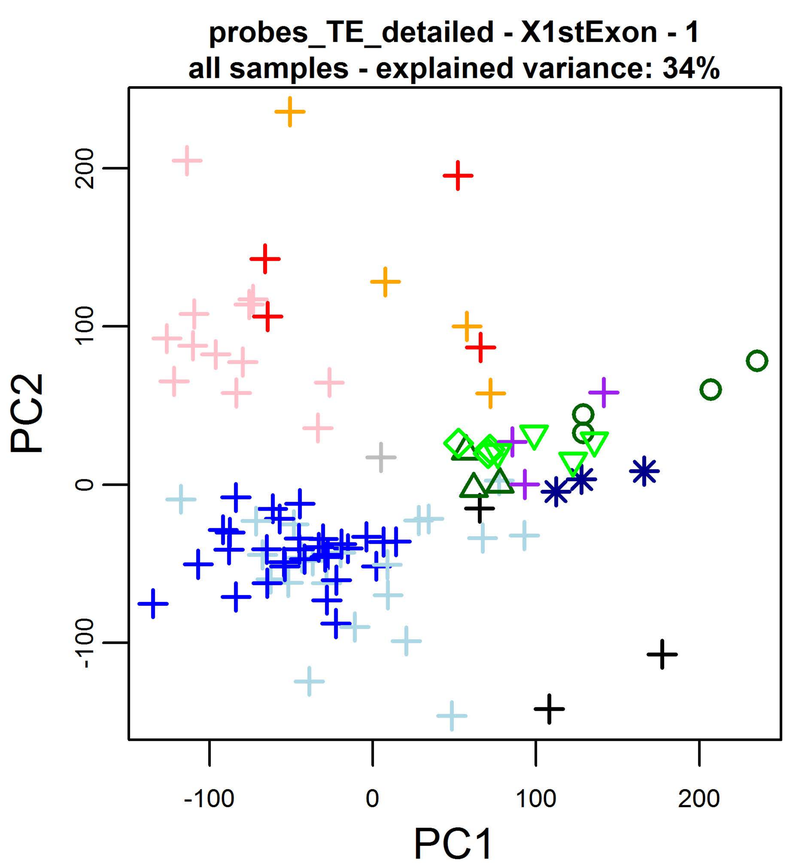

probes_TE_detailed - X5.UTR - 1
all samples - explained variance: 37%
PC2
PC1
-100
0
100
200
-200
-100
0
100
200
300
400

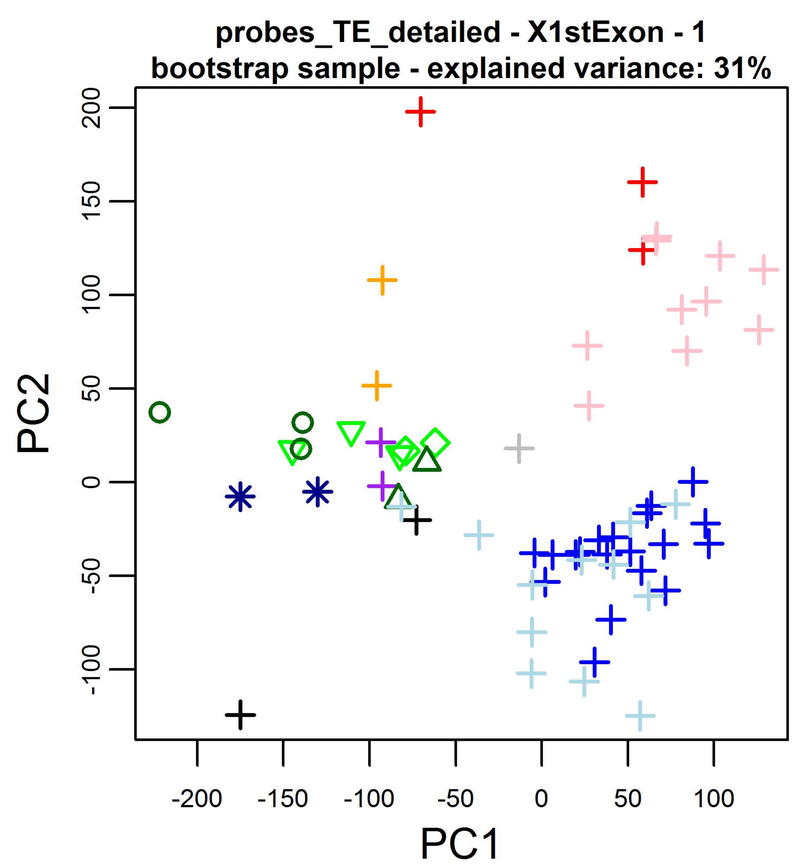

probes_TE_detailed - X5.UTR - 1
bootstrap sample - explained variance: 34%
PC2
PC1
-200
-150
-100
-50
0
50
100
-200
-100
0
100
200
300

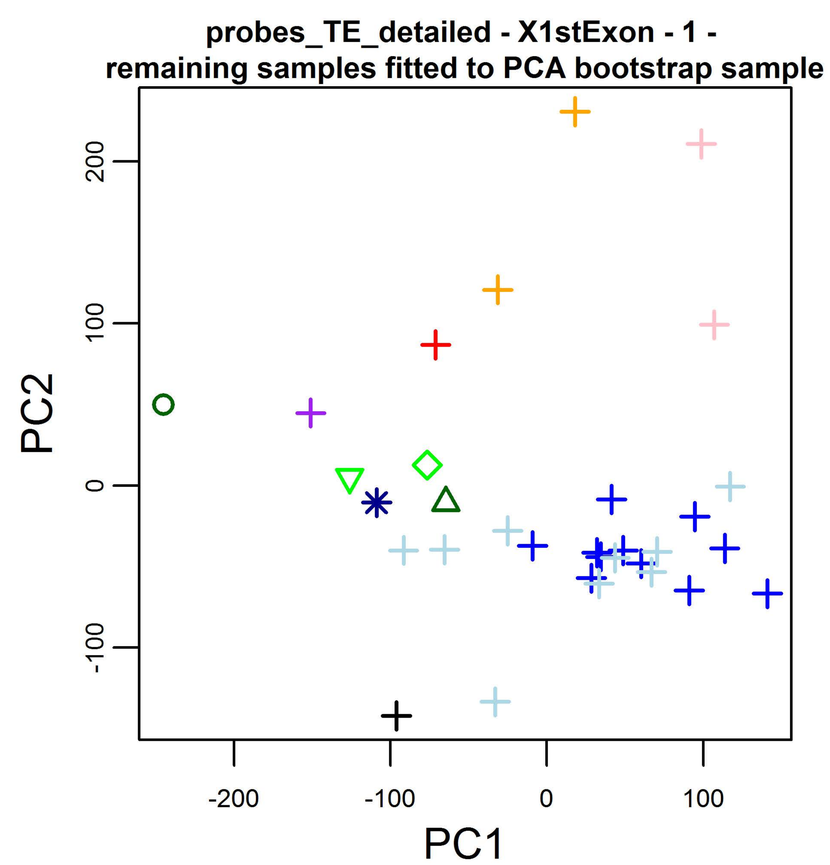

probes_TE_detailed - X5.UTR - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-200
-100
0
100
-200
-100
0
100
200
300
400

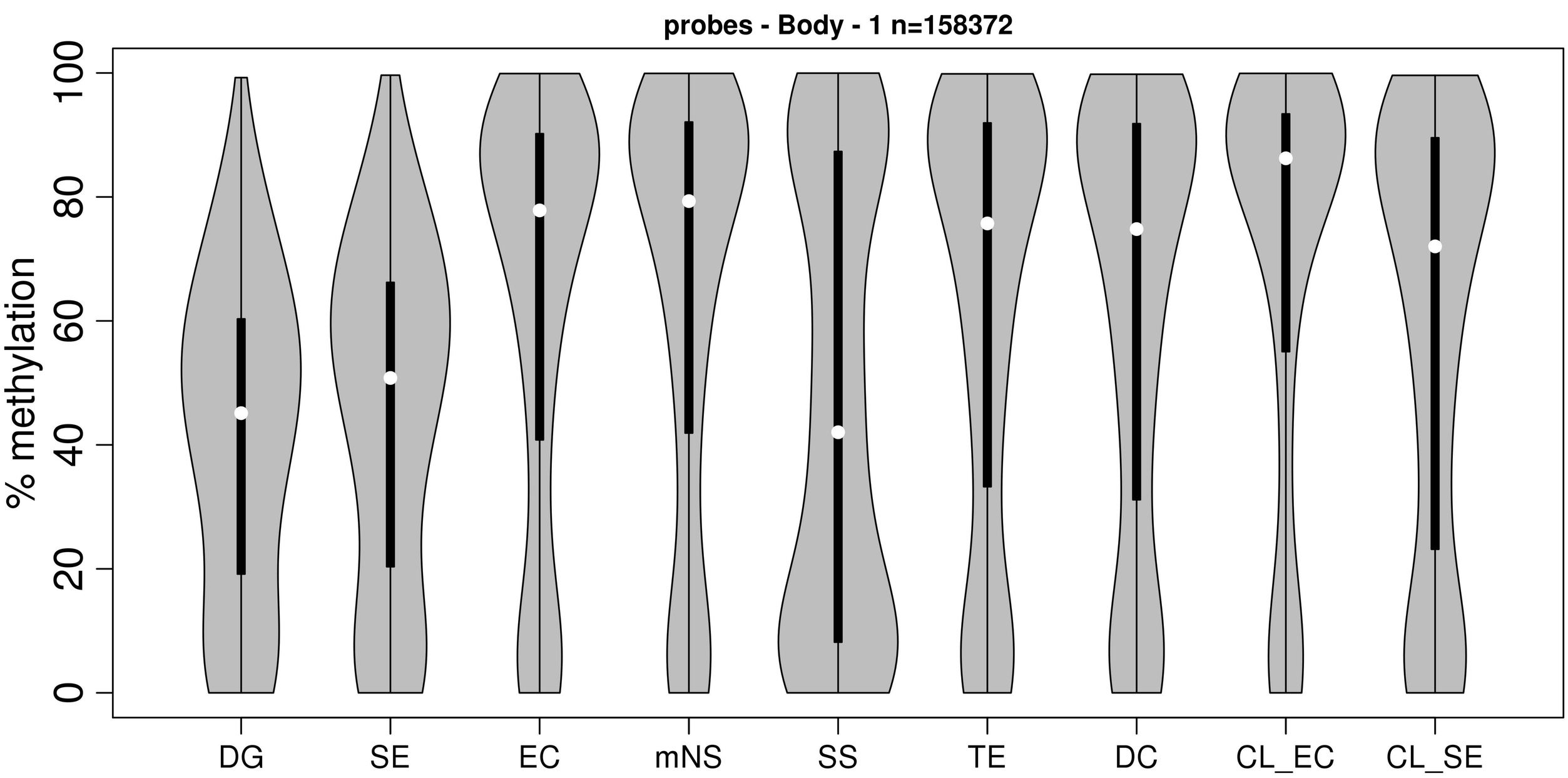

probes - X1stExon - 1 n=35836
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

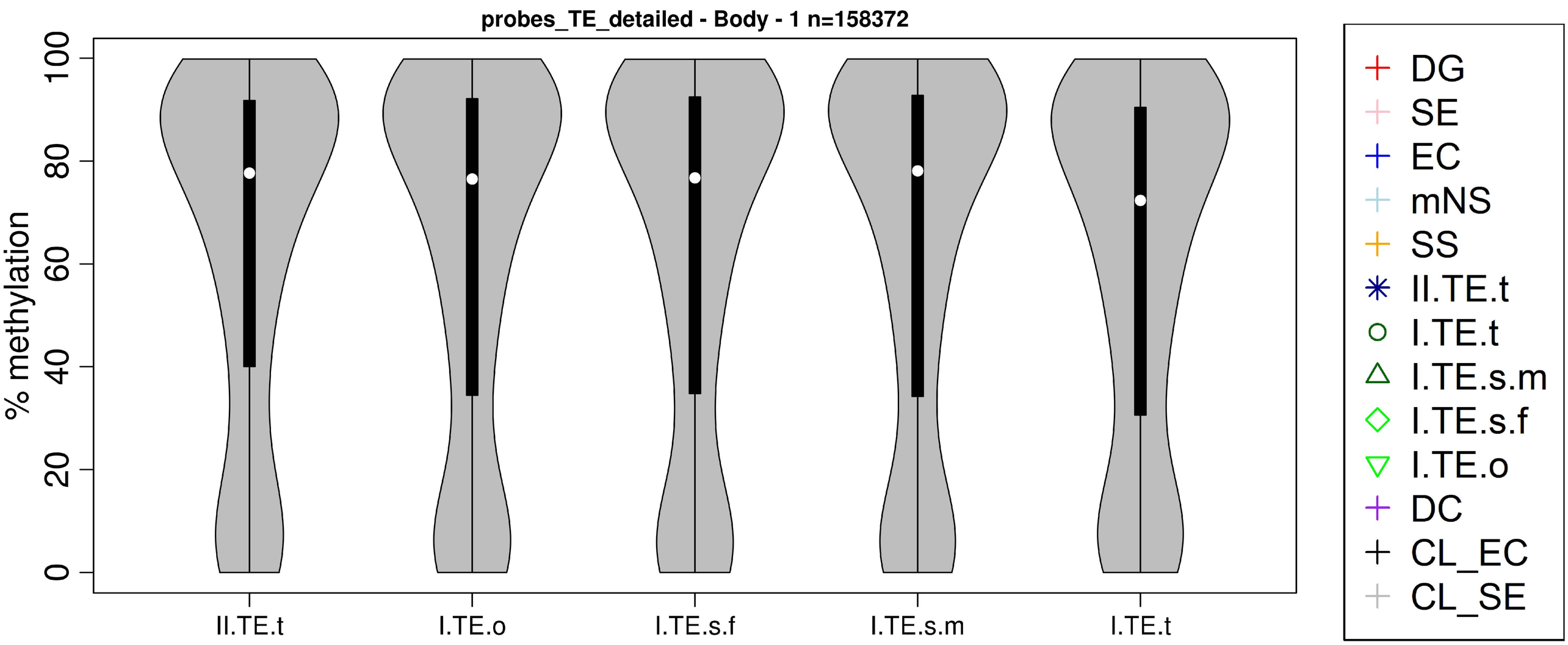

probes_TE_detailed - X1stExon - 1 n=35836
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

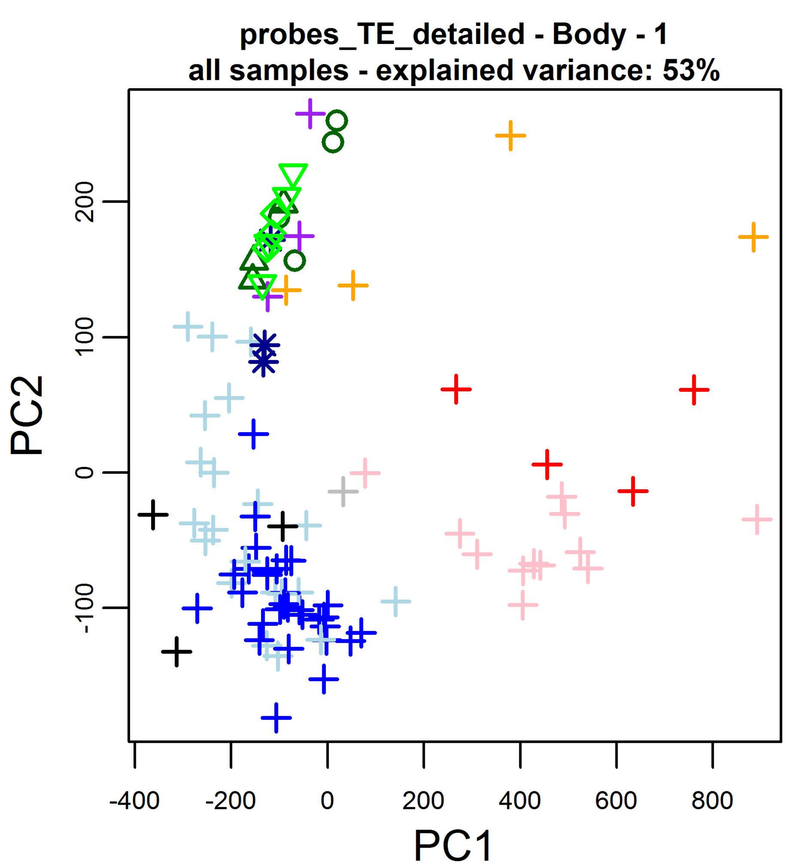

probes_TE_detailed - X1stExon - 1
all samples - explained variance: 34%
PC2
PC1
-100
0
100
200

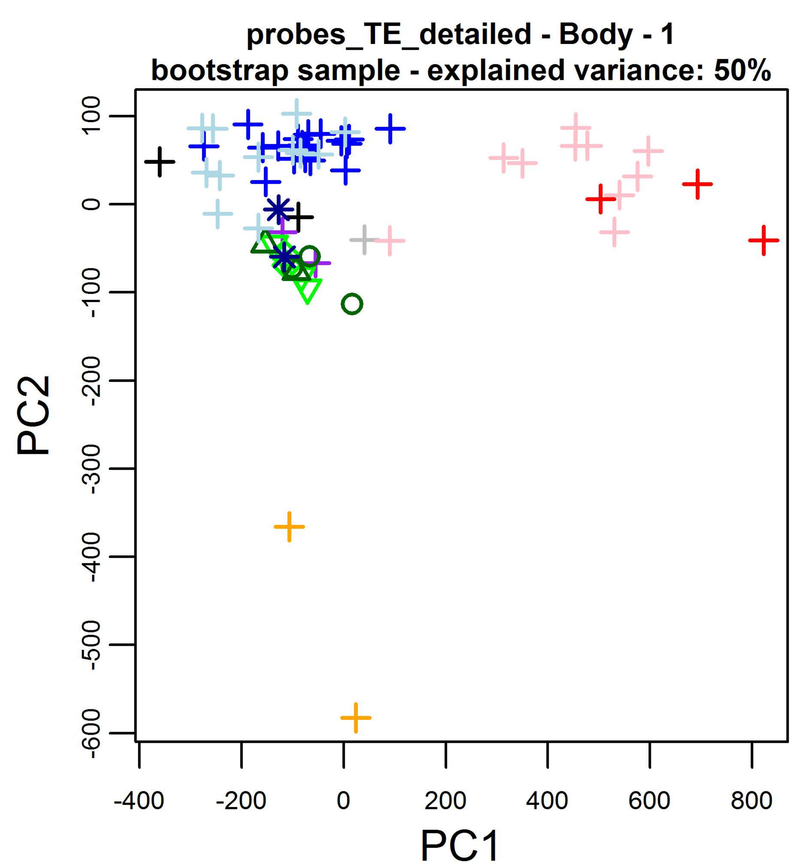

probes_TE_detailed - X1stExon - 1
bootstrap sample - explained variance: 31%
PC2
PC1
-100
-50
0
50
100
150
200
-200
-150

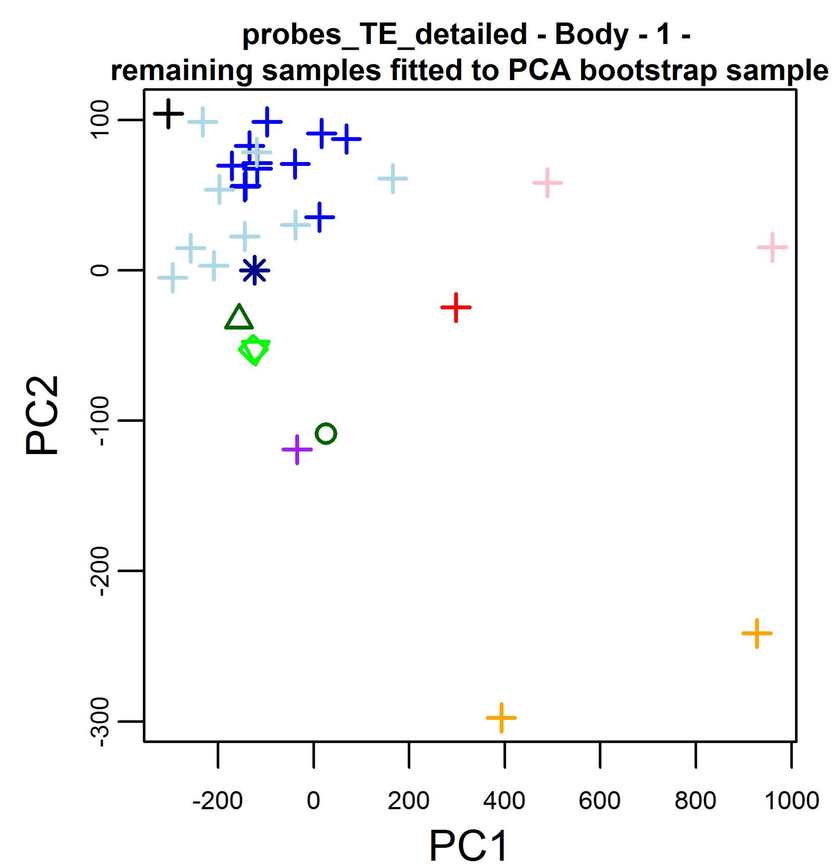

probes_TE_detailed - X1stExon - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-100
0
100
200
-200

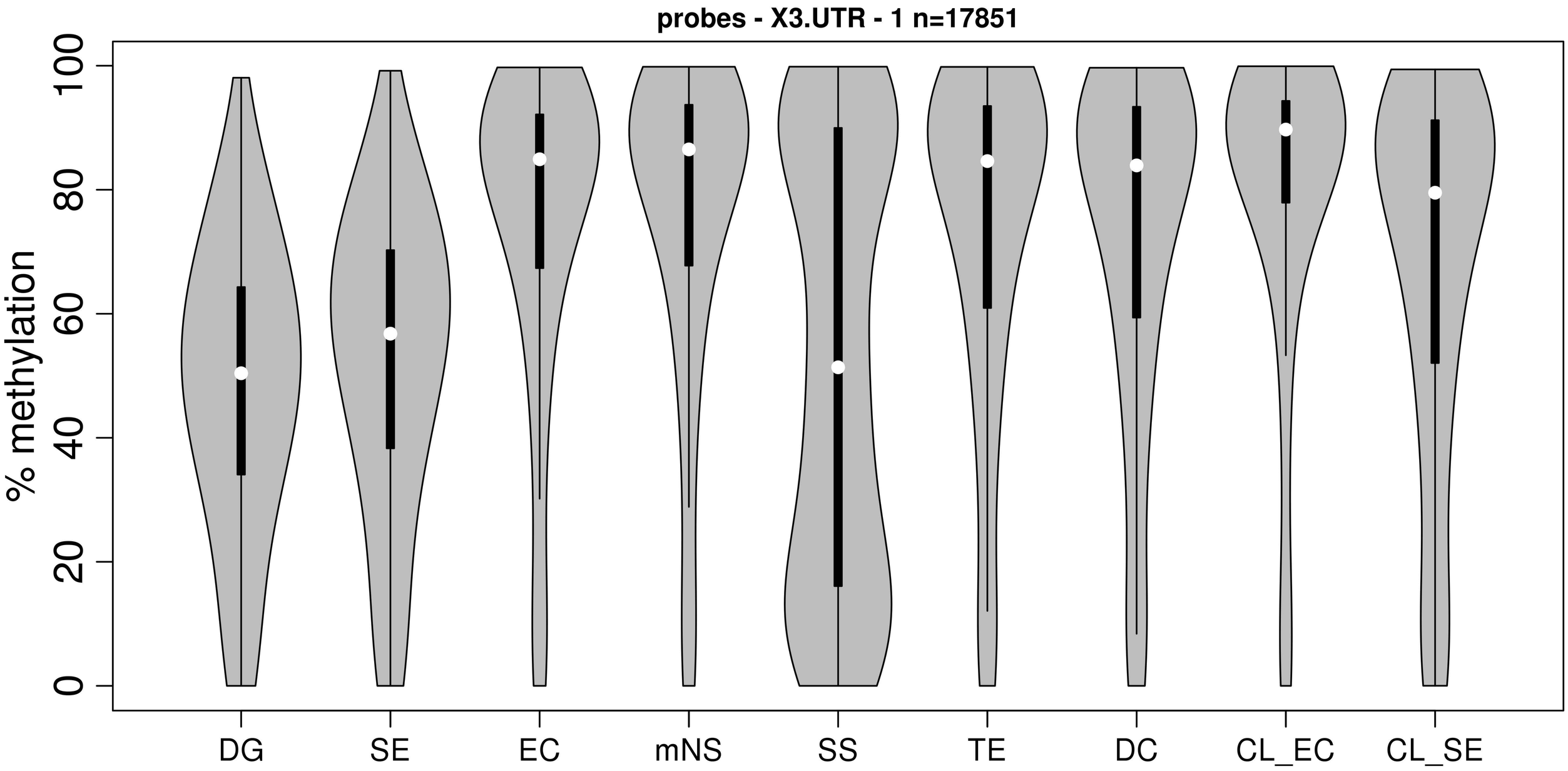

probes - Body - 1 n=158372
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

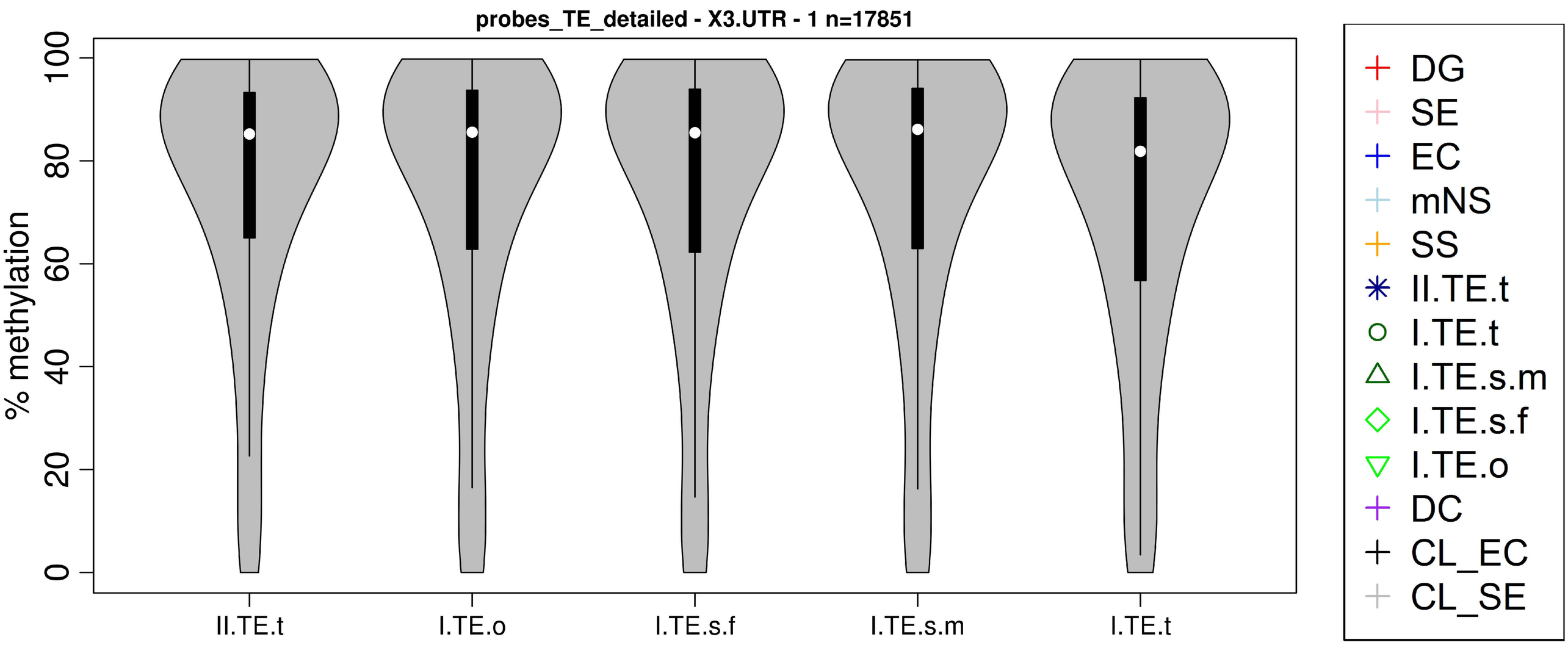

probes_TE_detailed - Body - 1 n=158372
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

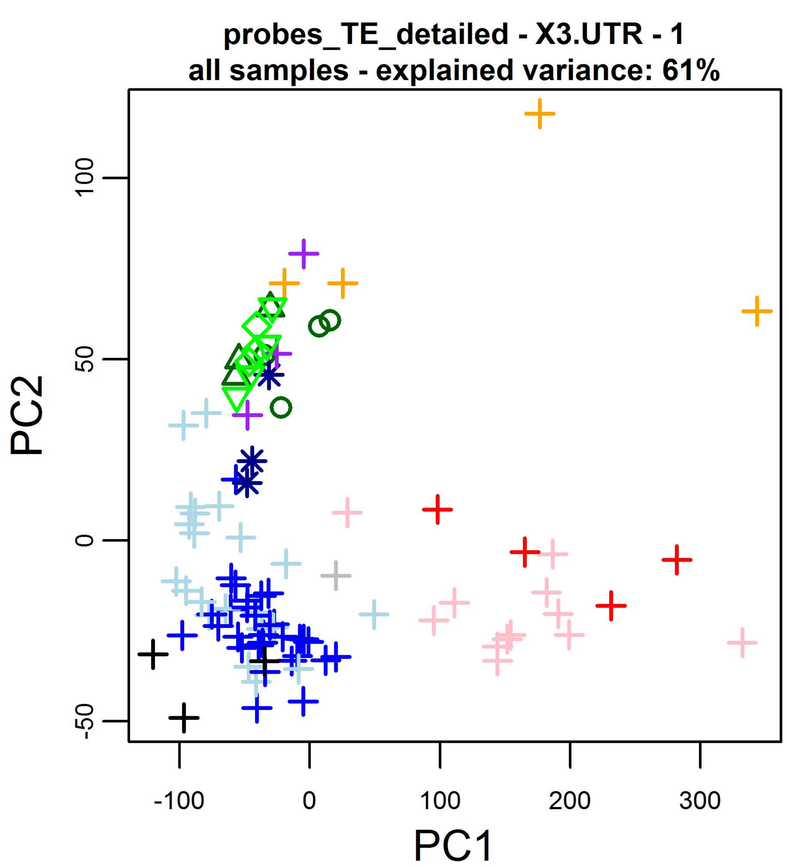

probes_TE_detailed - Body - 1
all samples - explained variance: 53%
PC2
PC1
-400
-200
0
200
400
600
800
-100
0
100
200

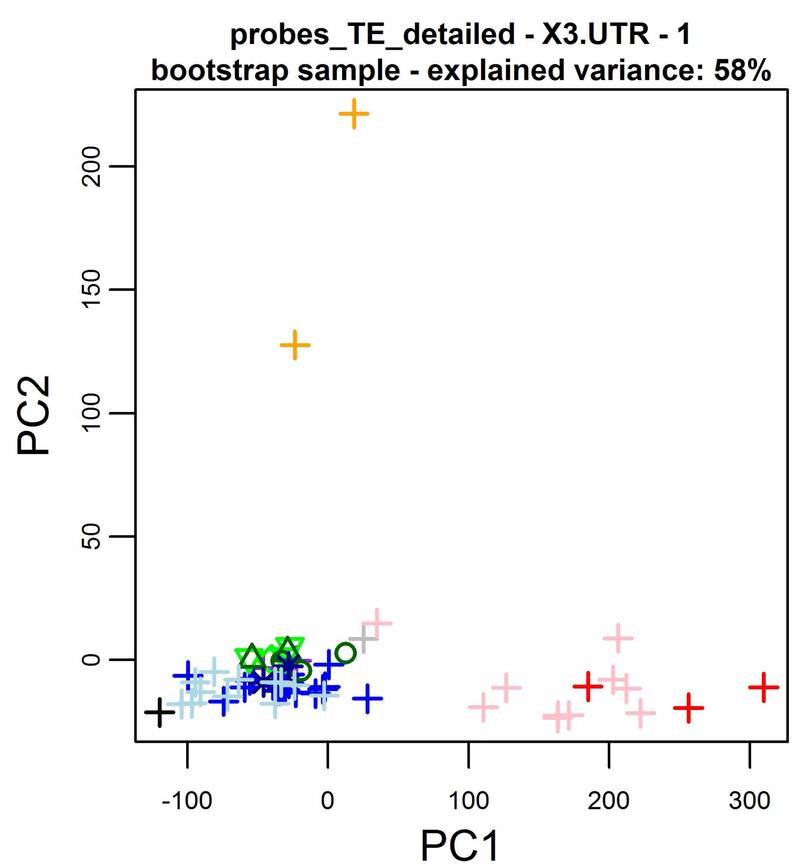

probes_TE_detailed - Body - 1
bootstrap sample - explained variance: 50%
PC2
PC1
-400
-200
0
200
400
600
800
100
0
-100
-200
-300
-400
-500
-600

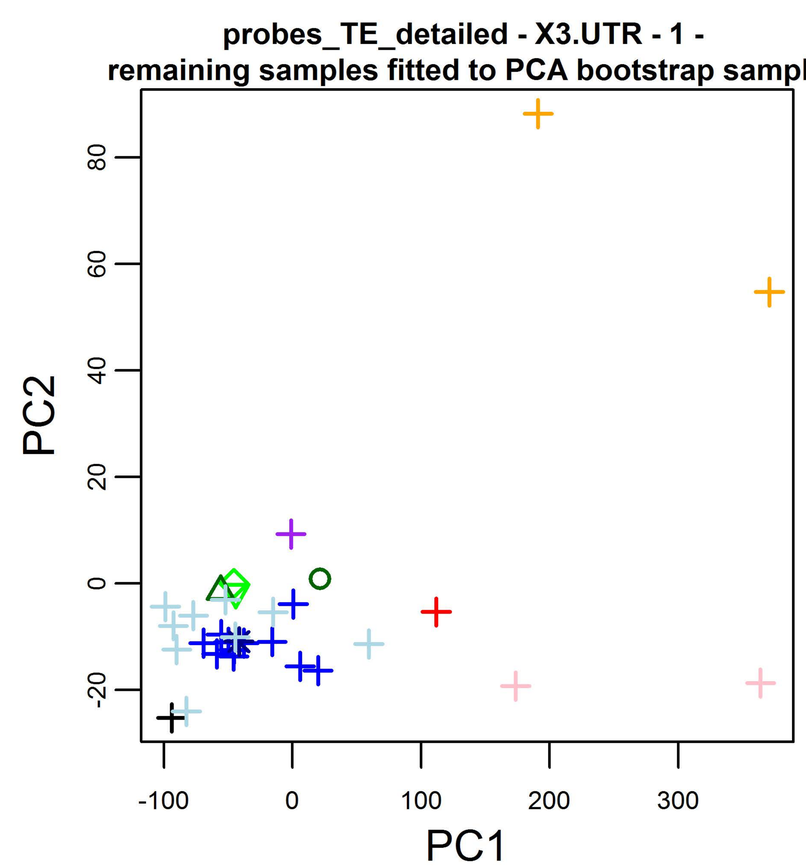

probes_TE_detailed - Body - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-200
0
200
400
600
800
1000
100
0
-100
-200
-300

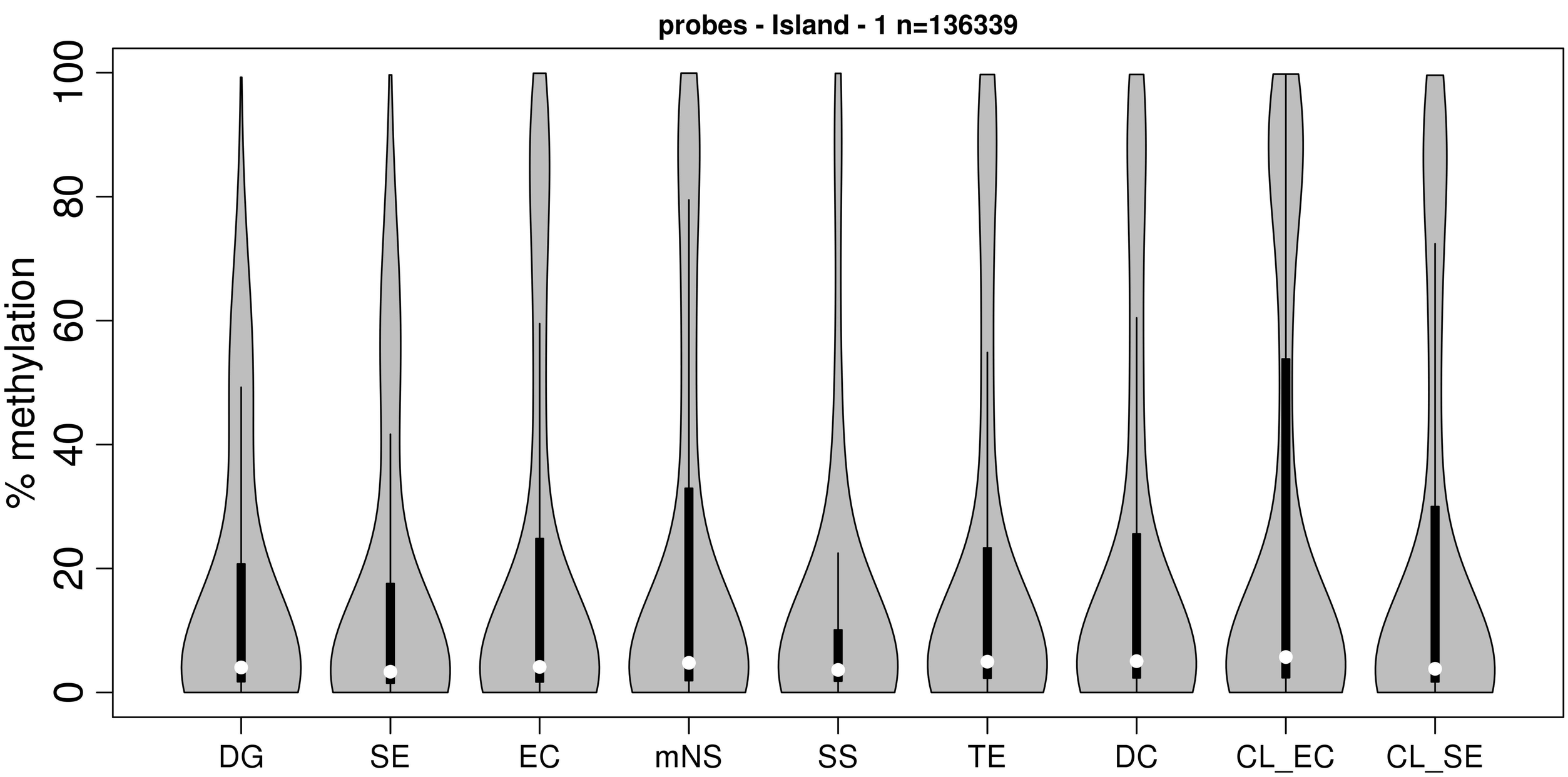

probes - X3.UTR - 1 n=17851
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

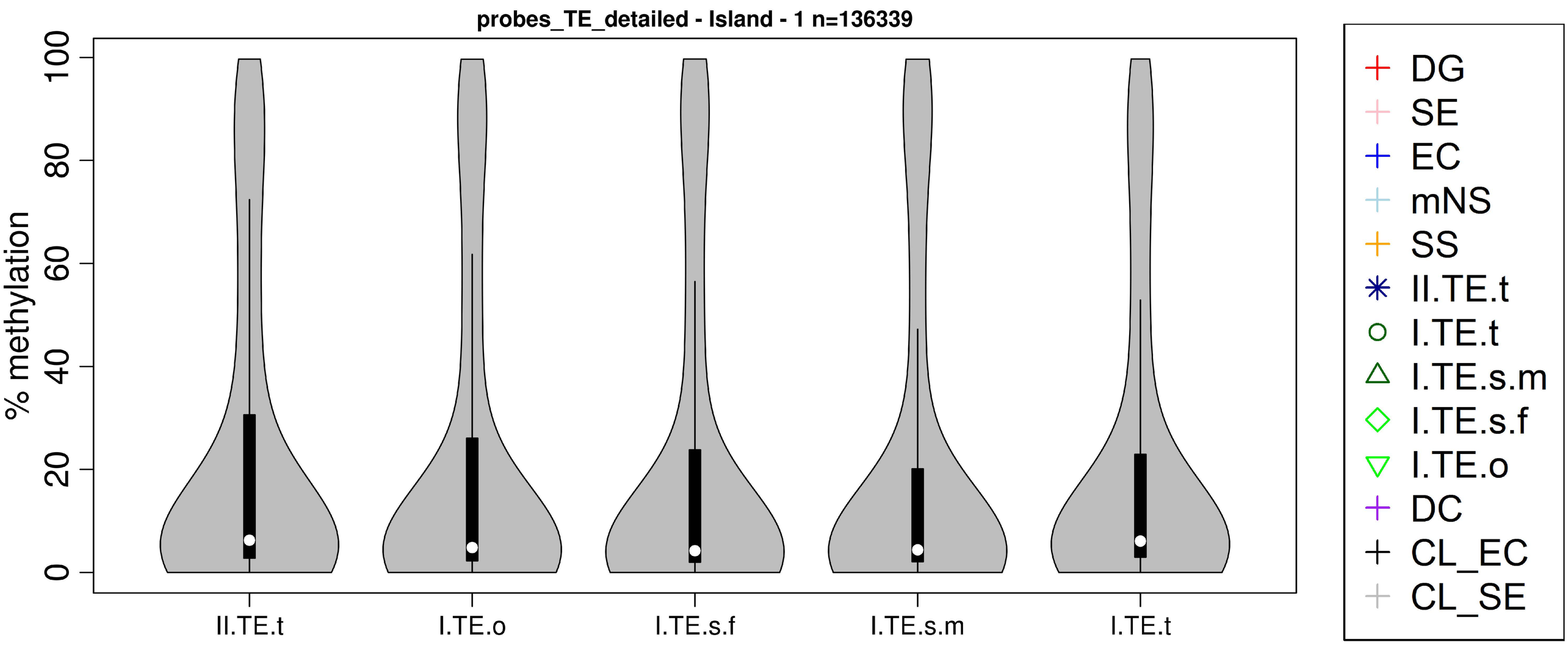

probes_TE_detailed - X3.UTR - 1 n=17851
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

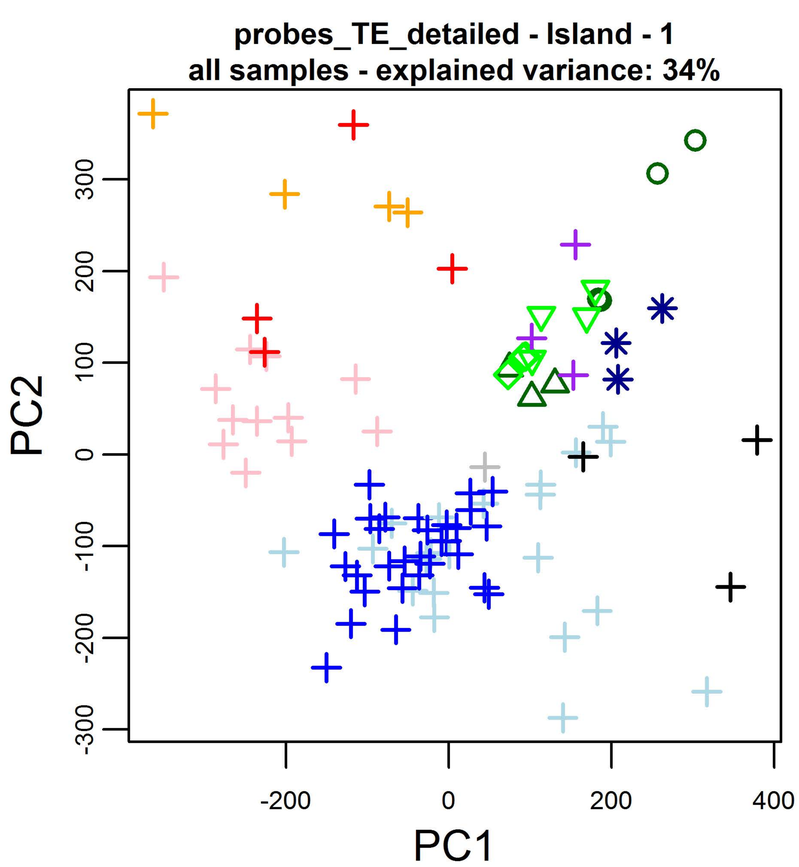

probes_TE_detailed - X3.UTR - 1
all samples - explained variance: 61%
PC2
PC1
-50
0
50
100
-100
0
100
200
300

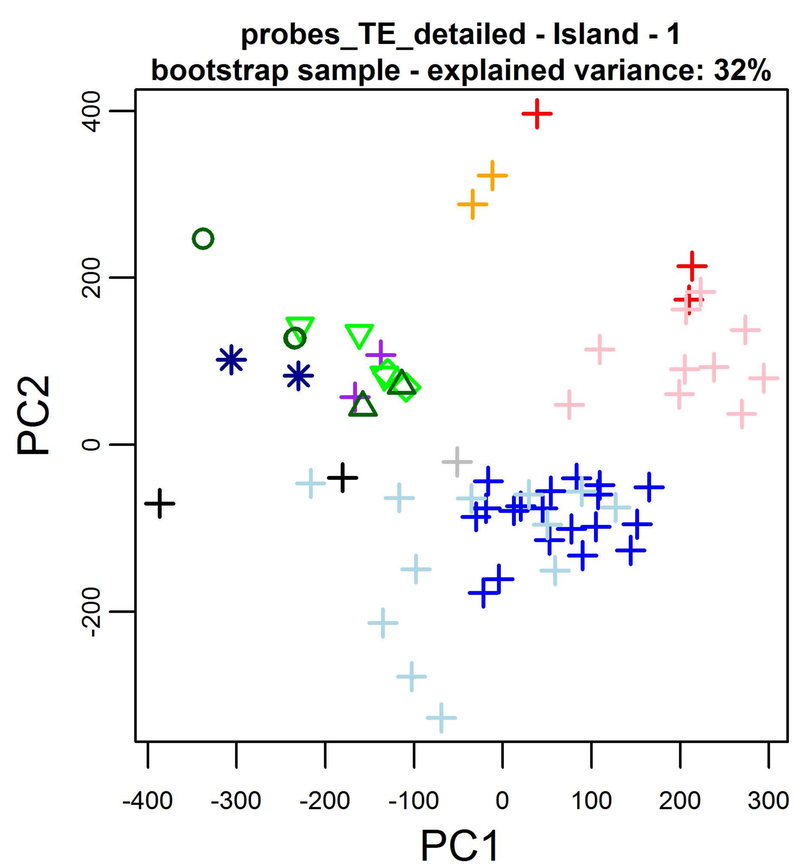

probes_TE_detailed - X3.UTR - 1
bootstrap sample - explained variance: 58%
PC2
PC1
0
50
100
150
200
-100
0
100
200
300

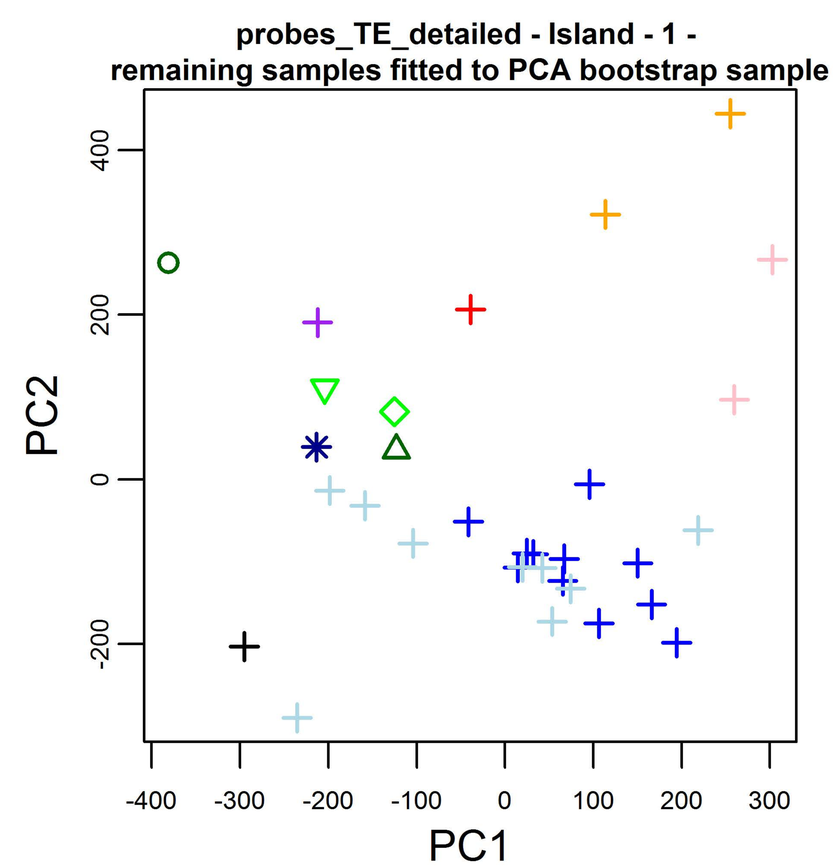

probes_TE_detailed - X3.UTR - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-20
0
20
40
60
80
-100
0
100
200
300

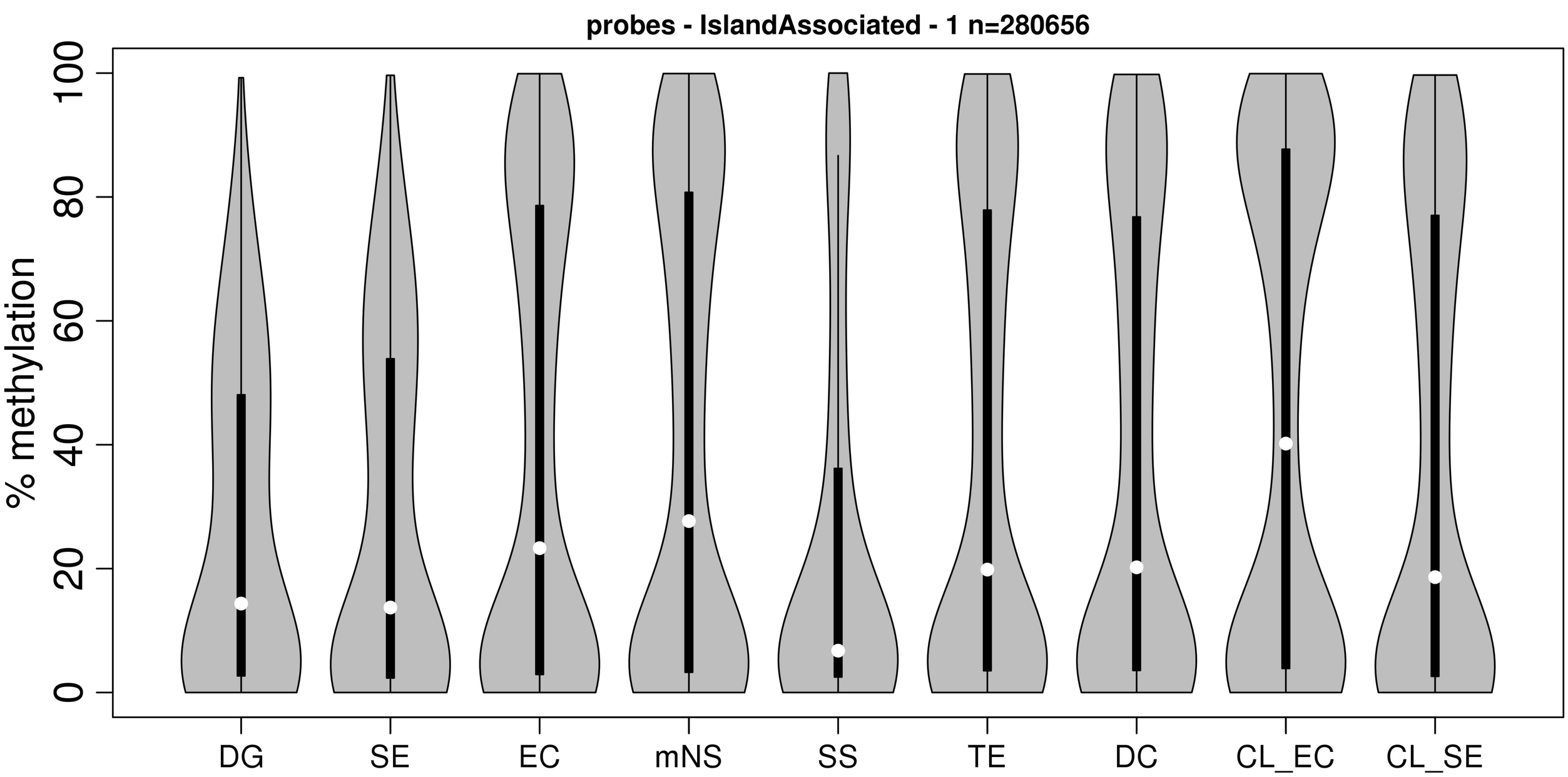

probes - Island - 1 n=136339
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

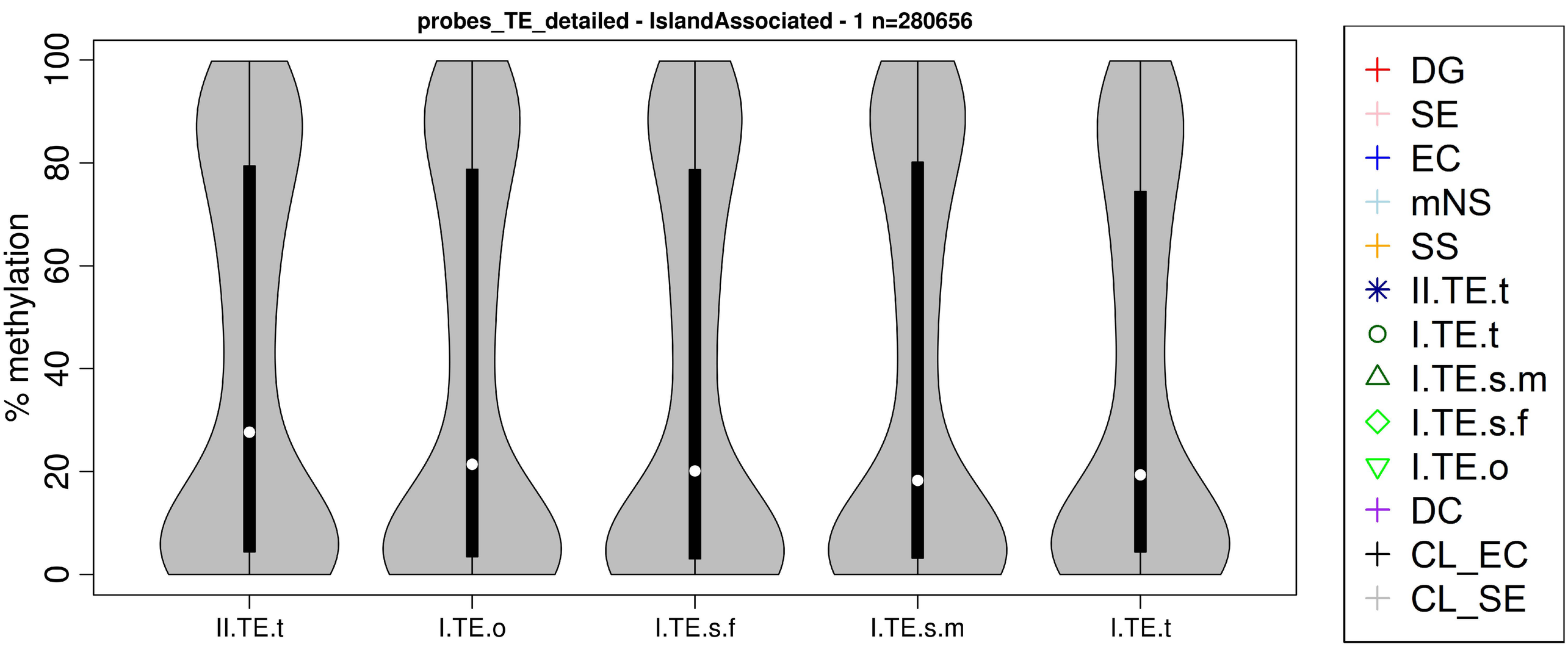

probes_TE_detailed - Island - 1 n=136339
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

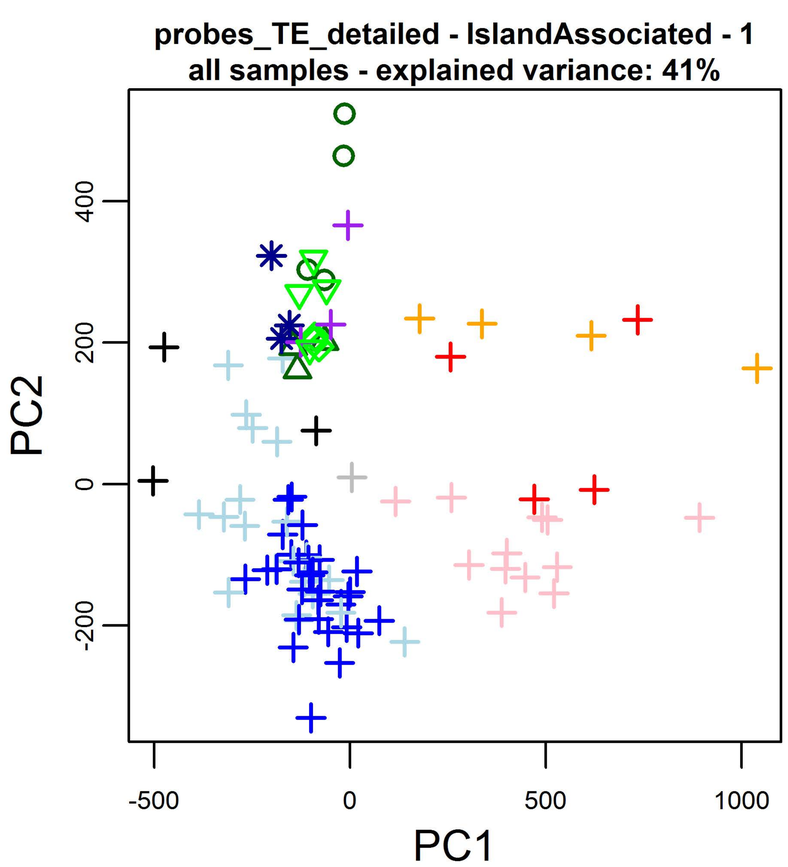

probes_TE_detailed - Island - 1
all samples - explained variance: 34%
PC2
PC1
-300
-200
-100
0
100
200
300
-200
0
200
400

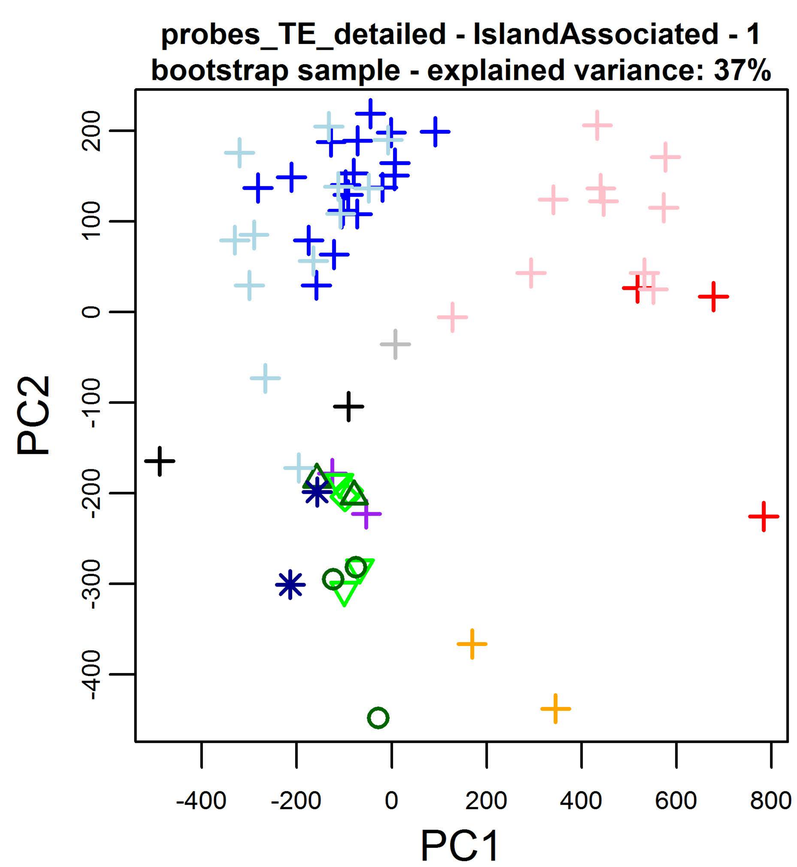

probes_TE_detailed - Island - 1
bootstrap sample - explained variance: 32%
PC2
PC1
-200
0
200
400
-400
-300
-200
-100
0
100
200
300

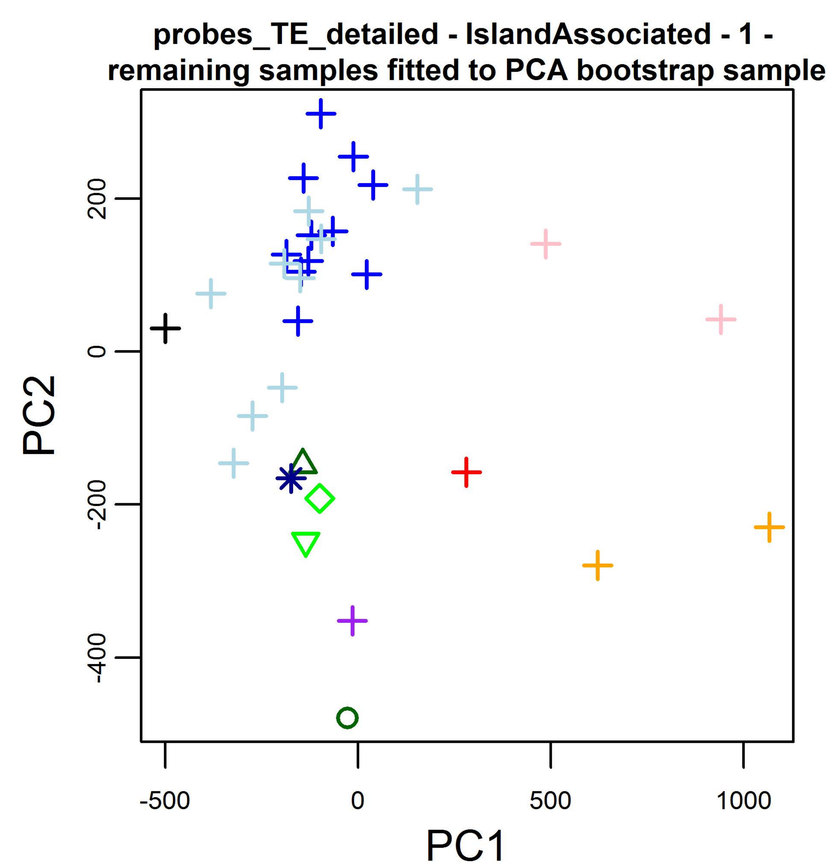

probes_TE_detailed - Island - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-200
0
200
400
-400
-300
-200
-100
0
100
200
300

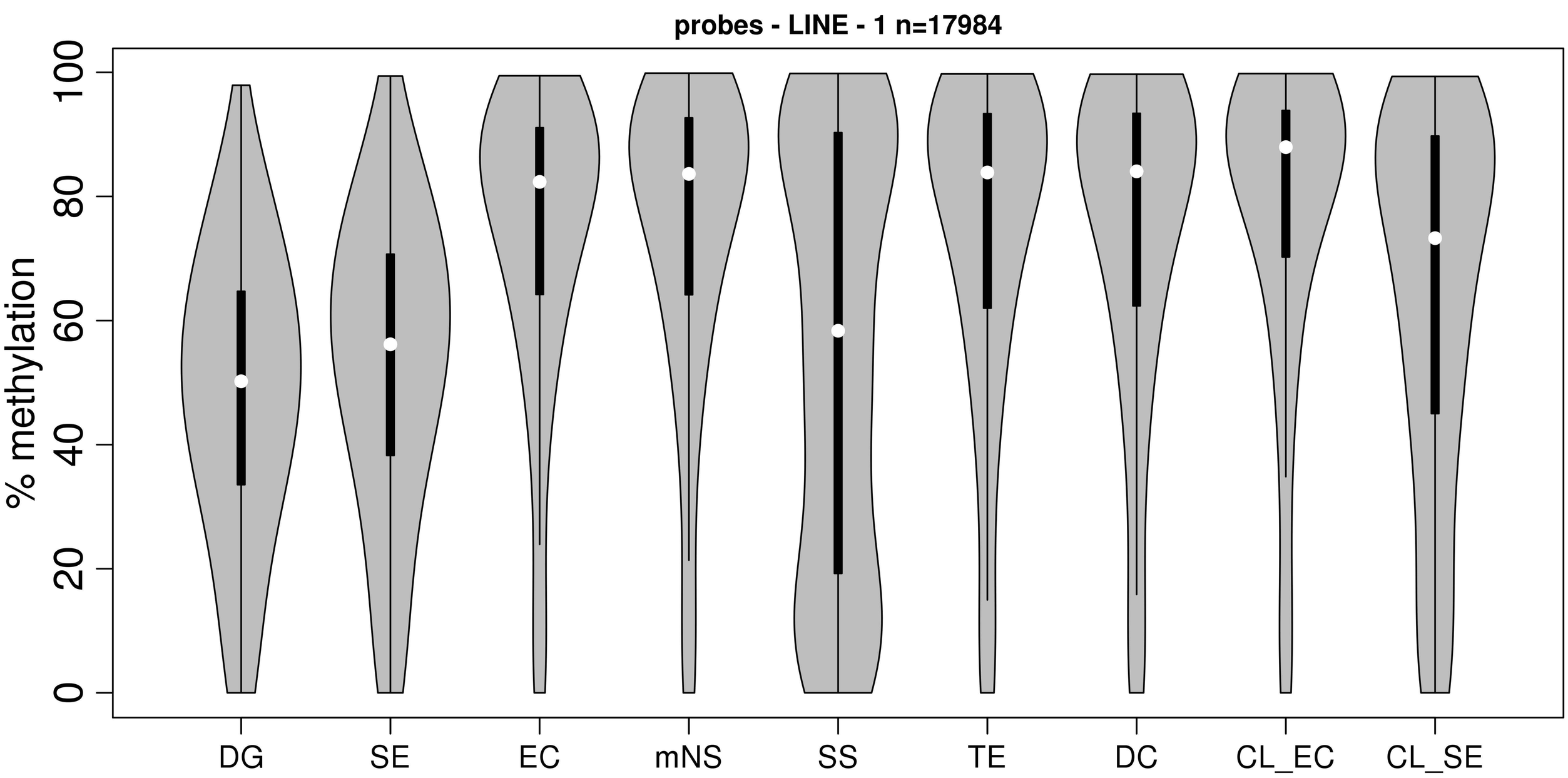

probes - IslandAssociated - 1 n=280656
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

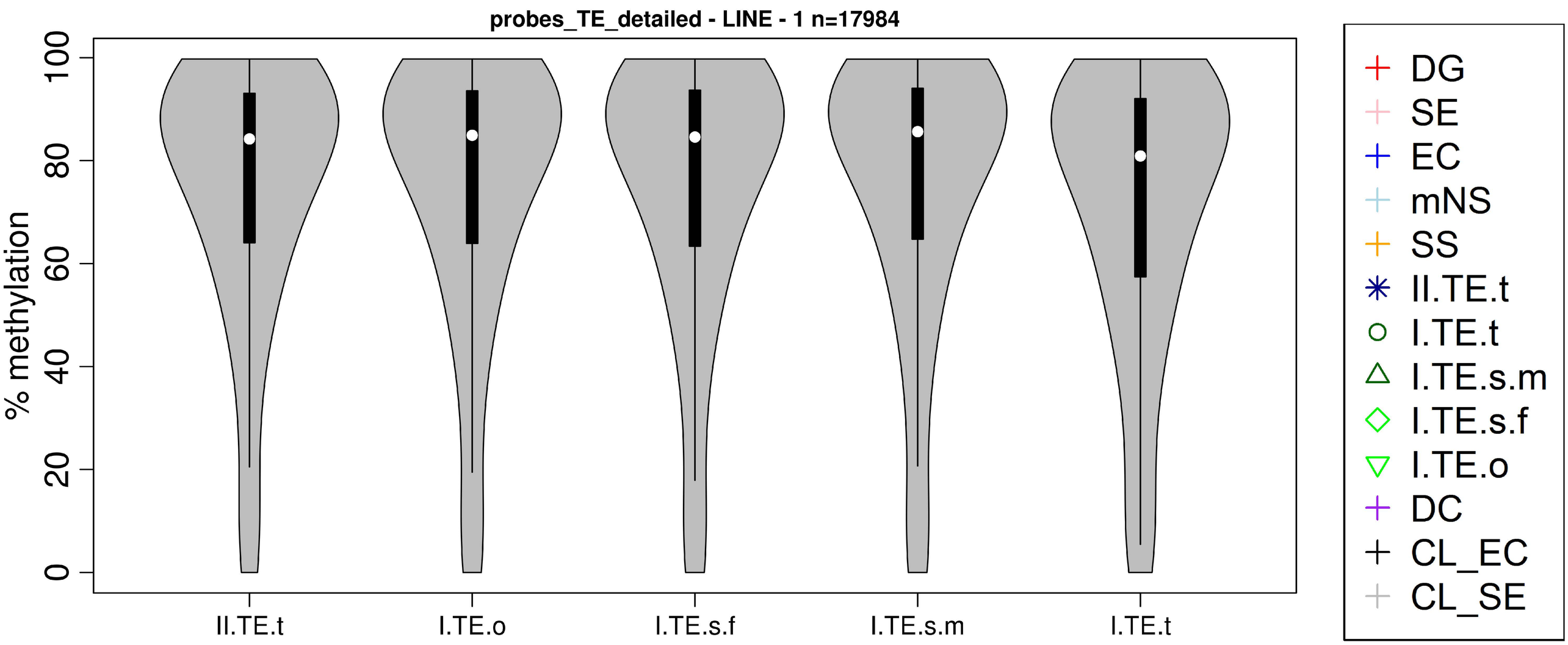

probes_TE_detailed - IslandAssociated - 1 n=280656
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

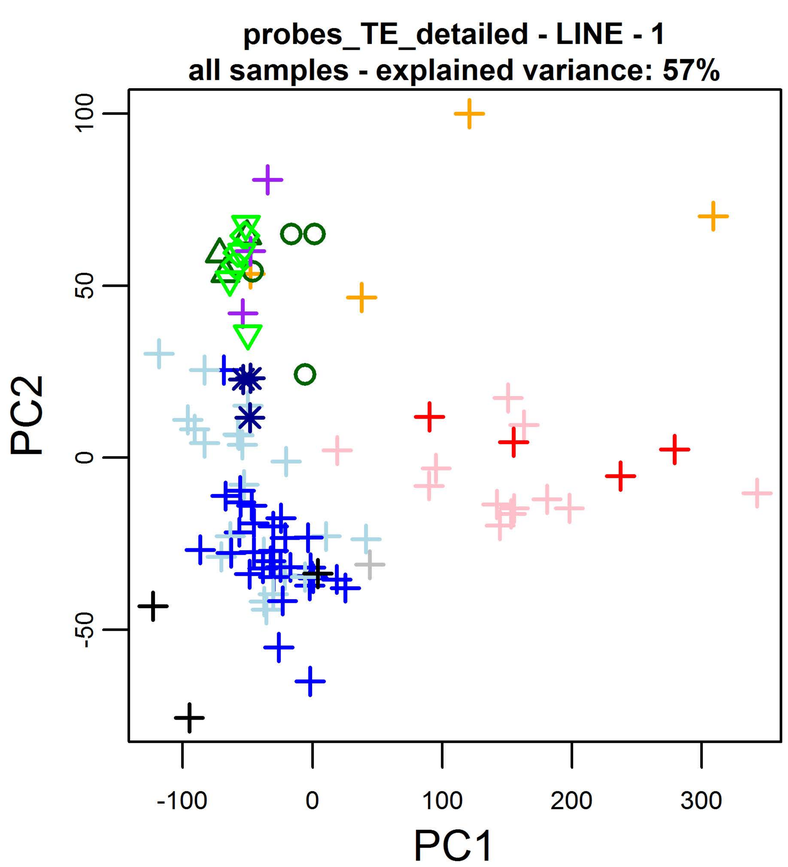

probes_TE_detailed - IslandAssociated - 1
all samples - explained variance: 41%
PC2
PC1
-500
0
500
1000
-200
0
200
400

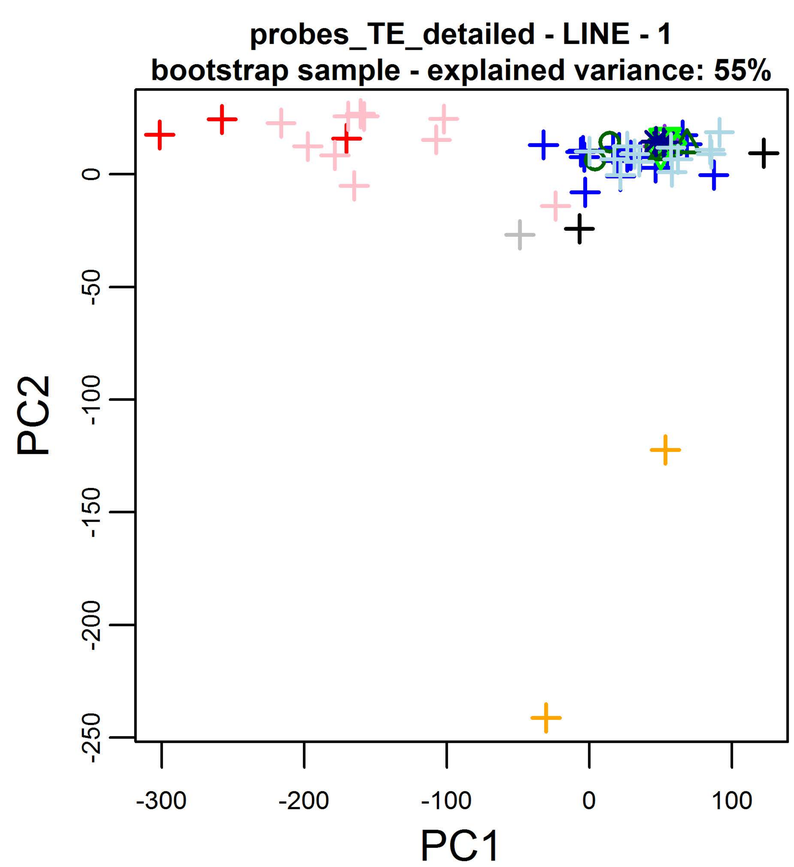

probes_TE_detailed - IslandAssociated - 1
bootstrap sample - explained variance: 37%
PC2
PC1
-400
-200
0
200
400
600
800
-400
-300
-200
-100
0
100
200

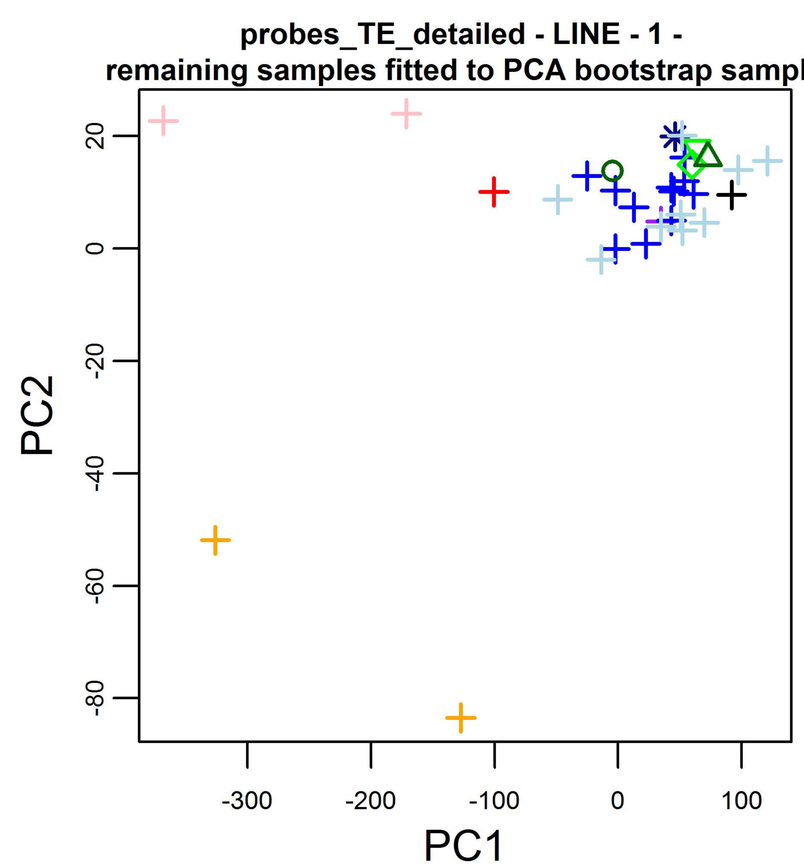

probes_TE_detailed - IslandAssociated - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-500
0
500
1000
-400
-200
0
200

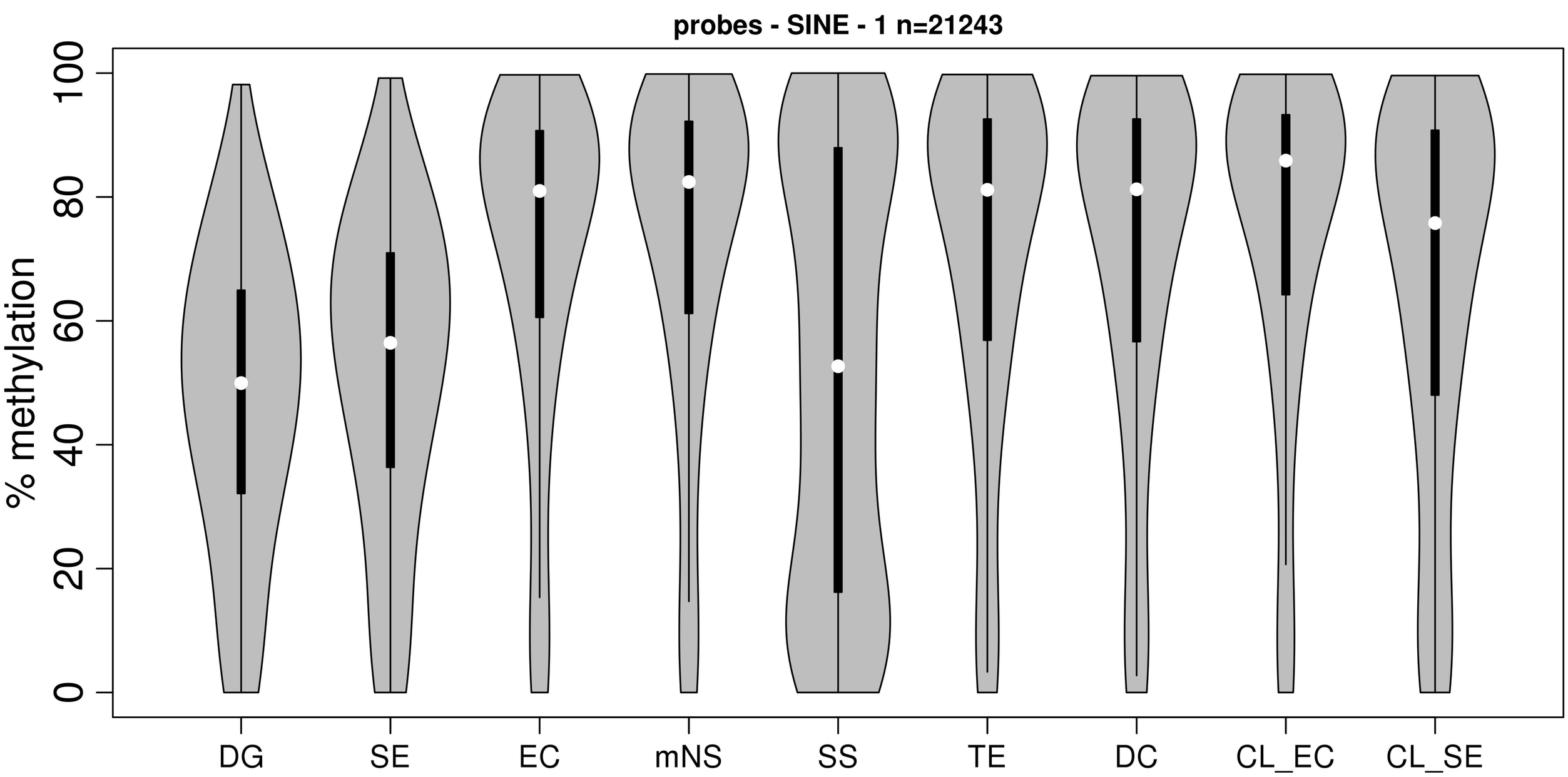

probes - LINE - 1 n=17984
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

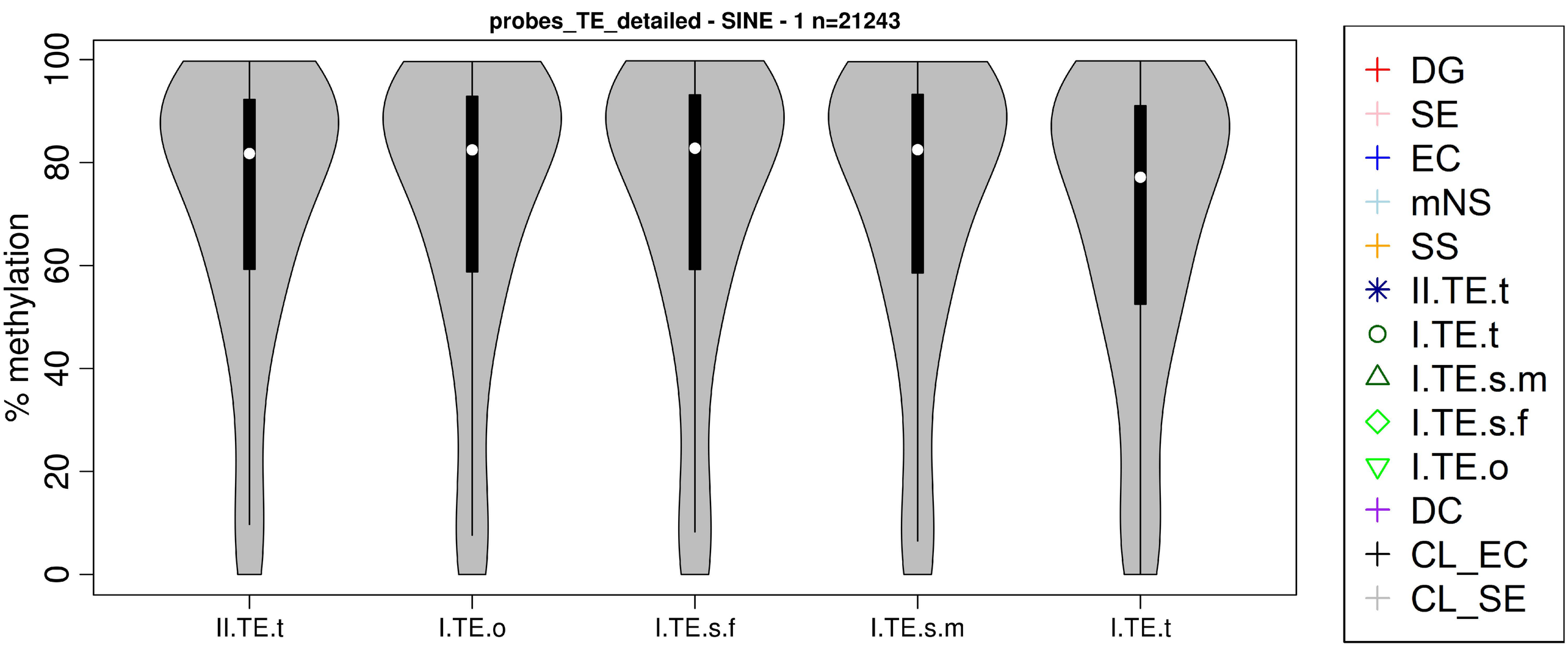

probes_TE_detailed - LINE - 1 n=17984
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

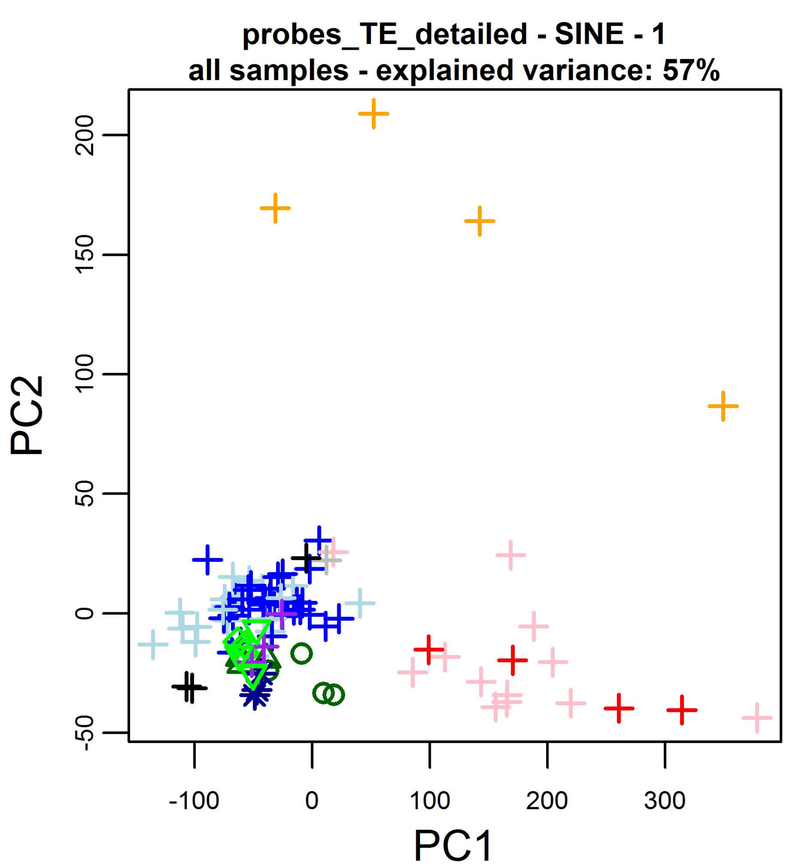

probes_TE_detailed - LINE - 1
all samples - explained variance: 57%
PC2
PC1
-50
0
50
100
-100
0
100
200
300

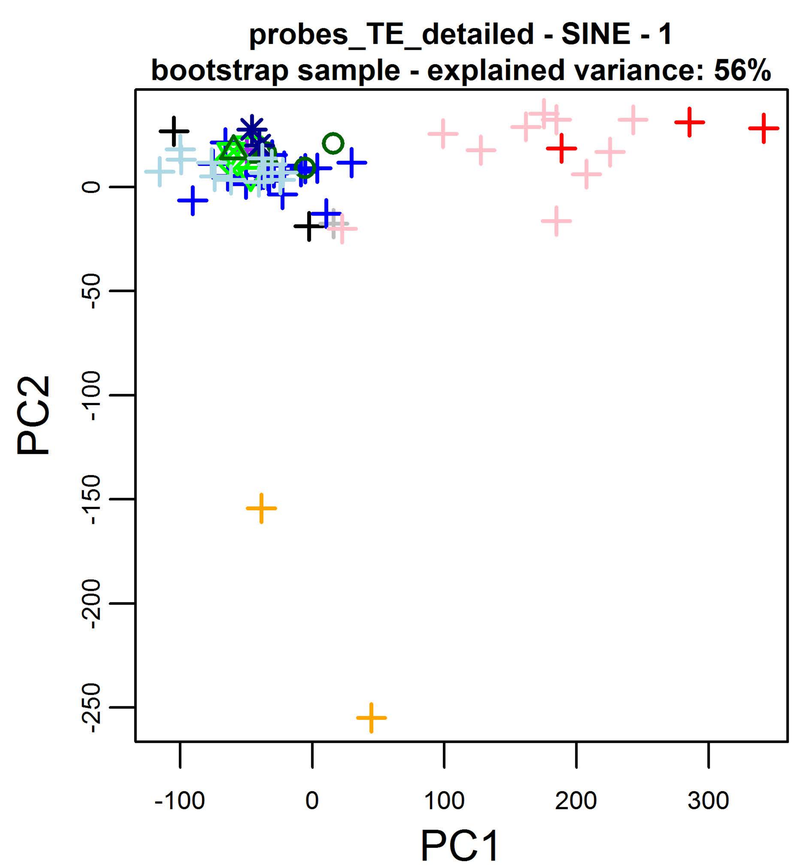

probes_TE_detailed - LINE - 1
bootstrap sample - explained variance: 55%
PC2
PC1
0
-50
-100
-150
-200
-250
-300
-200
-100
0
100

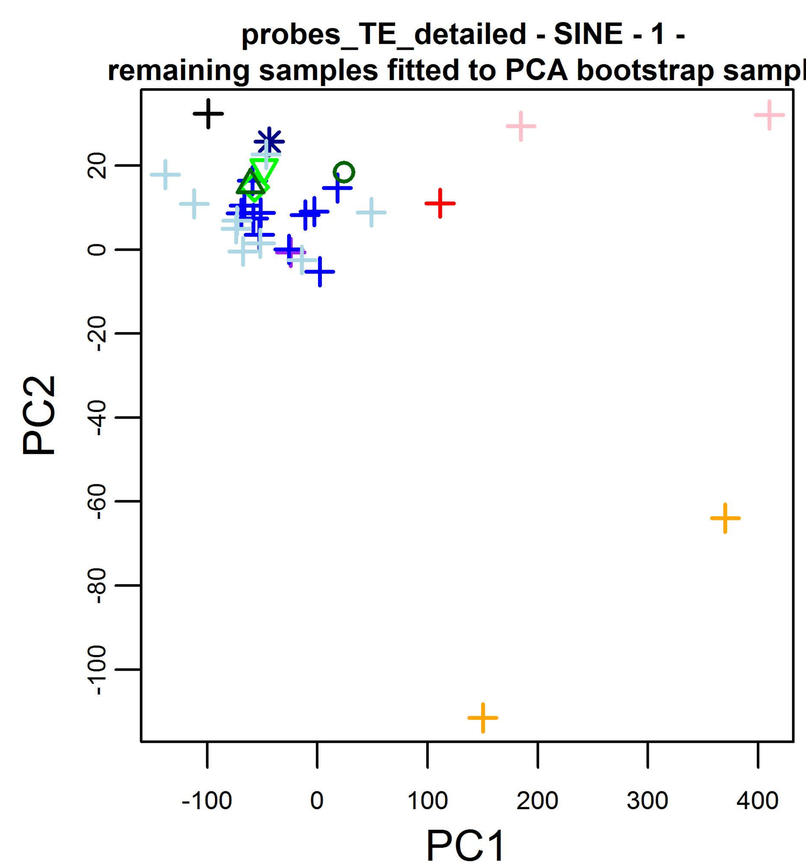

probes_TE_detailed - LINE - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
20
0
-20
-40
-60
-80
-300
-200
-100
0
100

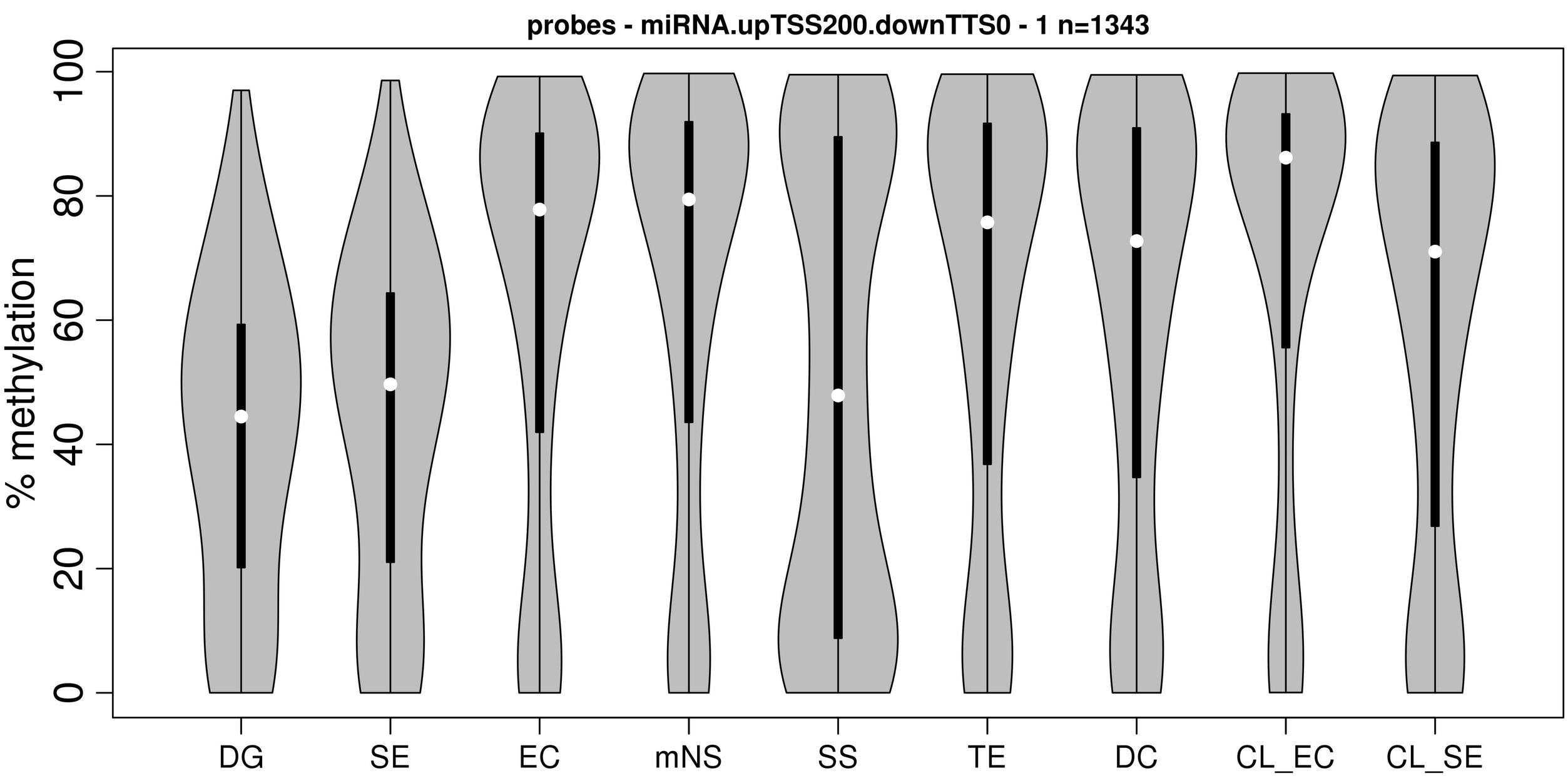

probes - SINE - 1 n=21243
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

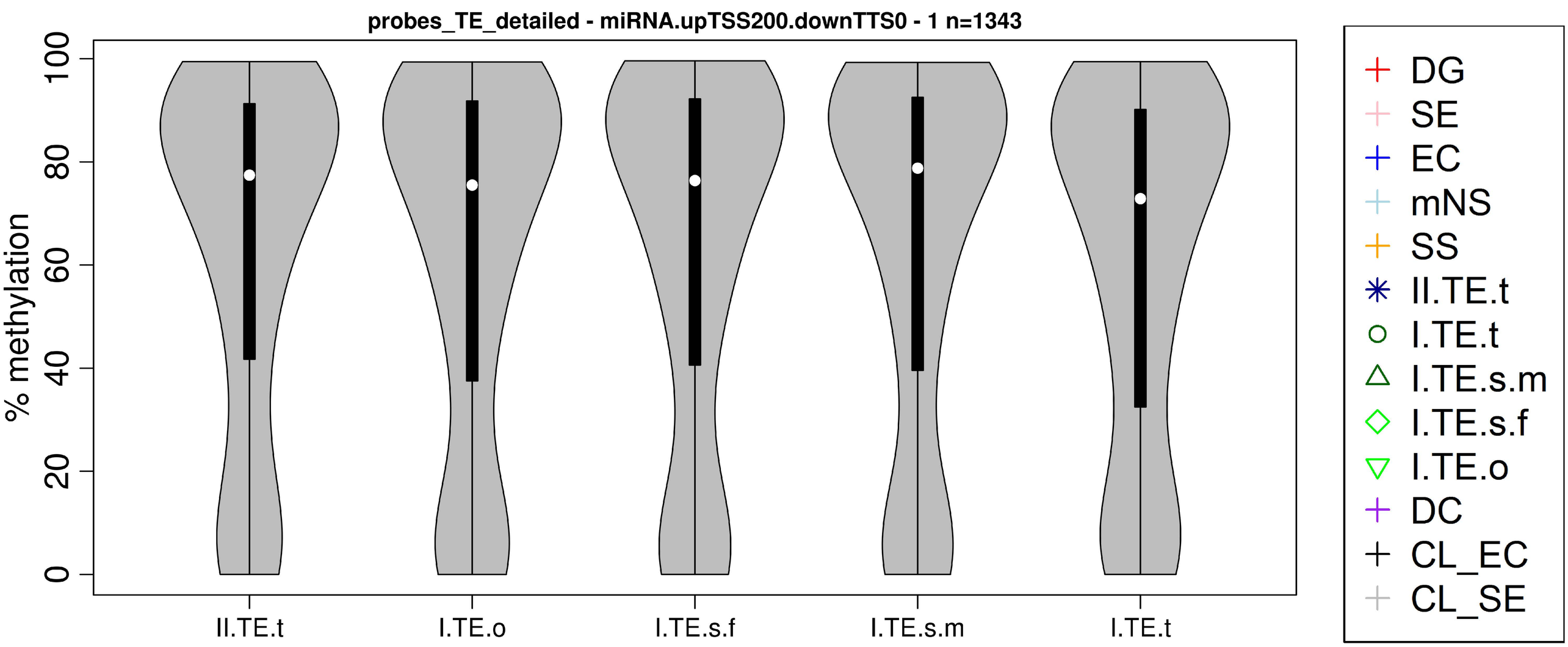

probes_TE_detailed - SINE - 1 n=21243
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

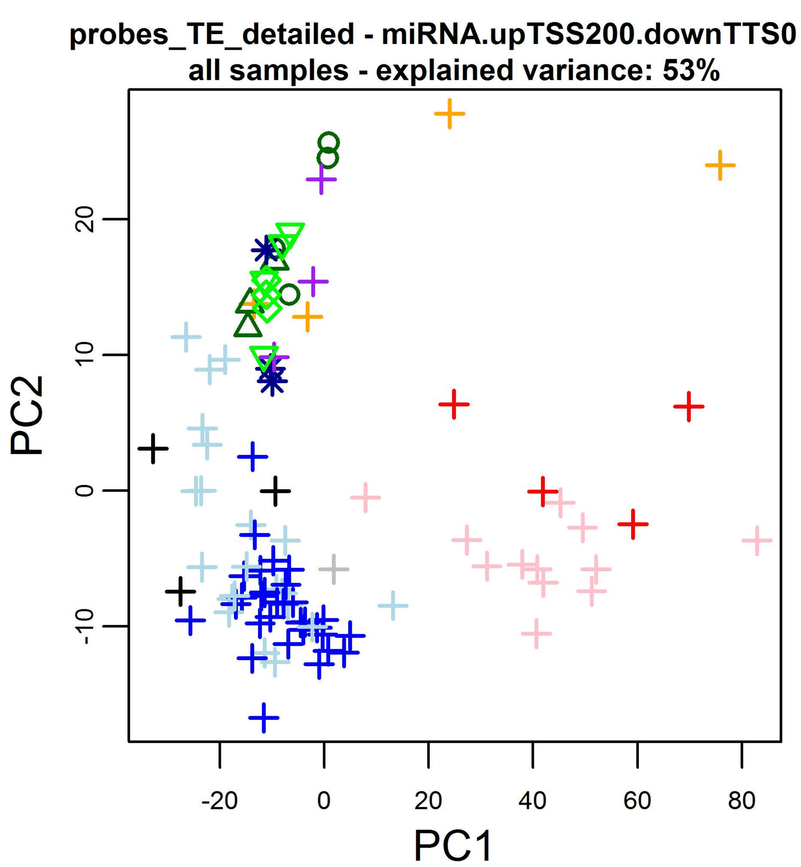

probes_TE_detailed - SINE - 1
all samples - explained variance: 57%
PC2
PC1
-50
0
50
100
150
200
-100
0
100
200
300

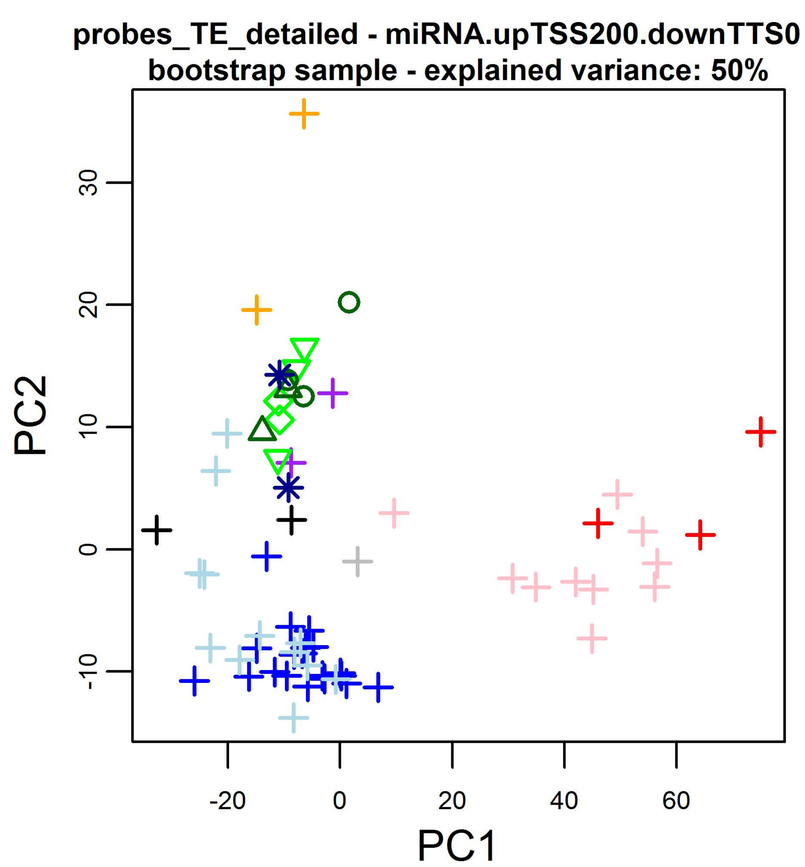

probes_TE_detailed - SINE - 1
bootstrap sample - explained variance: 56%
PC2
PC1
0
-50
-100
-150
-200
-250
-100
0
100
200
300

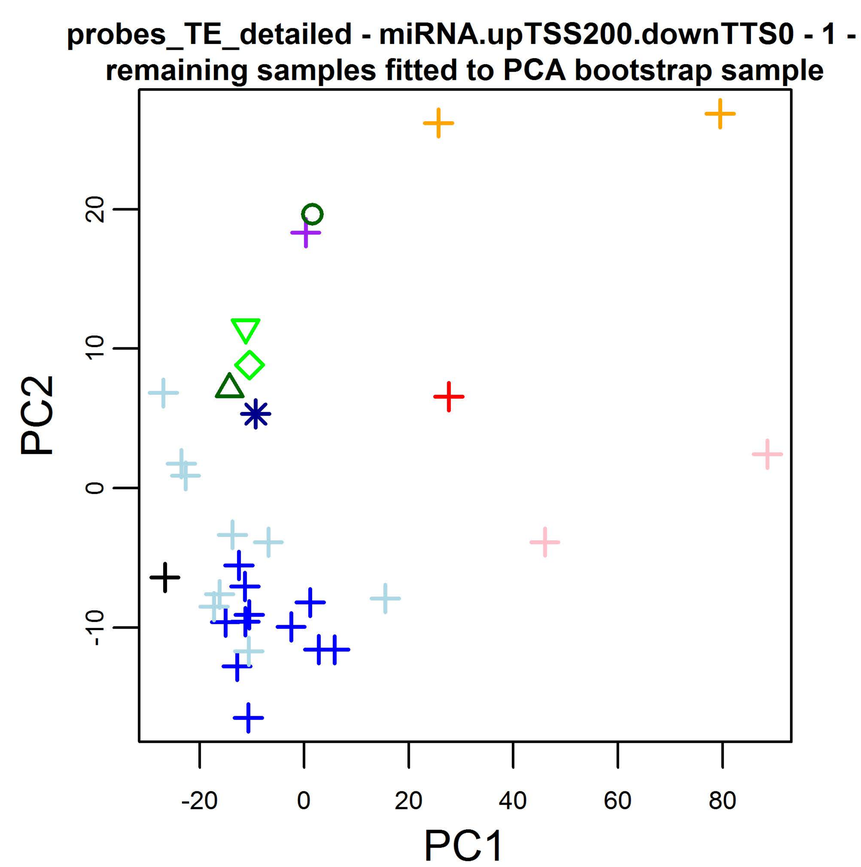

probes_TE_detailed - SINE - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
20
0
-20
-40
-60
-80
-100
-100
0
100
200
300
400

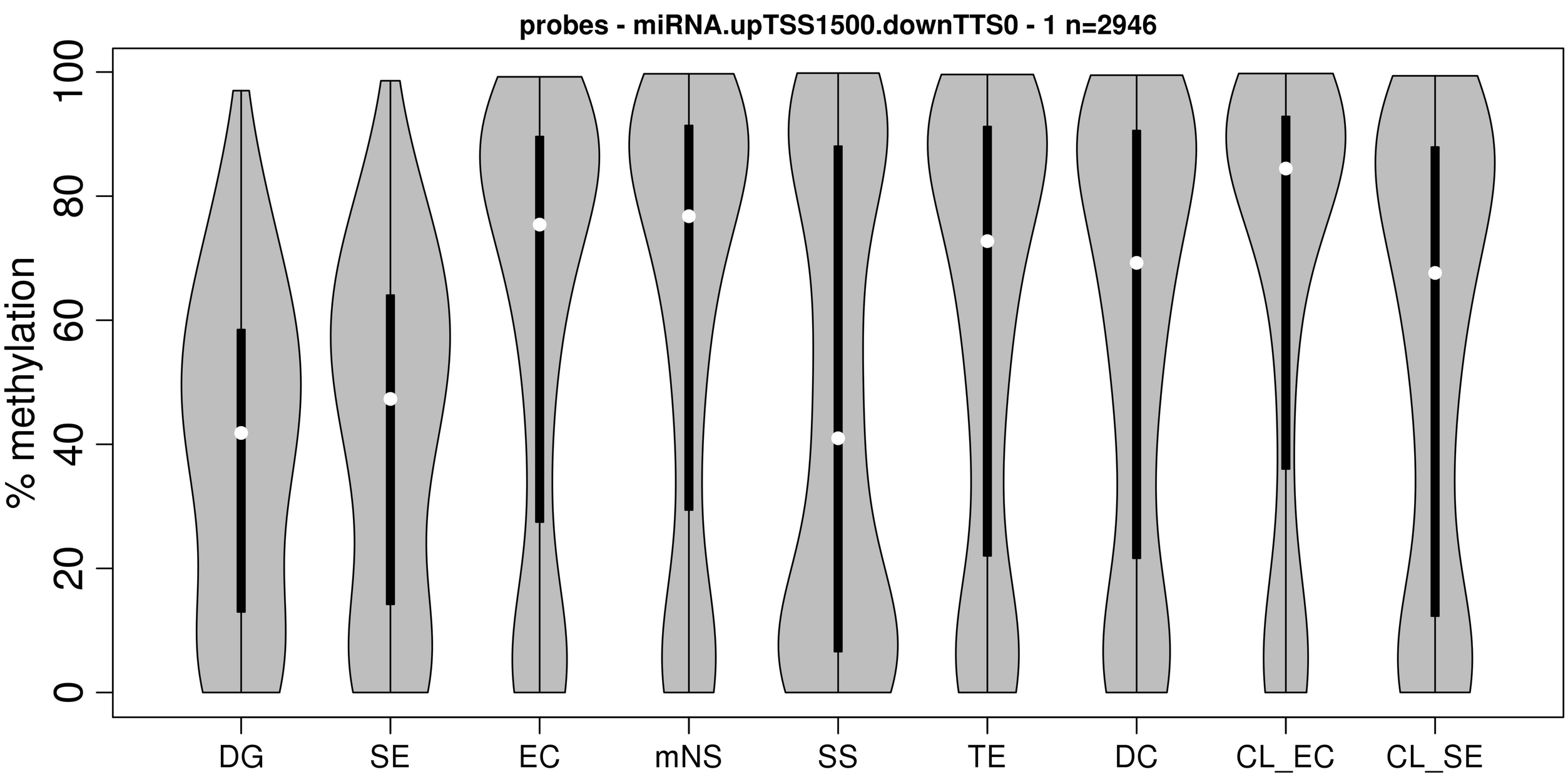

probes - miRNA.upTSS200.downTTS0 - 1 n=1343
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

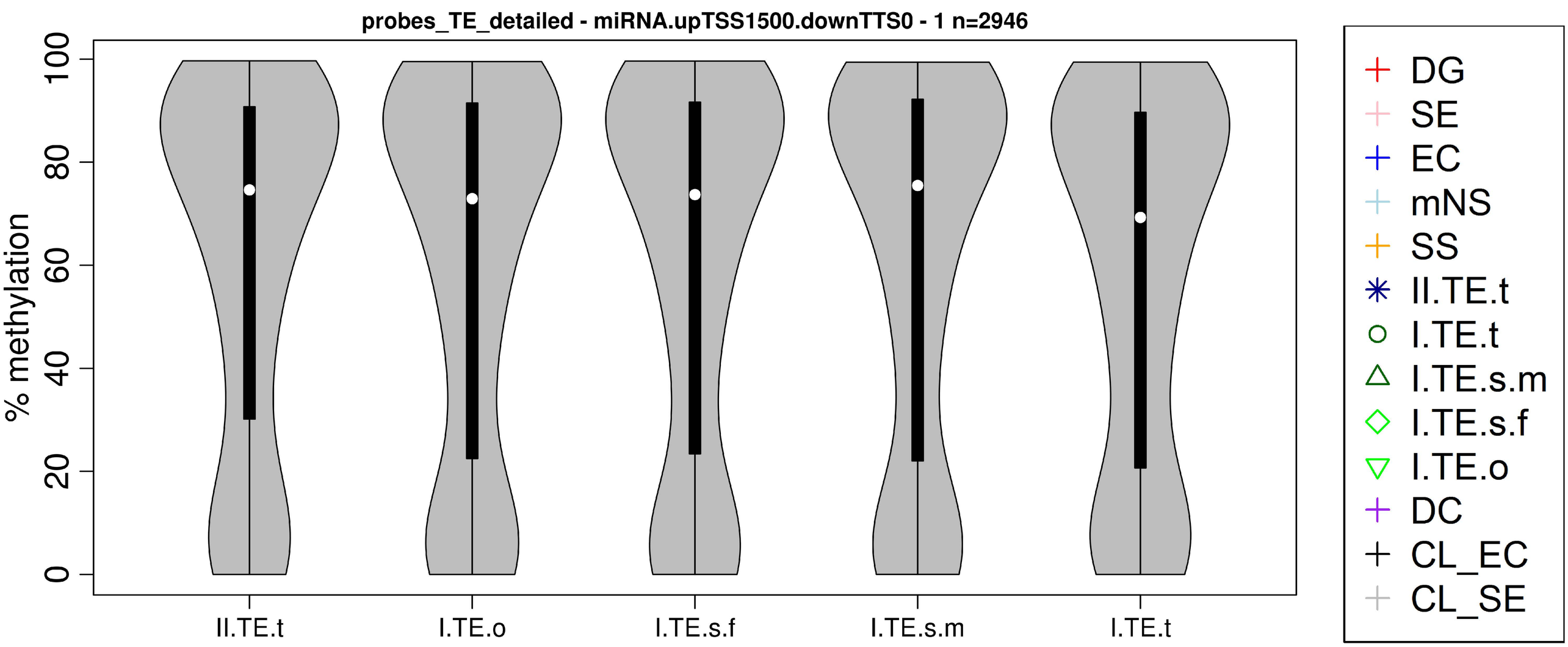

probes_TE_detailed - miRNA.upTSS200.downTTS0 - 1 n=1343
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

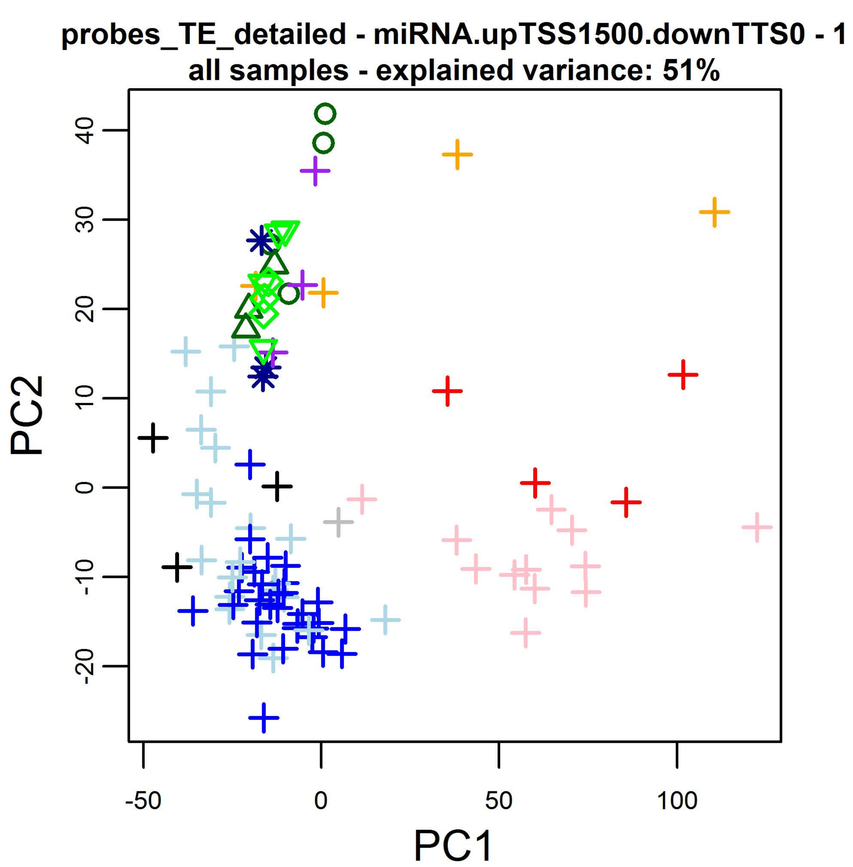

probes_TE_detailed - miRNA.upTSS200.downTTS0 - 1
all samples - explained variance: 53%
PC2
PC1
-20
0
20
40
60
80
-10
0
10
20

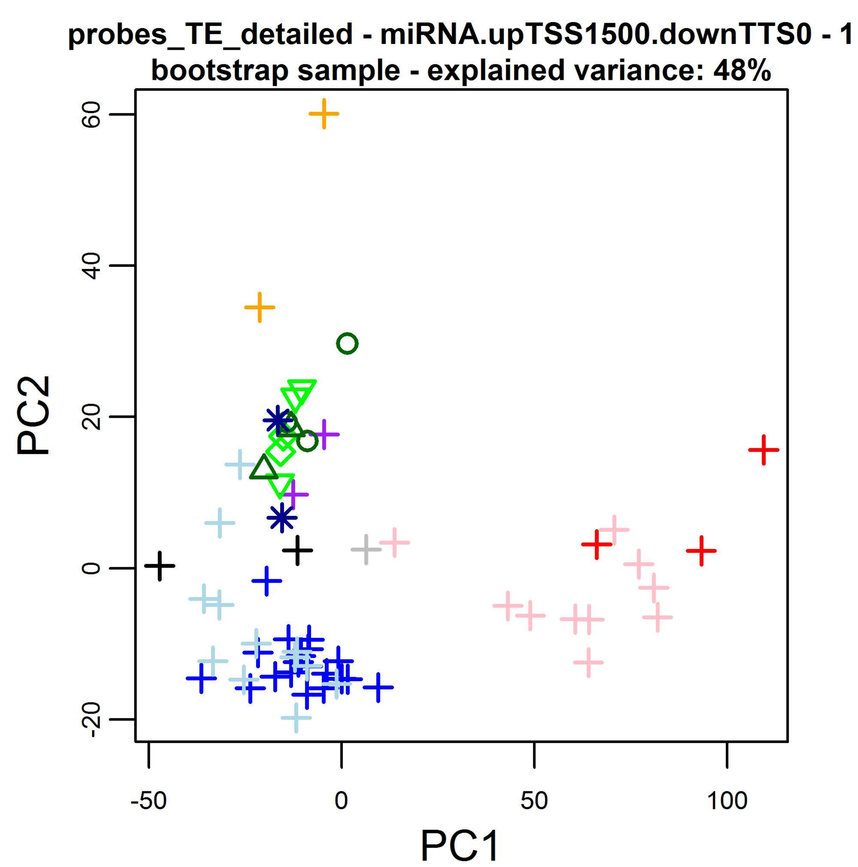

probes_TE_detailed - miRNA.upTSS200.downTTS0 - 1
bootstrap sample - explained variance: 50%
PC2
PC1
-20
0
20
40
60
-10
0
10
20
30

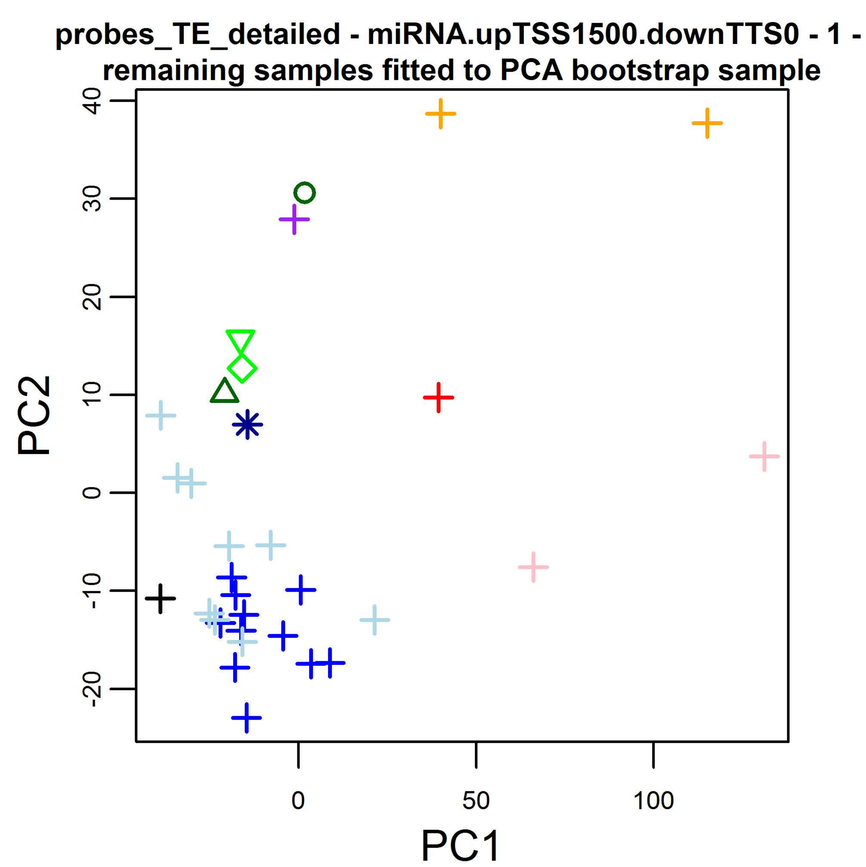

probes_TE_detailed - miRNA.upTSS200.downTTS0 - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-20
0
20
40
60
80
-10
0
10
20

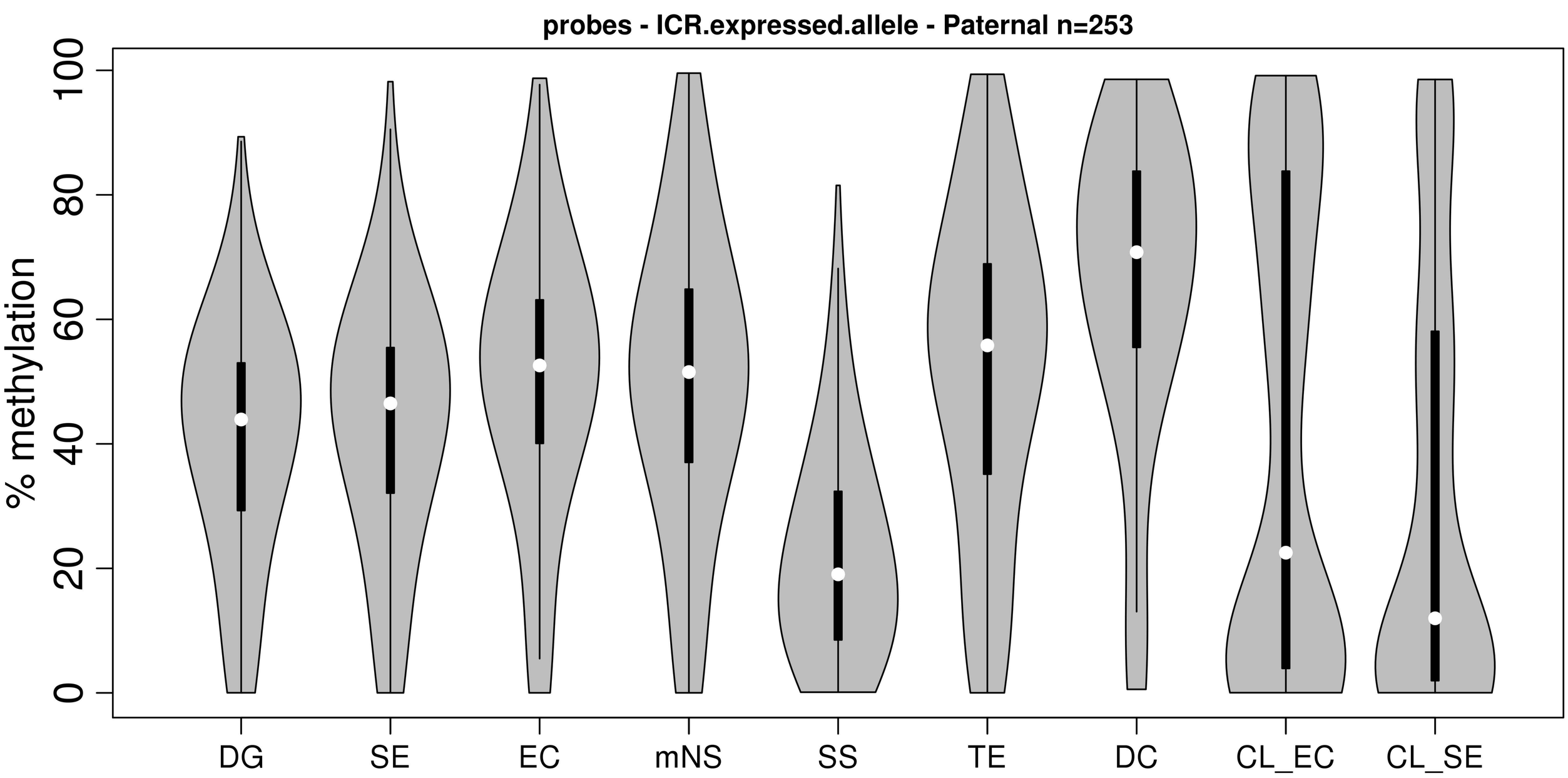

probes - miRNA.upTSS1500.downTTS0 - 1 n=2946
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

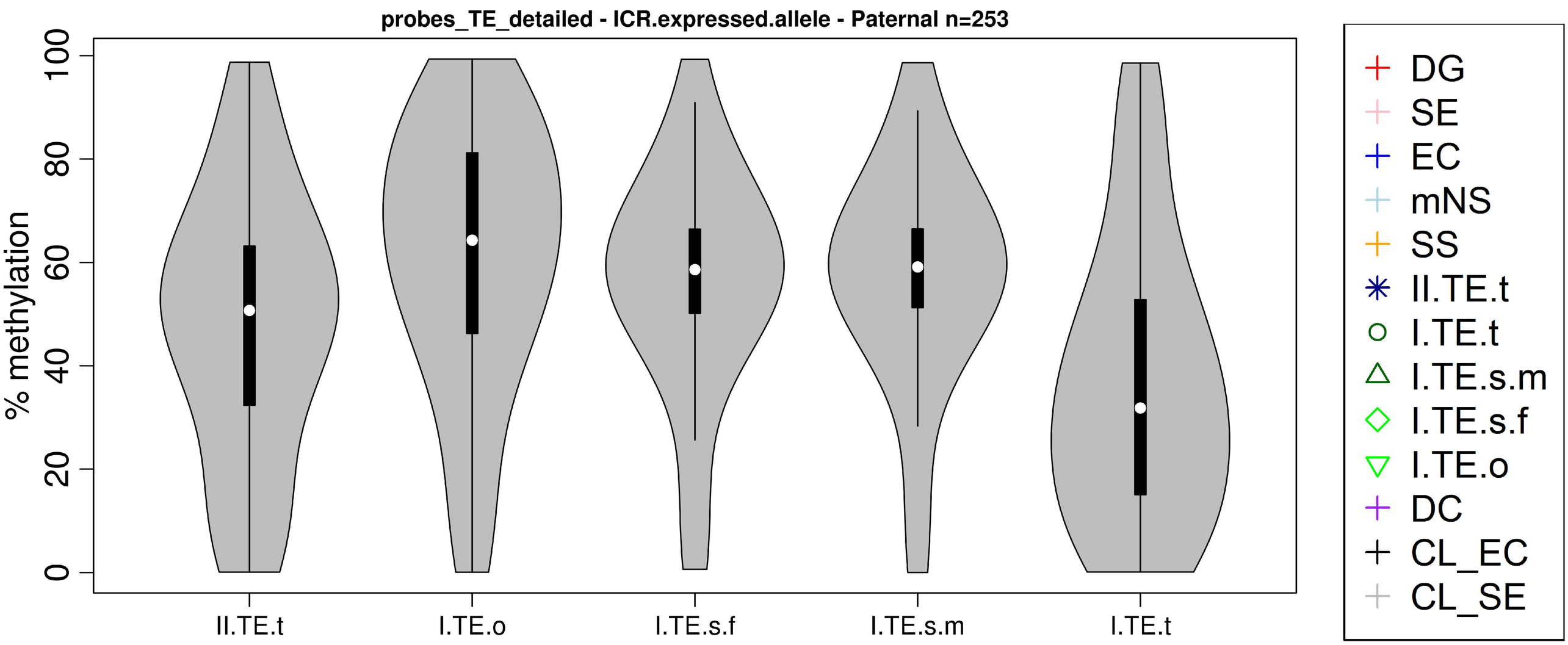

probes_TE_detailed - miRNA.upTSS1500.downTTS0 - 1 n=2946
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

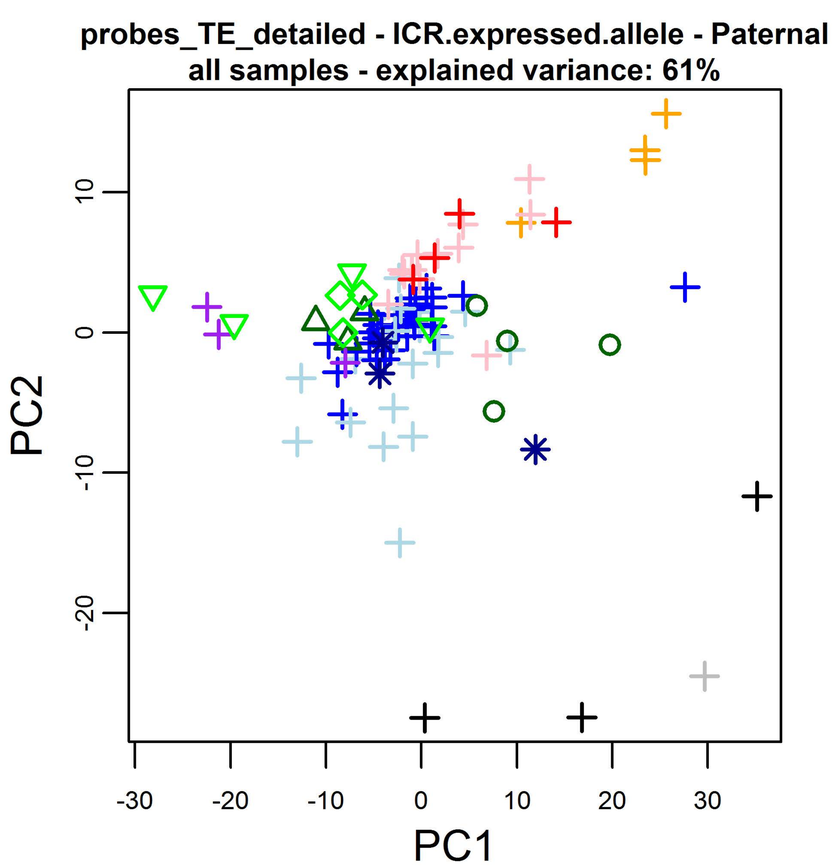

probes_TE_detailed - miRNA.upTSS1500.downTTS0 - 1
all samples - explained variance: 51%
PC2
PC1
-50
0
50
100
-20
-10
0
10
20
30
40

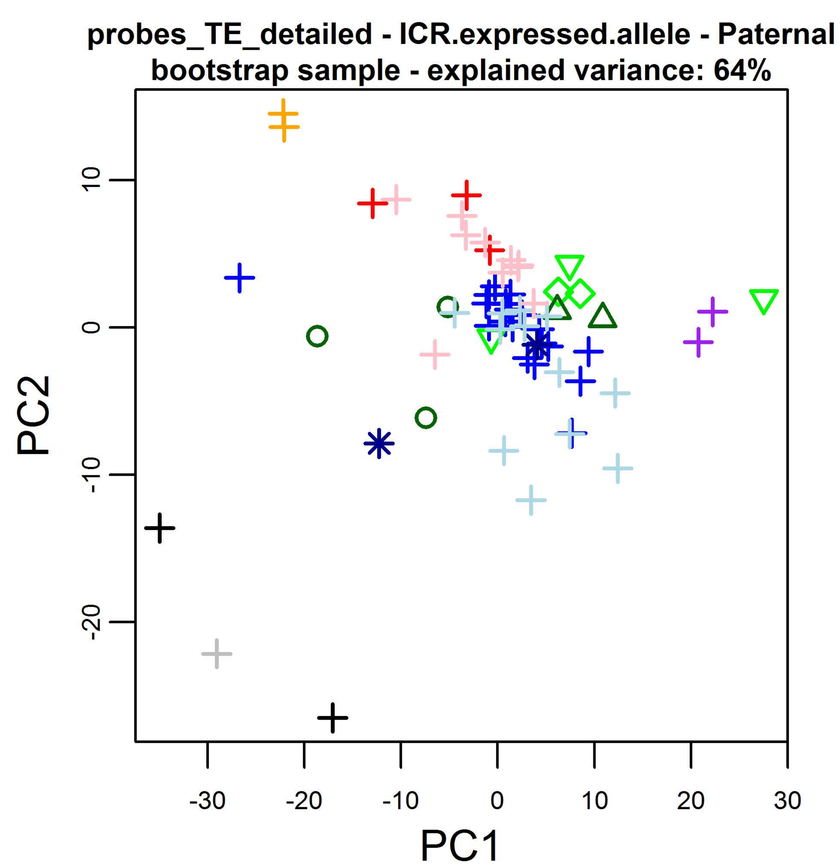

probes_TE_detailed - miRNA.upTSS1500.downTTS0 - 1
bootstrap sample - explained variance: 48%
PC2
PC1
-50
0
50
100
-20
0
20
40
60

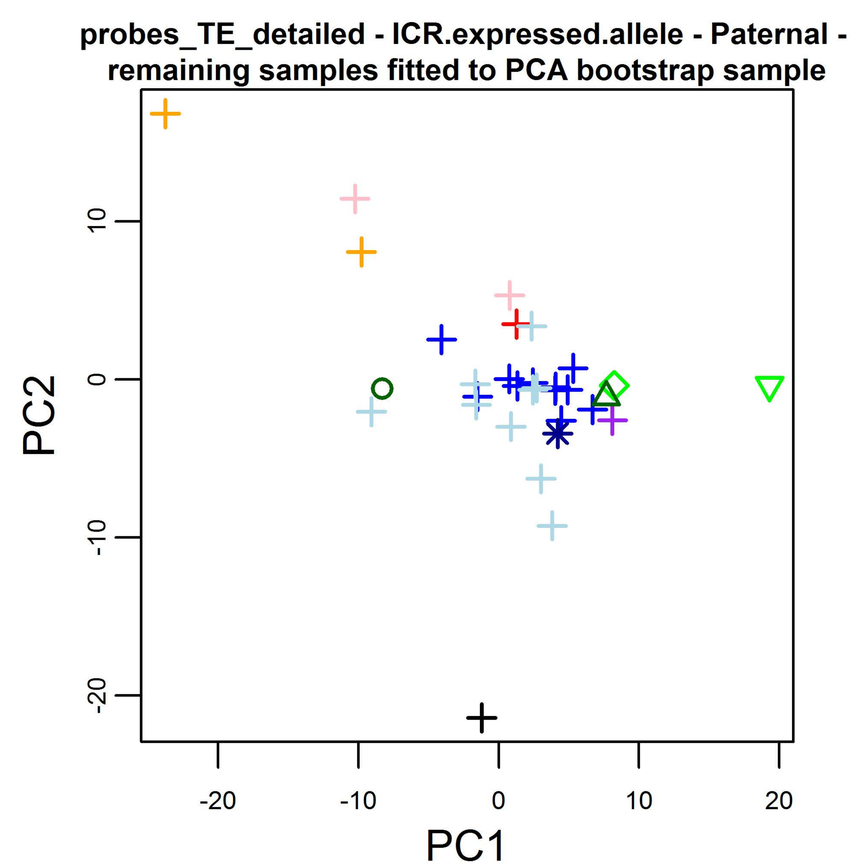

probes_TE_detailed - miRNA.upTSS1500.downTTS0 - 1 -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
0
50
100
-20
-10
0
10
20
30
40

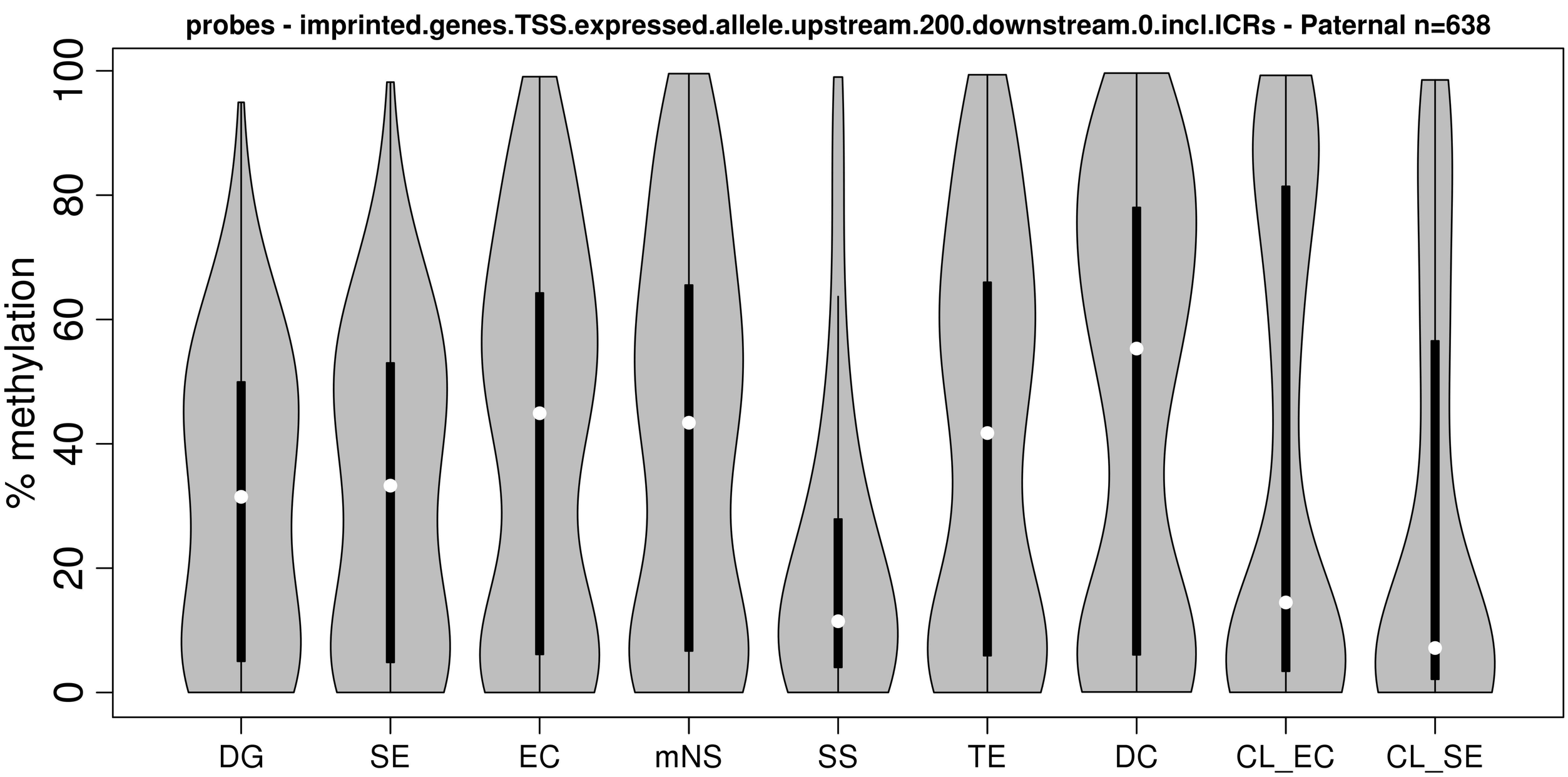

probes - ICR.expressed.allele - Paternal n=253
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

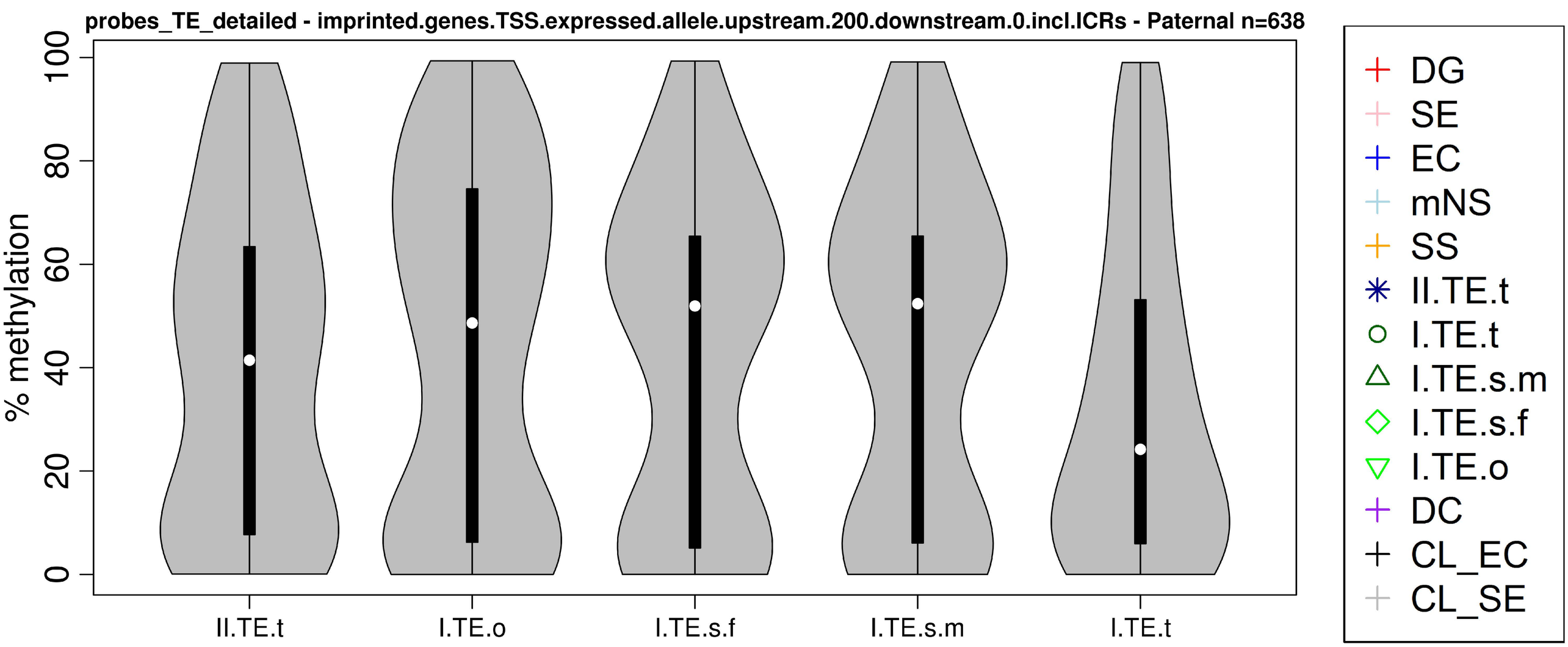

probes_TE_detailed - ICR.expressed.allele - Paternal n=253
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

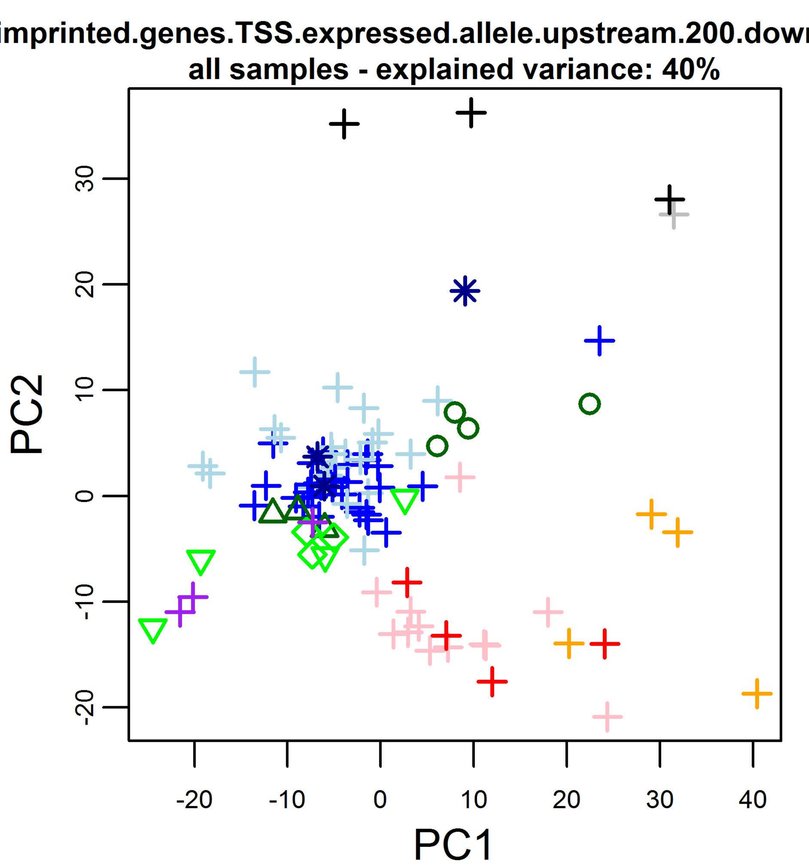

probes_TE_detailed - ICR.expressed.allele - Paternal
all samples - explained variance: 61%
PC2
PC1
-30
-20
-10
0
10
20
30

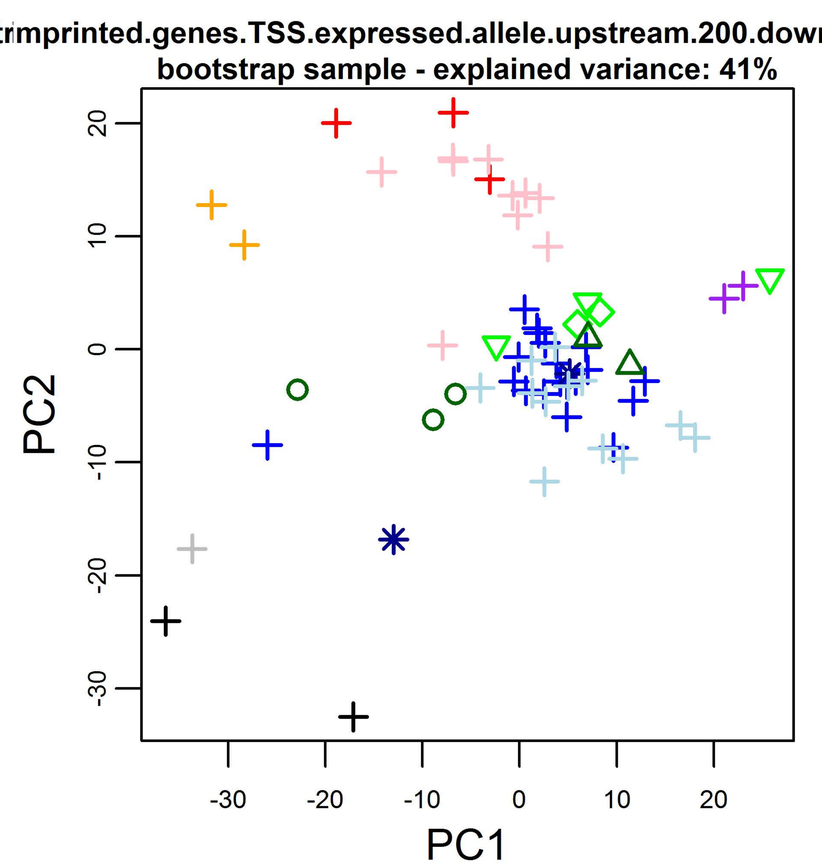

probes_TE_detailed - ICR.expressed.allele - Paternal
bootstrap sample - explained variance: 64%
PC2
PC1
-30
-20
-10
0
10
20
30

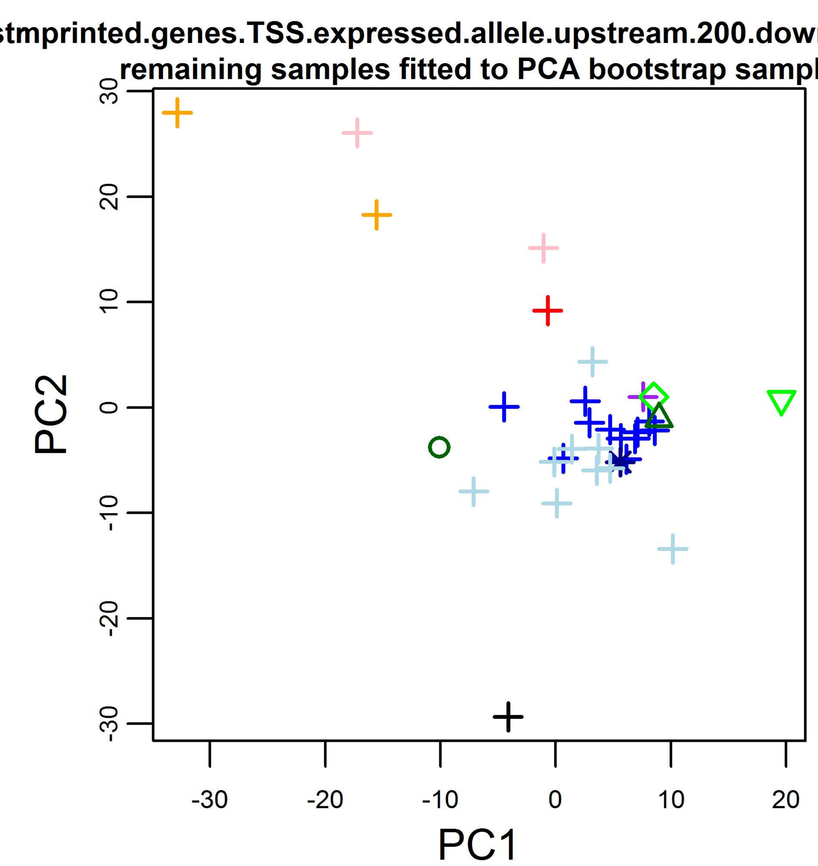

probes_TE_detailed - ICR.expressed.allele - Paternal -
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-20
-10
0
10
20

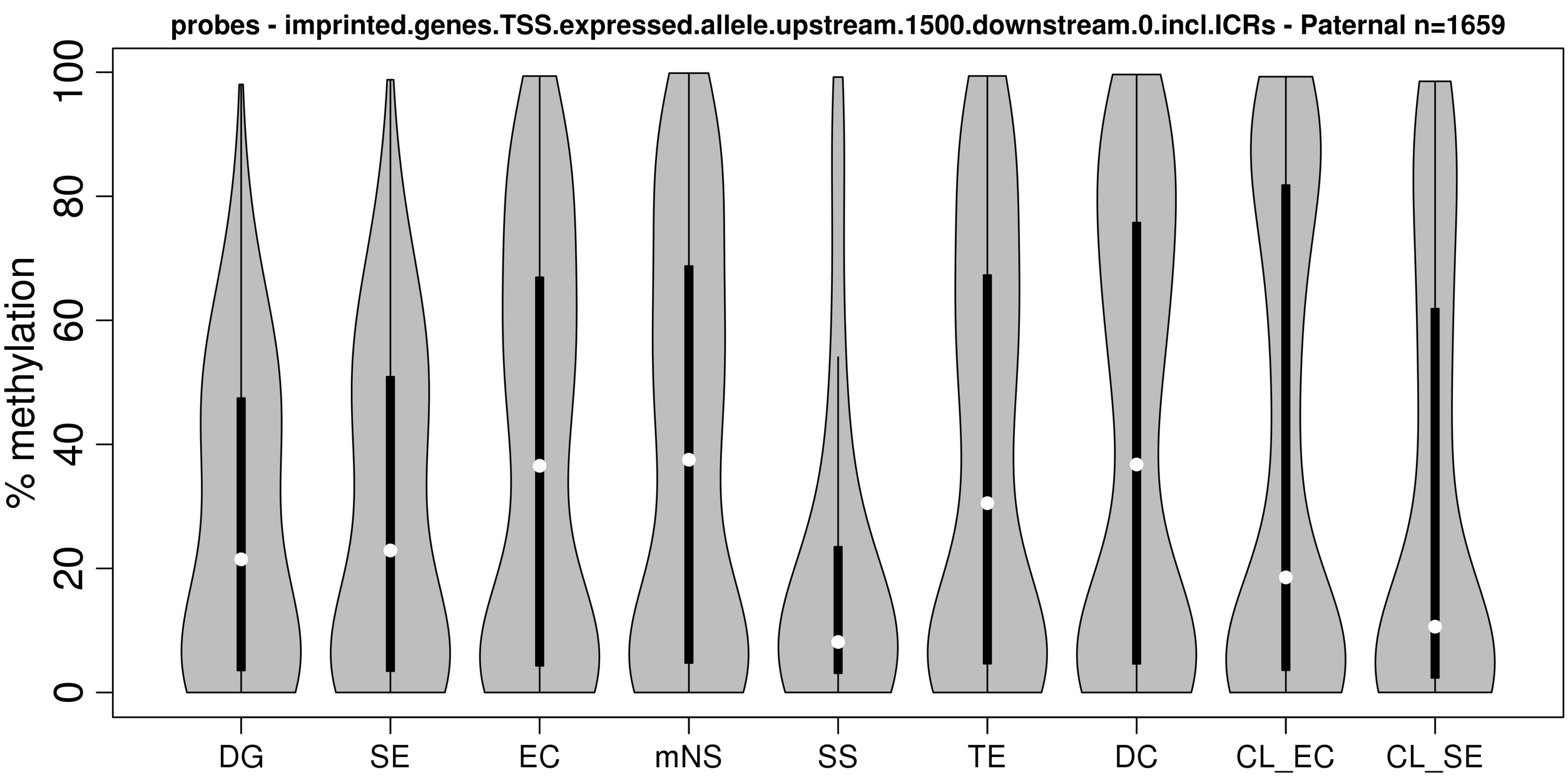

probes - imprinted.genes.TSS.expressed.allele.upstream.200.downstream.0.incl.ICRs - Paternal n=638
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

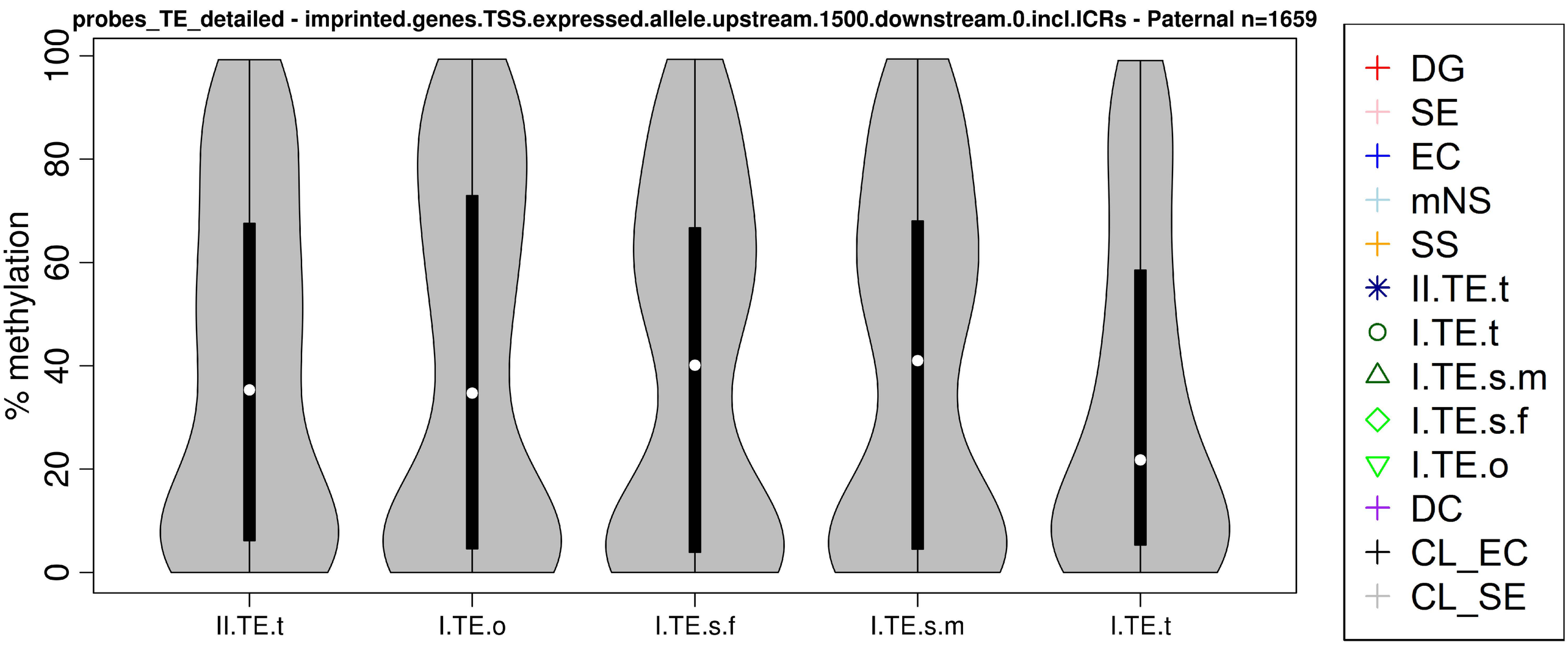

probes_TE_detailed - imprinted.genes.TSS.expressed.allele.upstream.200.downstream.0.incl.ICRs - Paternal n=638
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

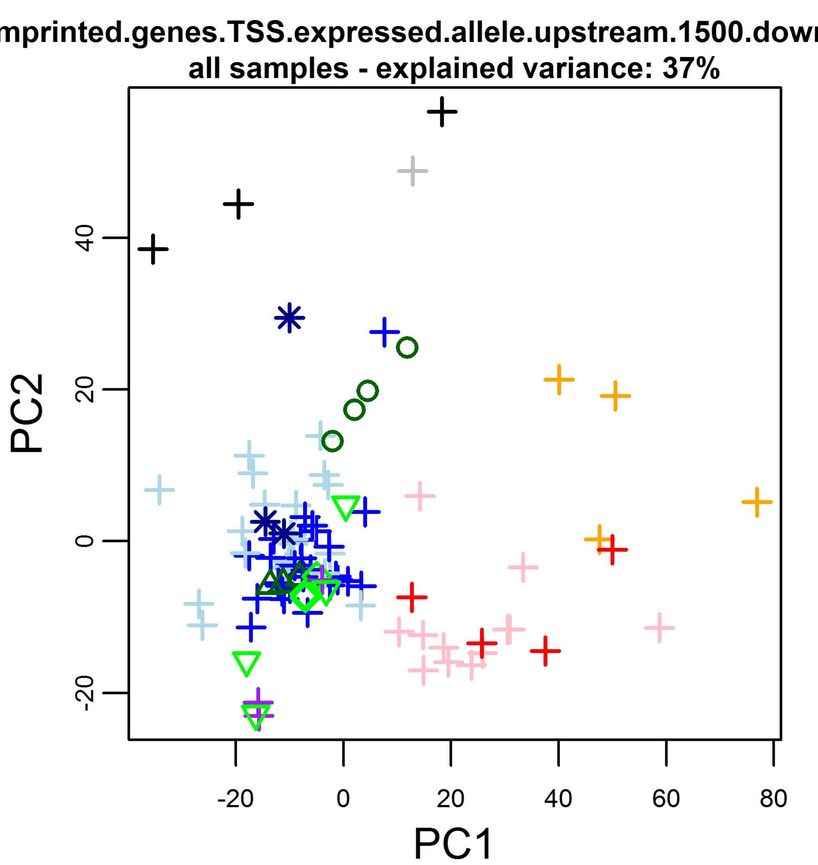

imprinted.genes.TSS.expressed.allele.upstream.200.downstr
all samples - explained variance: 40%
PC2
PC1

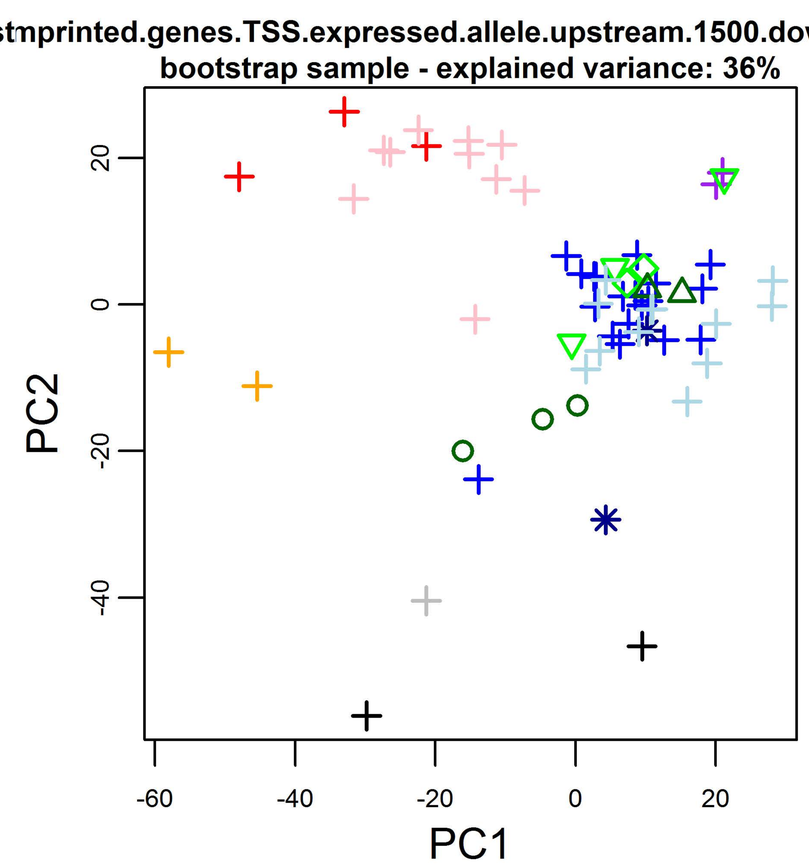

imprinted.genes.TSS.expressed.allele.upstream.200.downstm
bootstrap sample - explained variance: 41%
PC2
PC1

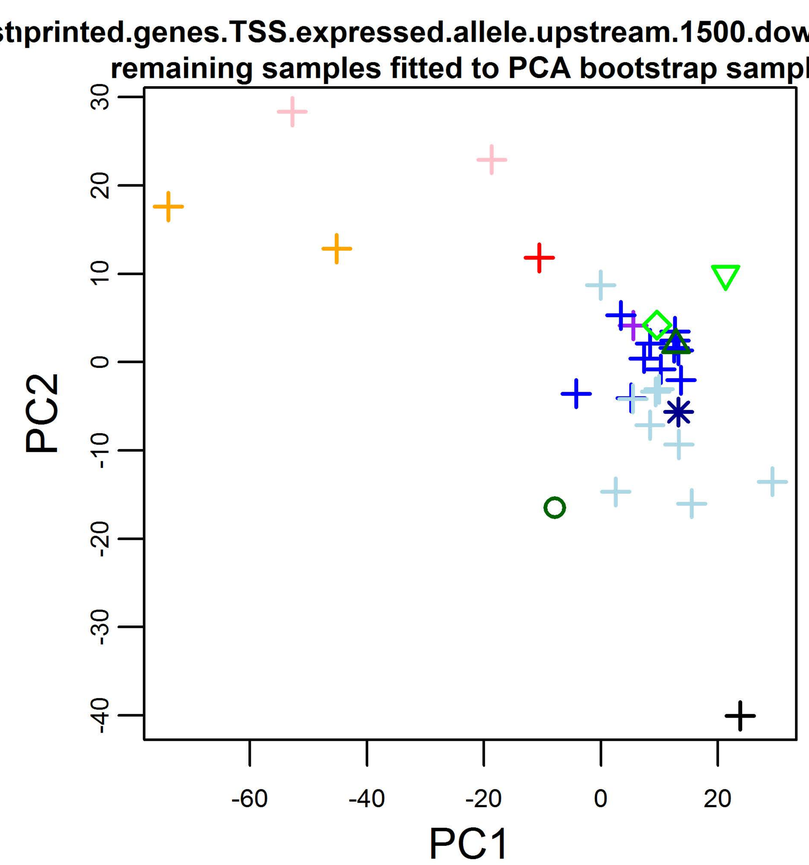

imprinted.genes.TSS.expressed.allele.upstream.200.downstre
remaining samples fitted to PCA bootstrap sample
PC2
PC1

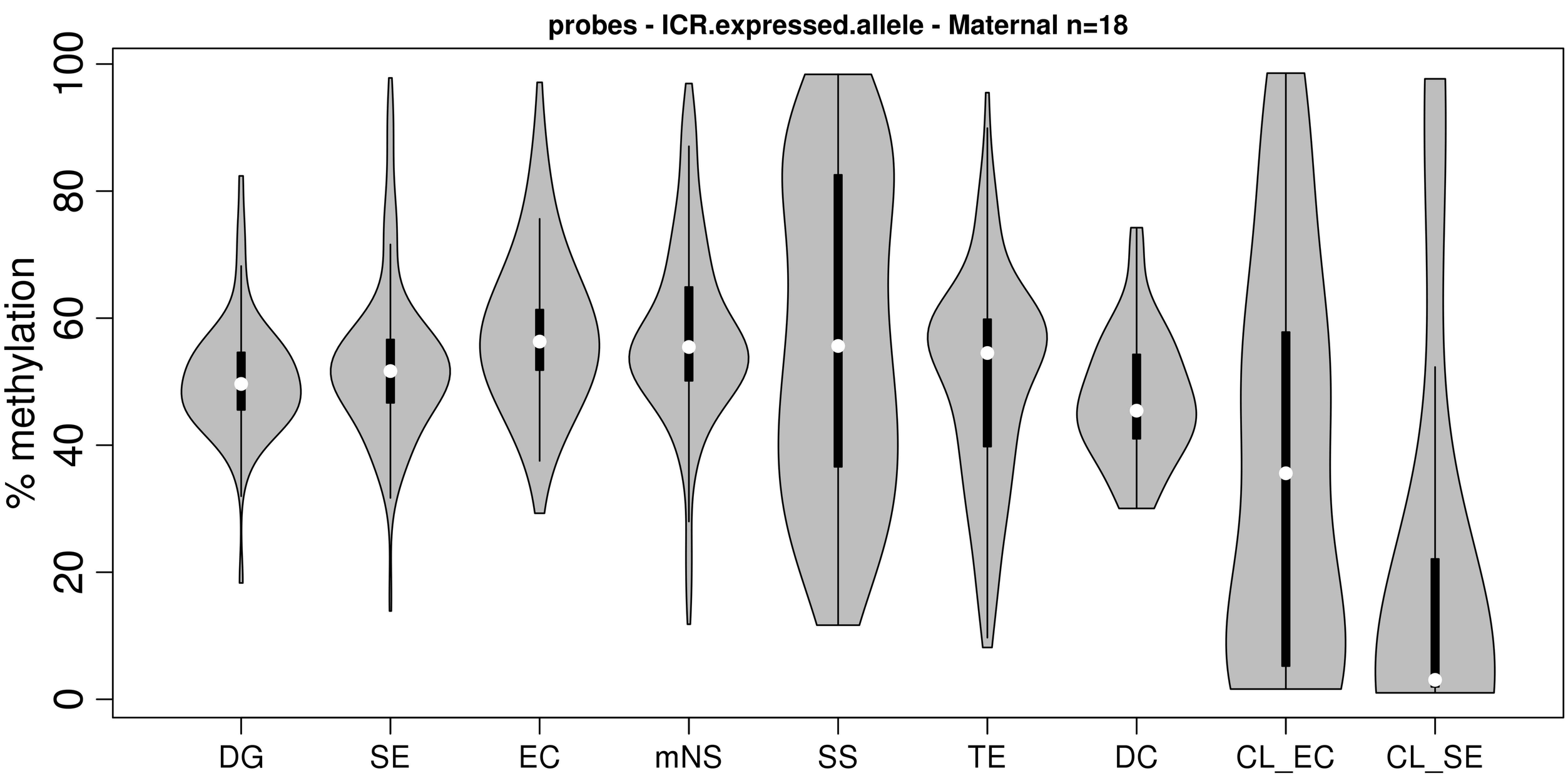

probes - imprinted.genes.TSS.expressed.allele.upstream.1500.downstream.0.incl.ICRs - Paternal n=1659
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

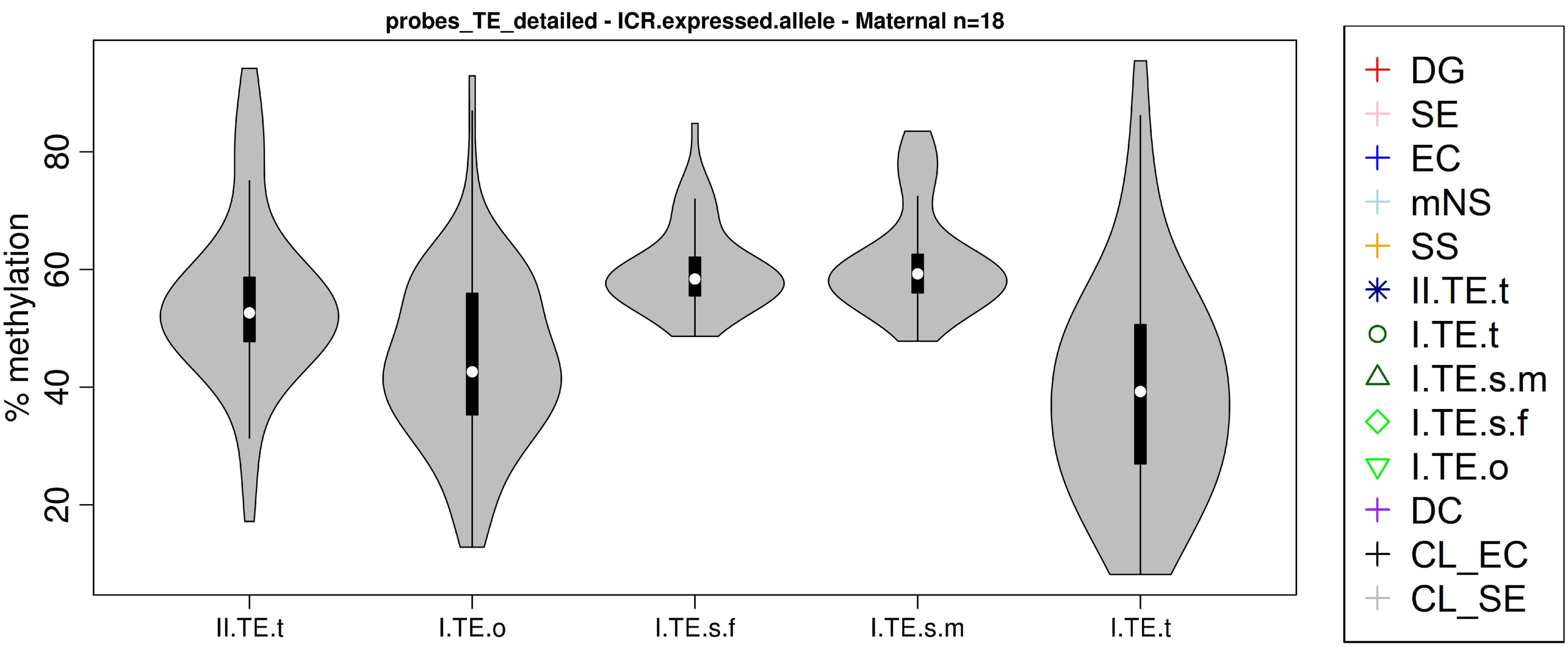

probes_TE_detailed - imprinted.genes.TSS.expressed.allele.upstream.1500.downstream.0.incl.ICRs - Paternal n=1659
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

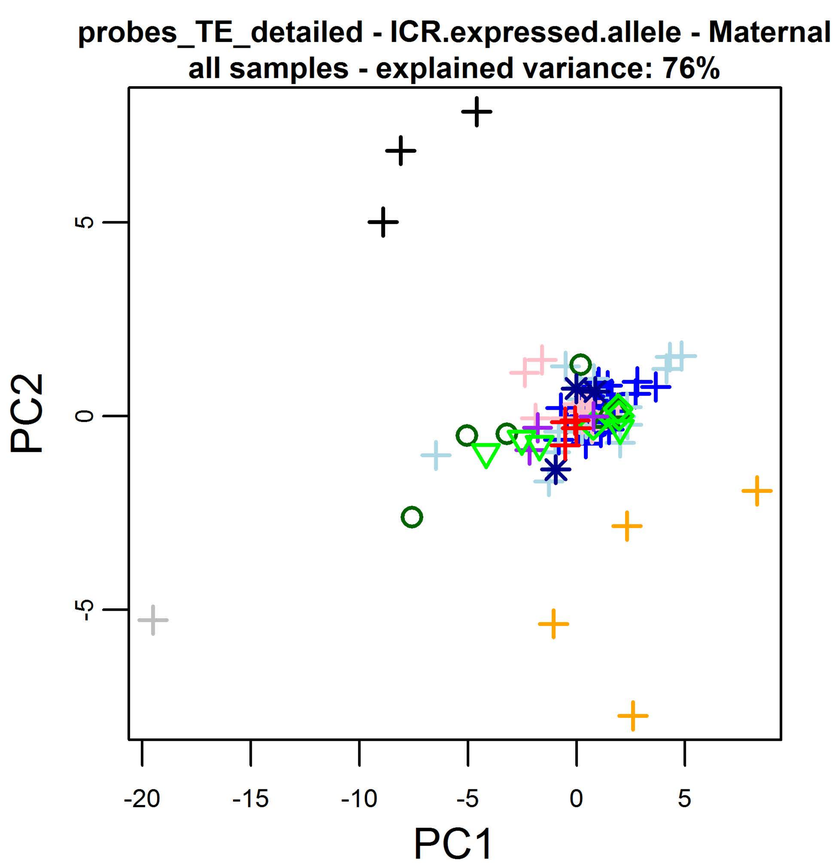

mprinted.genes.TSS.expressed.allele.upstream.1500.downst
all samples - explained variance: 37%
PC2
PC1
-20
0
20
40
60
80

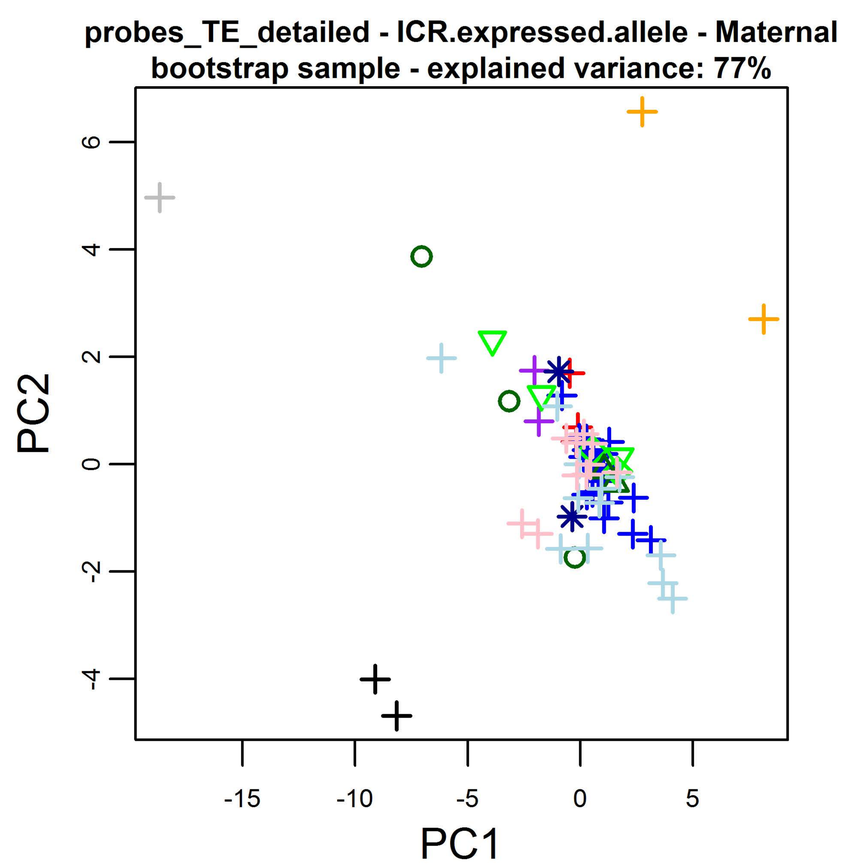

mprinted.genes.TSS.expressed.allele.upstream.1500.downst
bootstrap sample - explained variance: 36%
PC2
PC1
-60
-40
-20
0
20

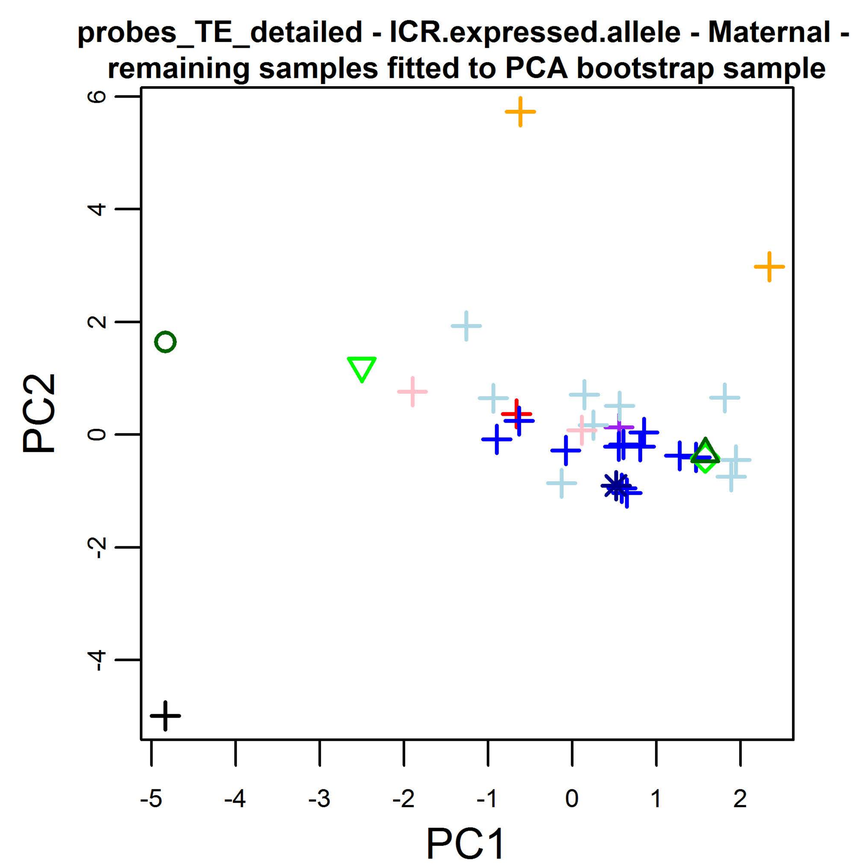

mprinted.genes.TSS.expressed.allele.upstream.1500.downstr
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-60
-40
-20
0
20
30
10
-10
-30

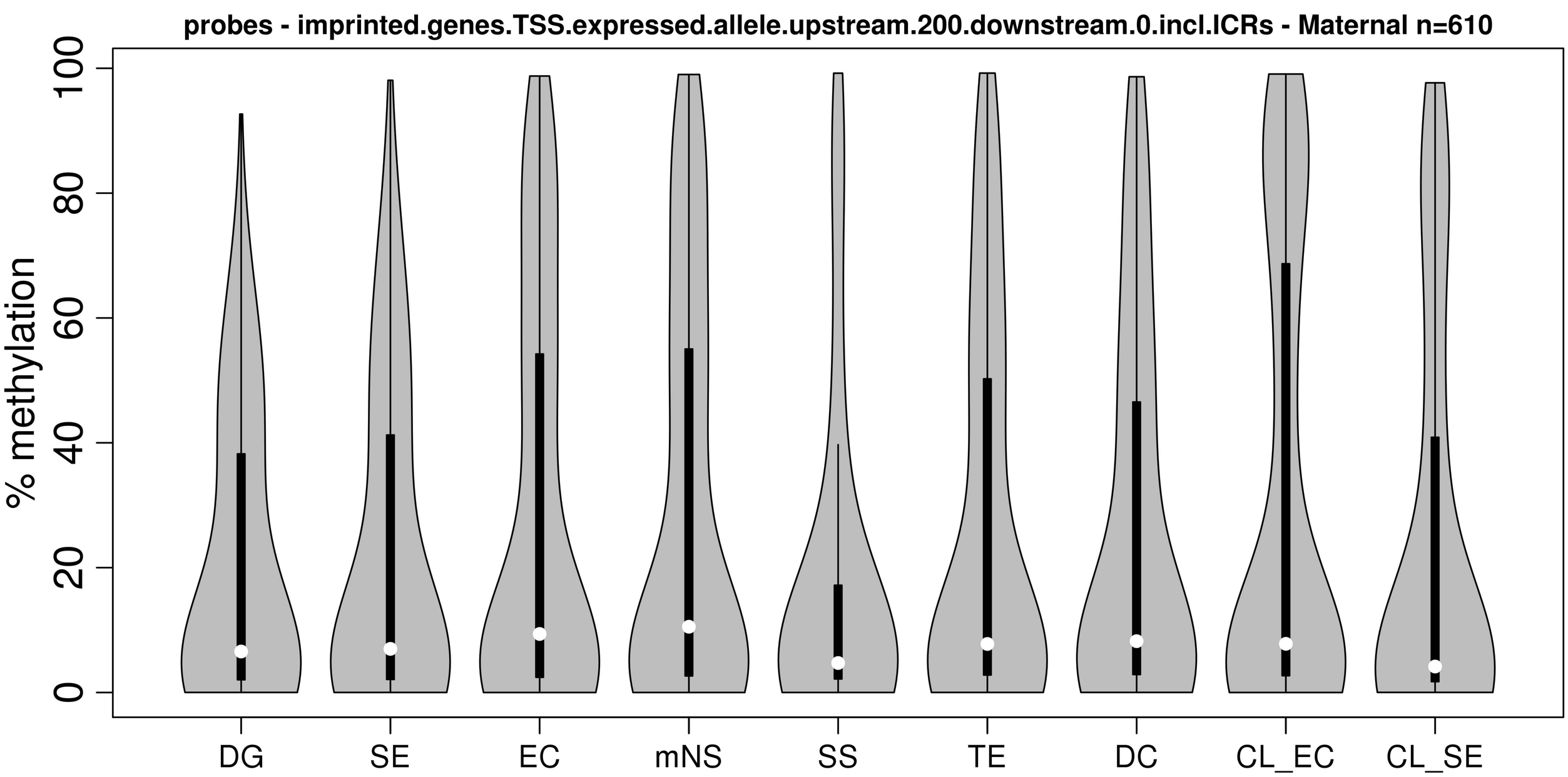

probes - ICR.expressed.allele - Maternal n=18
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

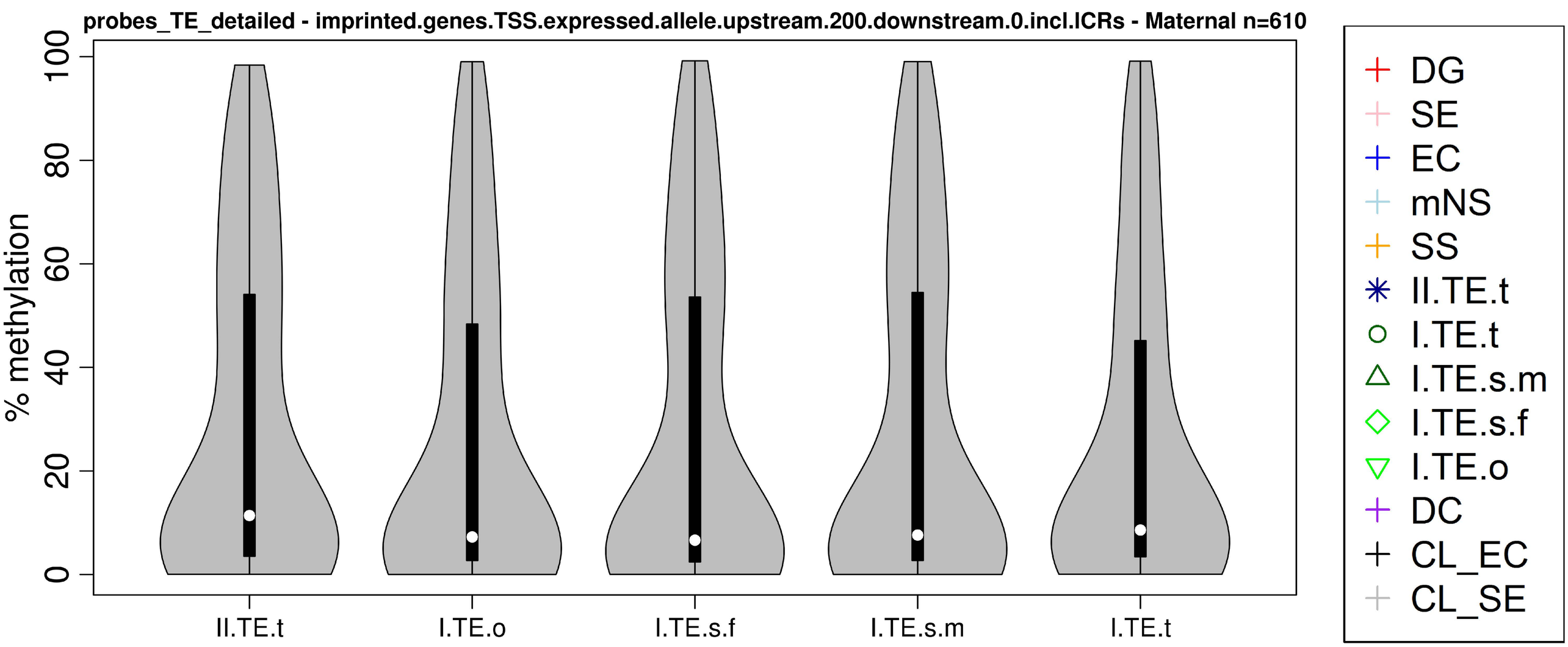

probes_TE_detailed - ICR.expressed.allele - Maternal n=18
% methylation
20
40
60
80
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

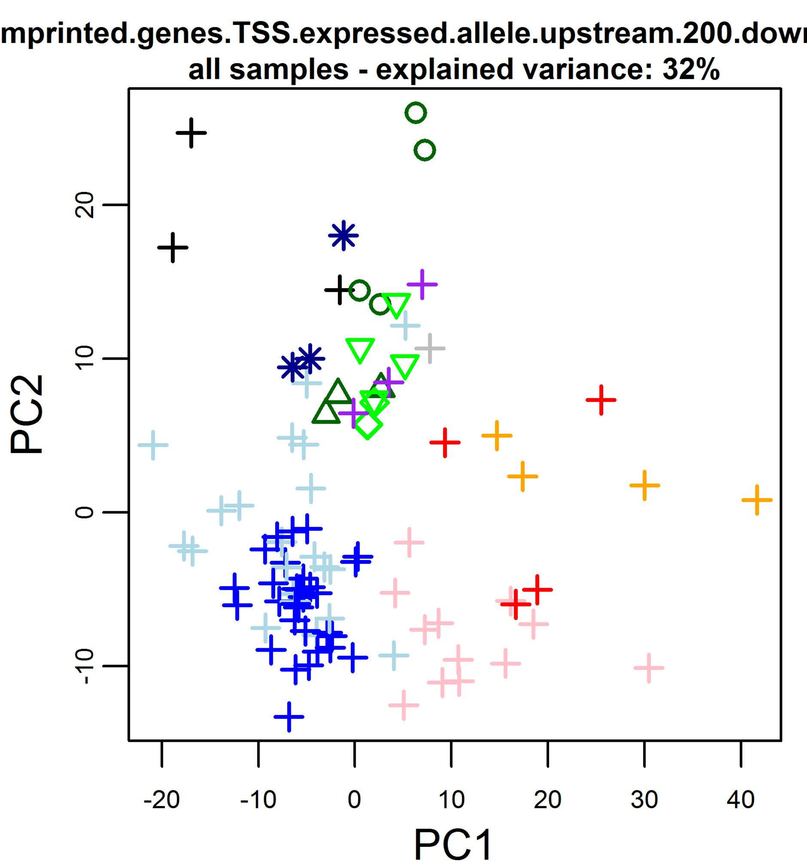

probes_TE_detailed - ICR.expressed.allele - Maternal
all samples - explained variance: 76%
PC2
PC1

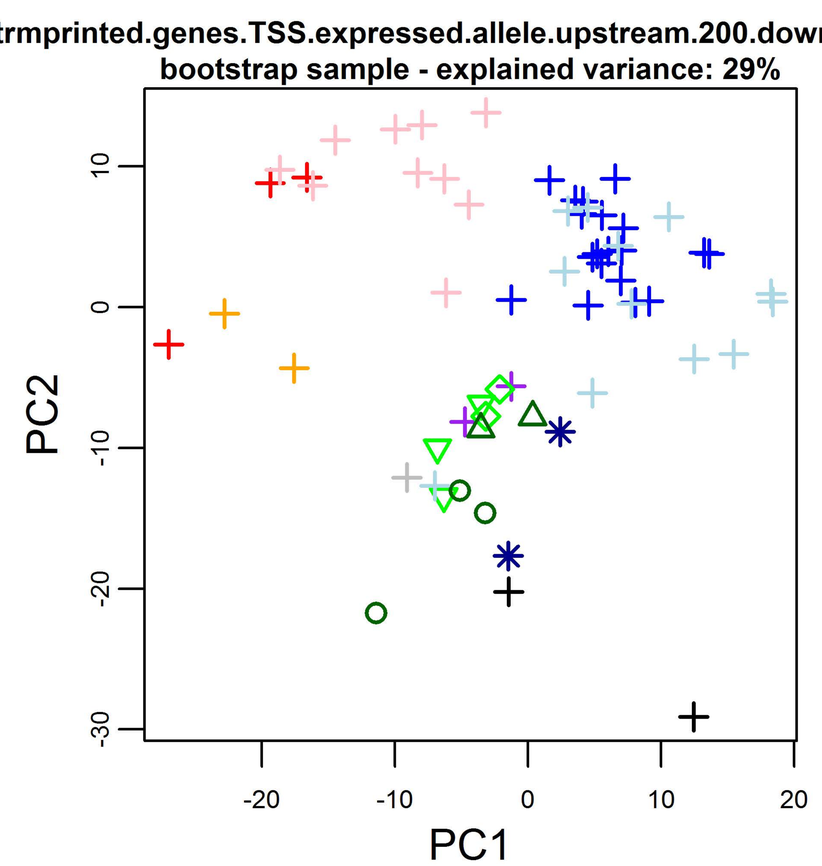

probes_TE_detailed - ICR.expressed.allele - Maternal
bootstrap sample - explained variance: 77%
PC2
PC1

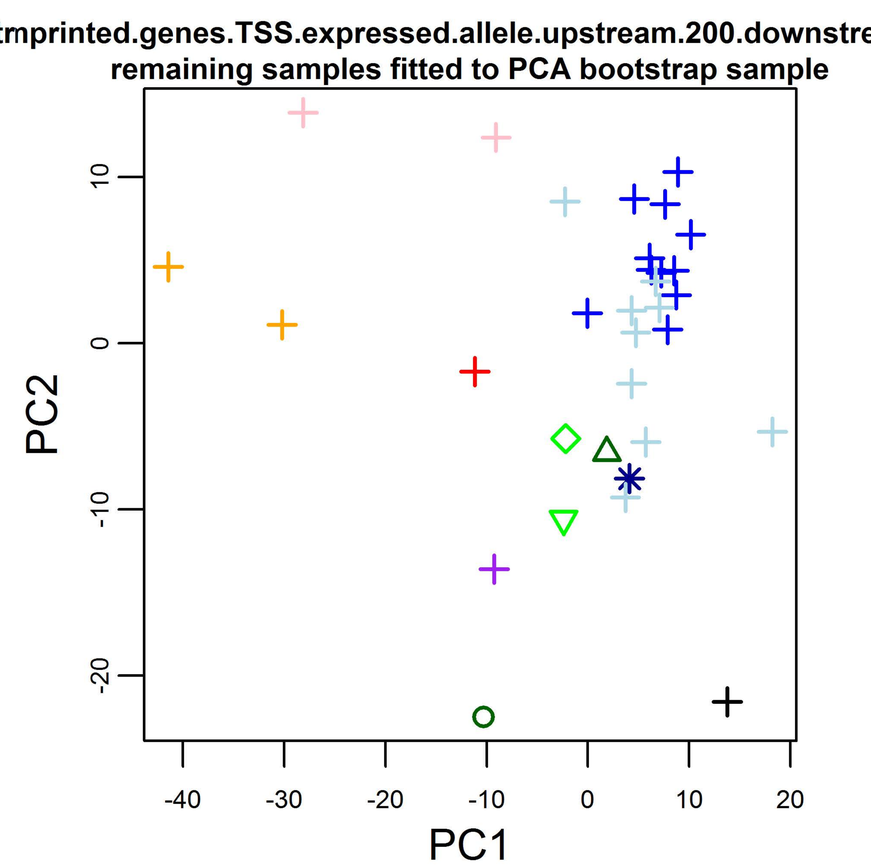

probes_TE_detailed - ICR.expressed.allele - Maternal -
remaining samples fitted to PCA bootstrap sample
PC2
PC1

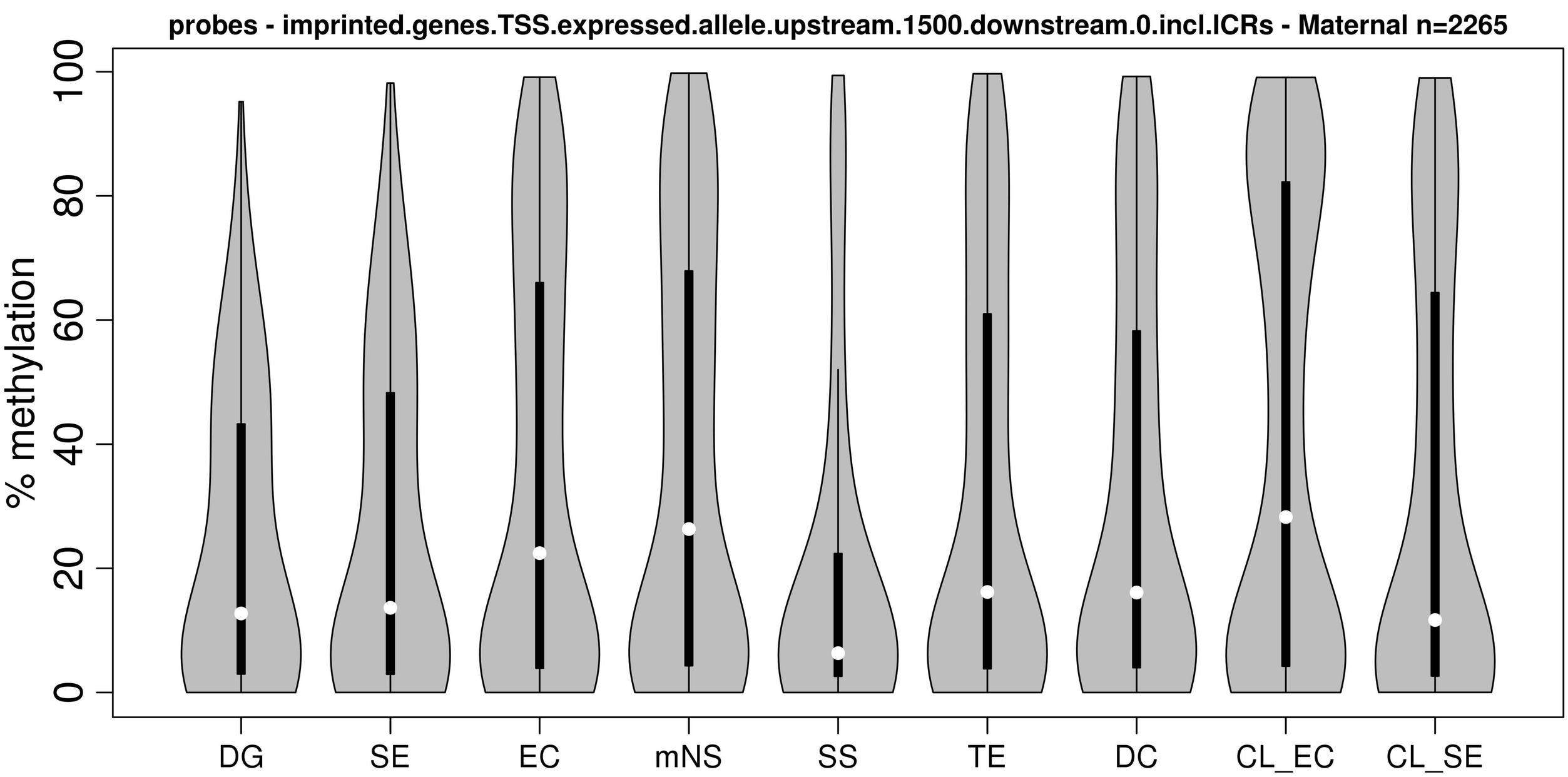

probes - imprinted.genes.TSS.expressed.allele.upstream.200.downstream.0.incl.ICRs - Maternal n=610
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE

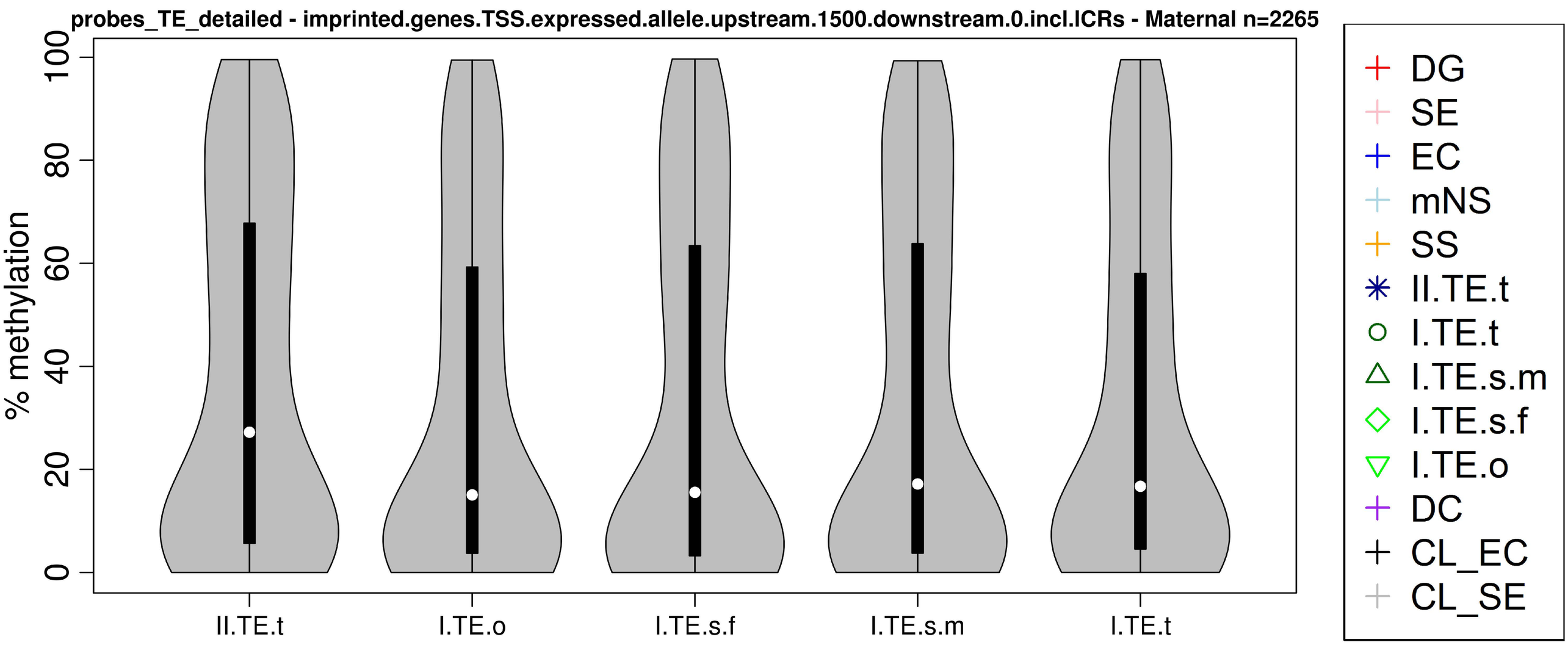

probes_TE_detailed - imprinted.genes.TSS.expressed.allele.upstream.200.downstream.0.incl.ICRs - Maternal n=610
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE

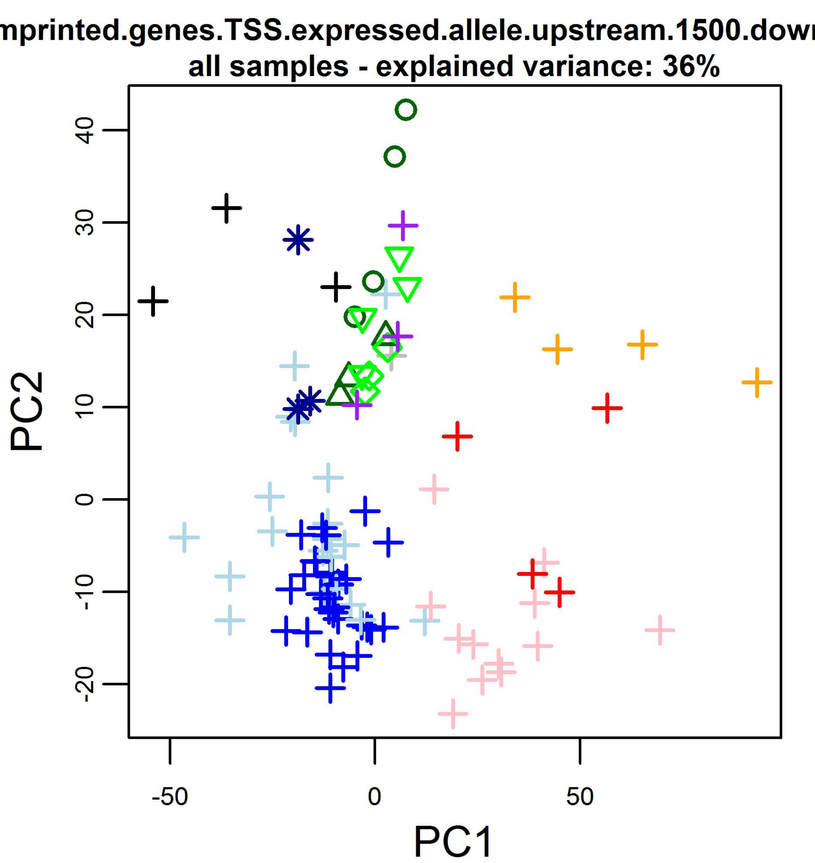

mprinted.genes.TSS.expressed.allele.upstream.200.downstr
all samples - explained variance: 32%
PC2
PC1
-20
-10
0
10
20
30
40

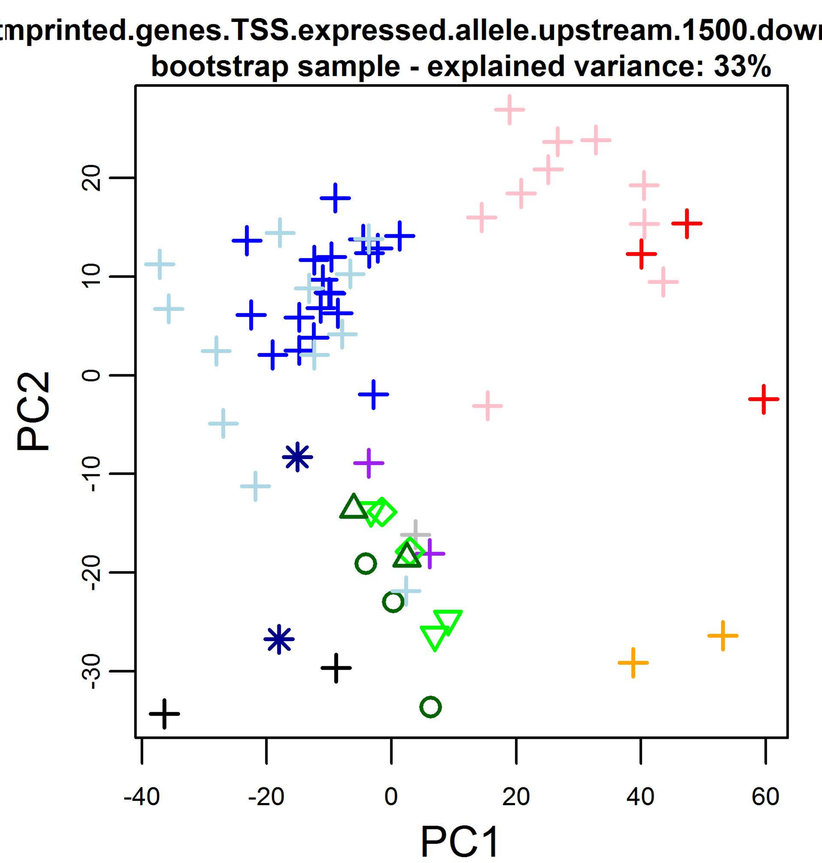

mprinted.genes.TSS.expressed.allele.upstream.200.downst
bootstrap sample - explained variance: 29%
PC2
PC1
-30
-20
-10
0
10
20

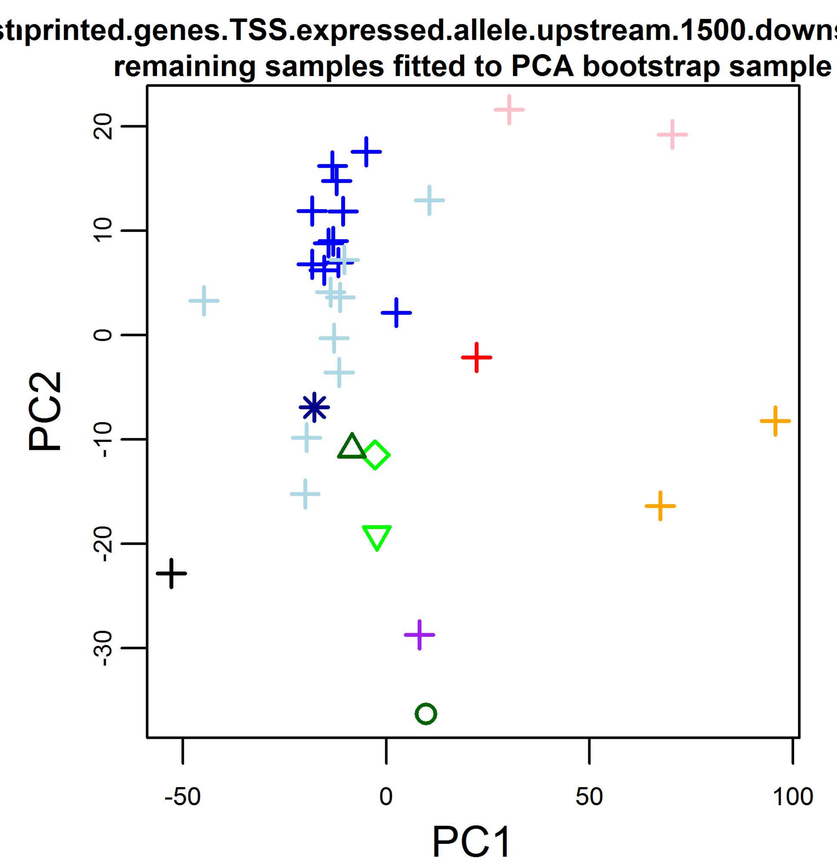

mprinted.genes.TSS.expressed.allele.upstream.200.downstre
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-40
-30
-20
-10
0
10
20


probes - imprinted.genes.TSS.expressed.allele.upstream.1500.downstream.0.incl.ICRs - Maternal n=2265
% methylation
0
20
40
60
80
100
DG
SE
EC
mNS
SS
TE
DC
CL_EC
CL_SE


probes_TE_detailed - imprinted.genes.TSS.expressed.allele.upstream.1500.downstream.0.incl.ICRs - Maternal n=2265
% methylation
0
20
40
60
80
100
II.TE.t
I.TE.o
I.TE.s.f
I.TE.s.m
I.TE.t
DG
SE
EC
mNS
SS
II.TE.t
I.TE.t
I.TE.s.m
I.TE.s.f
I.TE.o
DC
CL_EC
CL_SE


mprinted.genes.TSS.expressed.allele.upstream.1500.downst
all samples - explained variance: 36%
PC2
PC1
-50
0
50


mprinted.genes.TSS.expressed.allele.upstream.1500.downst
bootstrap sample - explained variance: 33%
PC2
PC1
-40
-20
0
20
40
60


printed.genes.TSS.expressed.allele.upstream.1500.downstre
remaining samples fitted to PCA bootstrap sample
PC2
PC1
-50
0
50
100