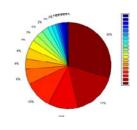


| Co-regulatory TF | Tissue          | -40g(P) |  |
|------------------|-----------------|---------|--|
| **               | **              | **      |  |
| CHIXTO           | erye            | 28.4156 |  |
| HNE-1            | kidney          | 23 6826 |  |
| COUP/TEANE-4     | kidney          | 22.6516 |  |
| PID/2            | 898             | 19.1804 |  |
| HNE.1            | small_intestine | 19 1628 |  |
| CROC             | 1010            | 18.5542 |  |
| HNF-4ALPHA       | locity          | 16 8834 |  |
| NK26-2           | smal_intestine  | 15 6923 |  |
| 1003             | small_intestine | 15.1010 |  |
| STAT5A           | 690             | 112.929 |  |
| EXR              | eye             | 12.8655 |  |
| TAL-1EETATIE-2   | <i>ay</i> 0     | 128105  |  |
| TAL-1EETAE-17    | aye             | 12,7791 |  |
| 45.1             | liver           | 12.23   |  |
| C/EBP            | muscle          | 11.6189 |  |
| PERSO            | thymus          | 11.0019 |  |
| OCT-1            | eye             | 10.7224 |  |
| MZF 1            | eye             | 10 6372 |  |
| 001-X            | eye             | 10.5787 |  |
| AP-1             | bladder         | 10.5385 |  |
| NE-AT            | smal_intestine  | 10.2656 |  |
| MYOD             | aya             | 10 2535 |  |
| RSRECA           | Jodney .        | 10.0576 |  |
| HEA              | lodney          | 10.0307 |  |
| TAL-18ETAITE-2   | muscle          | 9.93203 |  |
| TITE 1           | smal_intestine  | 9.75982 |  |
| ALPHA-CP1        | 690             | 9.5751  |  |
| GONE             | eye             | 9.4728  |  |
| HANDLEAT         | 0.0             | 943009  |  |



Distribution of Co-regulatory TFs

<u>Description</u>: this pie chart displays the distribution of co-regulatory transcription different bissues.

Color schema, the tissue with the largest percentage of co-regulatory TFs i whereas the tissue with the smallest percentage of co-regulatory TFs is colored to rissues with intermediate percentages of co-regulatory TFs are colored fit velow and coan and them to light blue.

## 242 Cis-Regulatory Module (CRM) detections in eye

## Download Table

| Chromosome<br>ID | CRM Start<br>Position | CRM End<br>Position | Gene Name | Transcription<br>Start Position | Orientation | Minimum<br>Energy | Transcription Factors                                 |
|------------------|-----------------------|---------------------|-----------|---------------------------------|-------------|-------------------|---|
| ▲ ▼              |                       |                     |           |                                 |             |                   |   |
| chr.1            | 68623595              | 68623680            | NM_000329 | 68627663                        | -1          | -1.10877          | FOXJ2 :: POU3F2 :: STAT5A :<br>SMAD-3 :: TATA         |
| chr.1            | 168352546             | 168352581           | NM_000261 | 168353430                       | -1          | -1.22283          | OCT-1 :: FOXJ2 :: POU3F2 ::<br>NR2E3 :: FOXO4         |
| chr.1            | 168352381             | 168352413           | NM_000261 | 168353430                       | -1          | -1.15567          | OCT-1 :: FOXJ2 :: POU3F2 ::<br>PBX1B :: FOXO1         |
| chr.1            | 168352357             | 168352368           | NM_000261 | 168353430                       | -1          | -1.01014          | FOXJ2 ::: OCT-1 :: POU3F2 ::<br>PBX1B :: FOXO1        |
| chr.1            | 193968043             | 193968048           | NM_012076 | 193969064                       | 1           | -1.00136          | FOXJ2 :: POU3F2 :: NKX6-2 ::<br>OCT-1 :: MEIS1A/HOXA9 |

### 289 RefSeq Genes are preferentially expressed in eye

#### Download Table

| RefSeq EST<br>Enrichmer |         | Gene<br>Symbol | Description  |  |  |
|-------------------------|---------|----------------|--|--|--|
| ▲ ▼                     |         | <b>A V</b>     |  |  |  |
| NM_032753               | 20.1971 | MGC15631       | Homo sapiens hypothetical protein MGC15631<br>(MGC15631), mRNA           |  |  |
| NM_021225               | 20.1971 | PROL1          | Homo sapiens proline rich, lacrimal 1 (PROL1), mRNA                      |  |  |
| NM_033277               | 20.1971 | LACRT          | Homo sapiens lacritin (LACRT), mRNA                                      |  |  |
| NM_007374               | 20.1971 | SIX6           | Homo sapiens sine oculis homeobox homolog 6<br>(Drosophila) (SIX6), mRNA |  |  |
| NM_030657               | 20.1971 | LIM2           | Homo sapiens lens intrinsic membrane protein 2<br>19kDa (LIM2), mRNA     |  |  |

# 307 transcription factor pairs co-regulate in eye

| Download Table<br>1st Factor | 2nd Factor | -log(P) |  |
|------------------------------|------------|---------|--|
|                              |            |         |  |
| FOXJ2                        | POU3F2     | 39.9539 |  |
| CHX10                        | CHX10      | 32.5137 |  |
| CHX10                        | CRX        | 28.4156 |  |
| FOXJ2                        | FOXJ2      | 20.8575 |  |
| FOXJ2                        | Oct-1      | 20.6056 |  |
| CRX                          | PITX2      | 19.1884 |  |
| CHX10                        | GATA-6     | 18.7433 |  |
| CRX                          | CRX        | 18.5542 |  |

# B. Transcription Factor View