**Supplementary Table 1. Patient Demographics**

| | **Discovery Cohort N=10** | **ELISA Test Cohort N=150** |
|---|---|---|
| **Recipient Age (mean, SD)** | 58 ± 9 | 49 ± 15 |
| **Race (% non-white)** | 10% | **44%** |
| **Male Gender (%)** | 90% | **41%** |
| **Previous transplantation (%)** | 60% | 40% |
| **HLA Sensitization[1] (%)** | 90% | 91% |
| **Mean % CPRA[2] (CDC-XM, FCXM)** | 18, 38 | 29, 39 |
| **Original ABO or HLA barrier[3]: (%)** | | |
| **ABOi** | 20% | 6% |
| **CDC-XM+** | 0 | 2% |
| **FCXM+** | 10% | 19% |
| **FCXM-, DSA+** | 40% | 45% |
| **NO DSA** | 50% | 34% |
| **Donor (Mean Age)** | 45 ± 12 | 40 ± 15 |
| **Live Donor (%)** | 70% | 55% |
| **Deceased Donor (%)** | 30% | 45% |
| **HLA-A;B;DR;DQ mismatch (mean)** | 5.0 | 4.7 |
| **Plasmapheresis Treatments:** | | |
| **No Pre- or Post- Treatments (%)** | 20% | 45% |
| **Pre-transplant (Mean, Median)** | 2.5, 1.5 | 1.0, 0.0 |
| **Post-transplant (Mean, Median)** | 4.4, 3.5 | 4.0, 2.0 |
| **anti-CD25 induction (% )** | 40% | 17% |
| **Thymoglobulin induction (% )** | 60% | 83% |
| **Rituximab induction (%)** | 30% | 36% |

[1] HLA-specific antibody detected on Luminex® platforms

[2] [2] Calculated panel reactive antibody (CPRA) was determined for HLA-antibodies of sufficient strength to yield a positive CDC crossmatch (CDC-XM) or flow cytometric crossmatch (FCXM)

[3] Original donor HLA-specific antibody (DSA) strength prior to desensitization treatments

**Supplementary Table 2. Protein array analysis of 14 AECA eluates derived from 10 Discovery Cohort Recipients**

| | Protein Name | Gene Symbol | Average RFU |
|---|---|---|---|
| 1. | Recombinant human CTLA-4/Fc | CTLA-4 | 58077.0 |
| 2. | tripartite motif-containing 21 (TRIM21) | TRIM21 | 39835.7 |
| 3. | hematopoietic SH2 domain containing (HSH2D) | HSH2D | 28572.5 |
| 4. | interferon, alpha-inducible protein 6 (IFI6) | IFI6 | 15892.2 |
| 5. | APEX nuclease (apurinic/apyrimidinic endonuclease) 2 (APEX2), nuclear gene encoding mitochondrial protein | APEX2 | 12493.3 |
| 6. | CAP-GLY domain containing linker protein family, member 4 (CLIP4) | CLIP4 | 10955.7 |
| 7. | UBX domain containing 8 (UBXD8) | UBXD8 | 8636.5 |
| 8. | zinc finger, MYM-type 5 (ZMYM5) | ZMYM5 | 8260.8 |
| 9. | **EGF-like repeats and discoidin I-like domains 3 (EDIL3)** | **EDIL3** | **8232.8** |
| 10 | ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) | UBE2V1 | 7955.9 |
| 11 | phosphoglycerate dehydrogenase (PHGDH) | PHGDH | 7405.2 |
| 12 | sciellin (SCEL) | SCEL | 7255.3 |
| 13 | Zinc finger CCHC domain-containing protein 8 | ZCCHC8 | 5908.2 |
| 14 | chromosome 22 open reading frame 33 (C22orf33) | C22orf33 | 5578.2 |
| 15 | cleavage and polyadenylation specific factor 3, 73kDa (CPSF3) | CPSF3 | 5425.6 |
| 16 | Uncharacterized protein C20orf96 | C20orf96 | 5031.8 |
| 17 | **endoglin (Osler-Rendu-Weber syndrome 1) (ENG)** | **ENG** | **4966.8** |
| 18 | Disks large homolog 3 | DLG3 | 4352.0 |
| 19 | cyclin G associated kinase (GAK) | GAK | 4298.4 |
| 20 | CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3) | CDC42EP3 | 4280.3 |
| 21 | ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), transcript variant 2 | ARFGAP1 | 4211.4 |
| 22 | baculoviral IAP repeat-containing 4 (BIRC4) | BIRC4 | 4108.5 |
| 23 | chromosome 2 open reading frame 47 (C2orf47) | C2orf47 | 3597.3 |
| 24 | quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 4 | QKI | 3493.8 |
| 25 | **intercellular adhesion molecule 4 (Landsteiner-Wiener blood group) (ICAM4), transcript variant 1** | **ICAM4** | 3412.4 |
| 26 | **fms-related tyrosine kinase 3 ligand (FLT3LG)** | **FLT3LG** | **3383.8** |
| 27 | hypothetical protein LOC51233, mRNA (cDNA clone MGC:75009 IMAGE:5170001), complete cds. | LOC51233 | 3331.7 |
| 28 | Parkinson disease 7 domain containing 1 (PDDC1) | PDDC1 | 3296.6 |
| 29 | forkhead box P1 (FOXP1) | FOXP1 | 3267.5 |
| 30 | nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1 (NUDT16L1) | NUDT16L1 | 3256.8 |
| 31 | ubiquilin 2 (UBQLN2) | UBQLN2 | 3129.8 |
| 32 | TOX high mobility group box family member 2 (TOX2), transcript variant 3 | TOX2 | 3102.1 |
| 33 | AF4/FMR2 family, member 4 (AFF4) | AFF4 | 3050.3 |

| | | | |
|---|---|---|---|
| 34 | CWF19-like 2, cell cycle control (S. pombe) (CWF19L2) | CWF19L2 | 2924.5 |
| 35 | glutaryl-Coenzyme A dehydrogenase (GCDH), nuclear gene encoding mitochondrial protein, transcript variant 1 | GCDH | 2666.8 |
| 36 | Protein FAM184A | C6orf60 | 2661.1 |
| 37 | SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae) (SUMO1), transcript variant 1 | SUMO1 | 2559.8 |
| 38 | chromogranin B (secretogranin 1) (CHGB) | CHGB | 2559.3 |
| 39 | zinc finger protein 695 (ZNF695) | ZNF695 | 2529.8 |
| 40 | LIM homeobox transcription factor 1, alpha (LMX1A) | LMX1A | 2476.6 |
| 41 | complexin 2 (CPLX2), transcript variant 2 | CPLX2 | 2435.8 |
| 42 | myotilin (MYOT) | MYOT | 2362.6 |
| 43 | sorting nexin 13 (SNX13) | SNX13 | 2324.0 |
| **44** | **intercellular adhesion molecule 4 (Landsteiner-Wiener blood group) (ICAM4)** | **ICAM4** | **2268.7** |
| 45 | centrosome and spindle pole associated protein 1 (CSPP1), transcript variant 2 | CSPP1 | 2256.9 |
| 46 | glycogenin 2 (GYG2) | GYG2 | 2227.8 |
| 47 | outer dense fiber of sperm tails 2 (ODF2) | ODF2 | 2226.6 |
| 48 | transcriptional adaptor 3 (NGG1 homolog, yeast)-like (TADA3L), transcript variant 2 | TADA3L | 2204.3 |
| 49 | aquaporin 2 (collecting duct) (AQP2) | AQP2 | 2197.4 |
| 50 | dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD), transcript variant Dp71b | DMD | 2136.8 |
| 51 | hypothetical protein FLJ22795 (FLJ22795) | FLJ22795 | 2117.2 |
| 52 | muted homolog (mouse) (MUTED) | MUTED | 2096.1 |
| 53 | proline/arginine-rich end leucine-rich repeat protein (PRELP), transcript variant 1 | PRELP | 2063.3 |
| 54 | major histocompatibility complex, class II, DP alpha 1 (HLA-DPA1) | HLA-DPA1 | 2053.5 |
| 55 | testis-specific serine kinase 2 (TSSK2) | TSSK2 | 2046.3 |