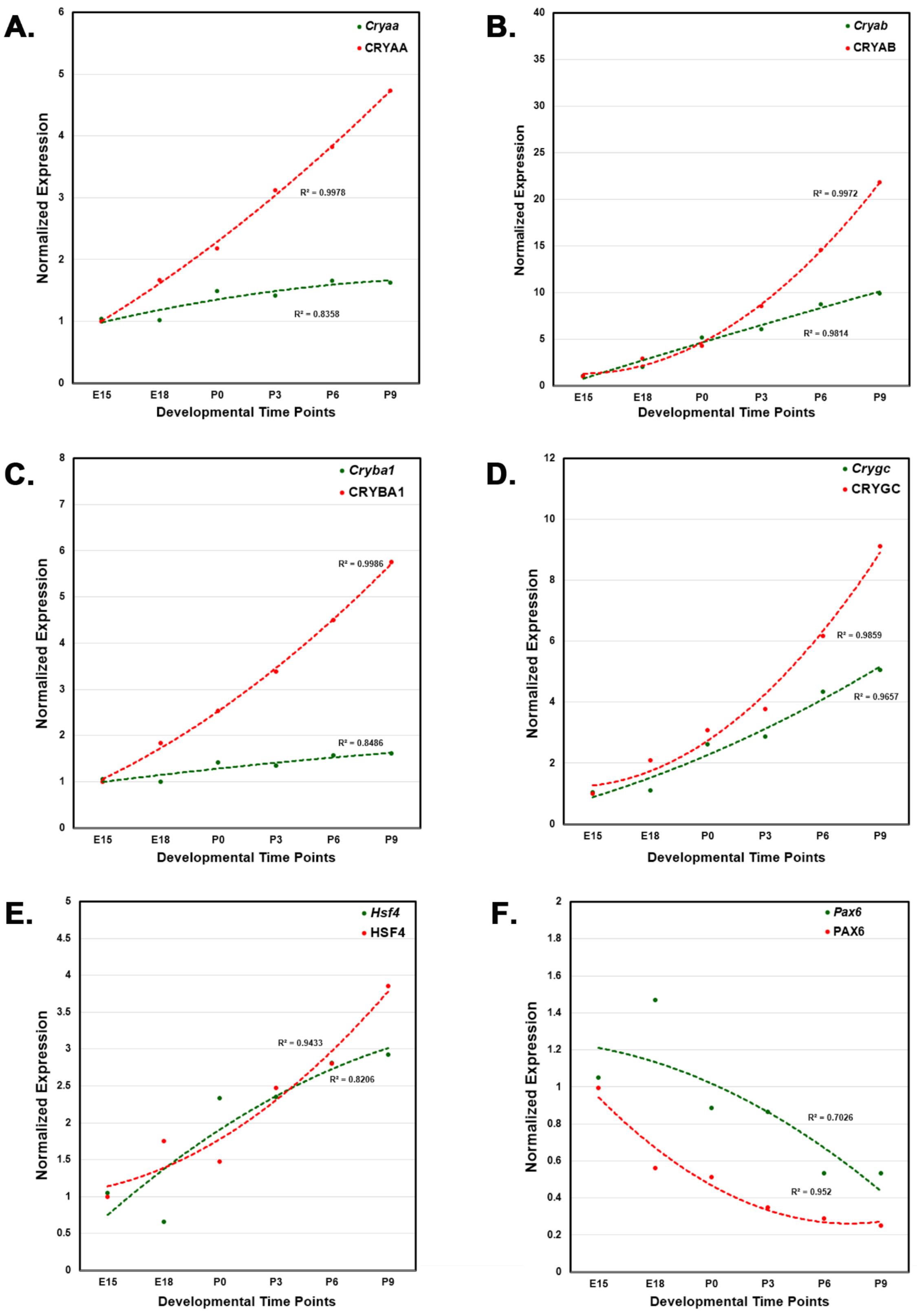
A.
Cryaa
CRYAA
R² = 0.9978
R² = 0.8358
Normalized Expression
Developmental Time Points
E15
E18
P0
P3
P6
P9
0
1
2
3
4
5
6
B.
Cryab
CRYAB
R² = 0.9972
R² = 0.9814
Normalized Expression
Developmental Time Points
0
5
10
15
20
25
30
35
40
C.
Cryba1
CRYBA1
R² = 0.9986
R² = 0.8486
Normalized Expression
Developmental Time Points
0
1
2
3
4
5
6
7
8
D.
Crygc
CRYGC
R² = 0.9859
R² = 0.9657
Normalized Expression
Developmental Time Points
0
2
4
6
8
10
12
E.
Hsf4
HSF4
R² = 0.9433
R² = 0.8206
Normalized Expression
Developmental Time Points
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
5
F.
Pax6
PAX6
R² = 0.7026
R² = 0.952
Normalized Expression
Developmental Time Points
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
1.8
2

Supplementary Figure 4: Illustrating the expression correlation trend in developing mouse lens transcriptome and proteome datasets at two embryonic (E15 and E18) and four postnatal (P0, P3, P6, and P9) time points. A-D) Graphs illustrating the normalized expression of crystallin proteins (crystallin alpha A (CryαA), crystallin alpha B (CryαB), crystallin beta A1 (CryβA1) and crystallin gamma C (CryγC)) at transcript and protein levels in developing mouse lens. The analyses identified an up-regulation trend for all crystallins at transcript and protein level in postnatal mouse lens. E-F) Showing the normalized expression values of HSF4, a heat shock transcription factor 4 and PAX6, a paired box 6 transcription factor in developing mouse lens transcriptome and proteome. The analysis identified an up-regulation of HSF4 at postnatal developmental time points in transcriptome and proteome datasets. Whereas, a down-regulation trend for PAX6 was identified in postnatal time points in transcriptome and proteome datasets. Green and red dots represent the transcripts and proteins normalized expression value in each graph. Whereas the green and red dotted lines represent the polynomial regression illustrating the differential expression trend across six developmental time points in mouse lens. The earliest developmental time point, E15, was set as the starting point, and the other five-time points were individually compared to E15, yielding each transcript and protein’s fold changes as development progressed. The y-axis depicts the normalized expression of transcript/protein, and the x-axis represent the developmental time points from two embryonic (E15 and E18) and four postnatal (P0, P3, P6, and P9) time points.