

Supporting Information

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SI Text

Materials and Methods Red-green color correction and alignment A two-dimensional lookup table routine, implemented in Matlab (Mathworks Inc.), was used to spatially register the coordinates of quantum dots tracked through sequences of red and green images. The lookup table was first constructed by simultaneously acquiring red and green images of a 0.19 μm multicolored fluorescent bead (Ultra Rainbow Particles; Spherotech) on a glass cover slip. A piezoelectric x-y translation stage was used to move the bead around the microscope's field of view in a grid pattern with 1.7 μm spacing. An image was acquired with the bead at each point in the grid, and the series was merged into a single image for each channel (Fig. S9A).

A particle image velocimetry routine (1) (mpiv toolbox by Nobuhito Mori, distributed under GNU public license) was used, which was developed for fluid flow applications to determine the displacement of particles between two images by 2D cross-correlation. The cross-correlation involved taking a 120 pixel, square window in both the red and green images and rastering

these windows simultaneously through the two images with 85% overlap for one window position to the next. This routine created an array of 126 vectors defining the correction offsets required at each location within the red channel image to match up with the green channel image (Fig. S9B). This array was then cubically interpolated to provide offsets for each pixel in both the horizontal and vertical dimensions (Fig. S9C). The procedure was repeated nineteen times with different grid images, and the standard deviations of horizontal and vertical offsets were used as a measure of local uncertainty of the lookup table, with greater standard deviations indicative of greater uncertainty (Fig. S9D).

Each dual-colored FLB-myov head position trace was then aligned by taking the x and y coordinates of the red quantum dot-labeled head at each time point and correcting its position relative to the green quantum dot-labeled head by the appropriate horizontal and vertical correction offsets (Fig. S9C) with sub-pixel resolution.

1. Michalek AJ, Buckley MR, Bonassar LJ, Cohen I, & Iatridis JC (2009) Measurement of local strains in intervertebral disc anulus fibrosus tissue under dynamic shear: contributions of matrix fiber orientation and elastin content. *J Biomech* 42(14):2279–2285.

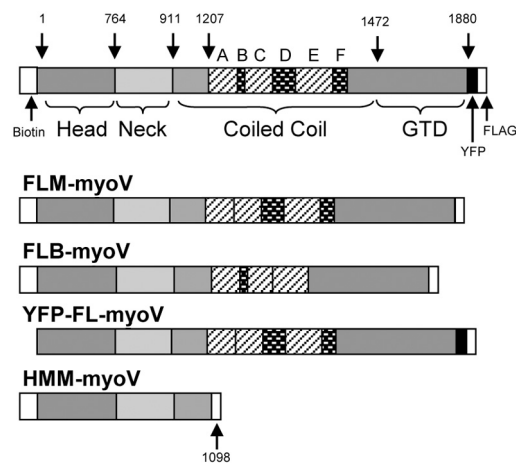


Fig. S1. MyoV constructs. (Top) The full-length myoV transcript containing all exons, an N-terminal biotin tag for conjugation with streptavidin-Qdots, and a C-terminal YFP and FLAG tag for purification. Alternatively spliced exons A–G are labeled. The melanocyte splice variant (FLM-myov) expresses exons ACDEF without the YFP whereas the brain splice variant (FLB-myov) expresses exons ABCE without the YFP. A FLM-myov YFP construct (YFP-FLM-myov) without the N-terminal biotin was used as a control for artifacts potentially created by the addition of a Qdot to the N-terminus of the motor. The HMM-myov construct is truncated at amino acid 1098, prior to the PEST site within the coiled-coil tail.

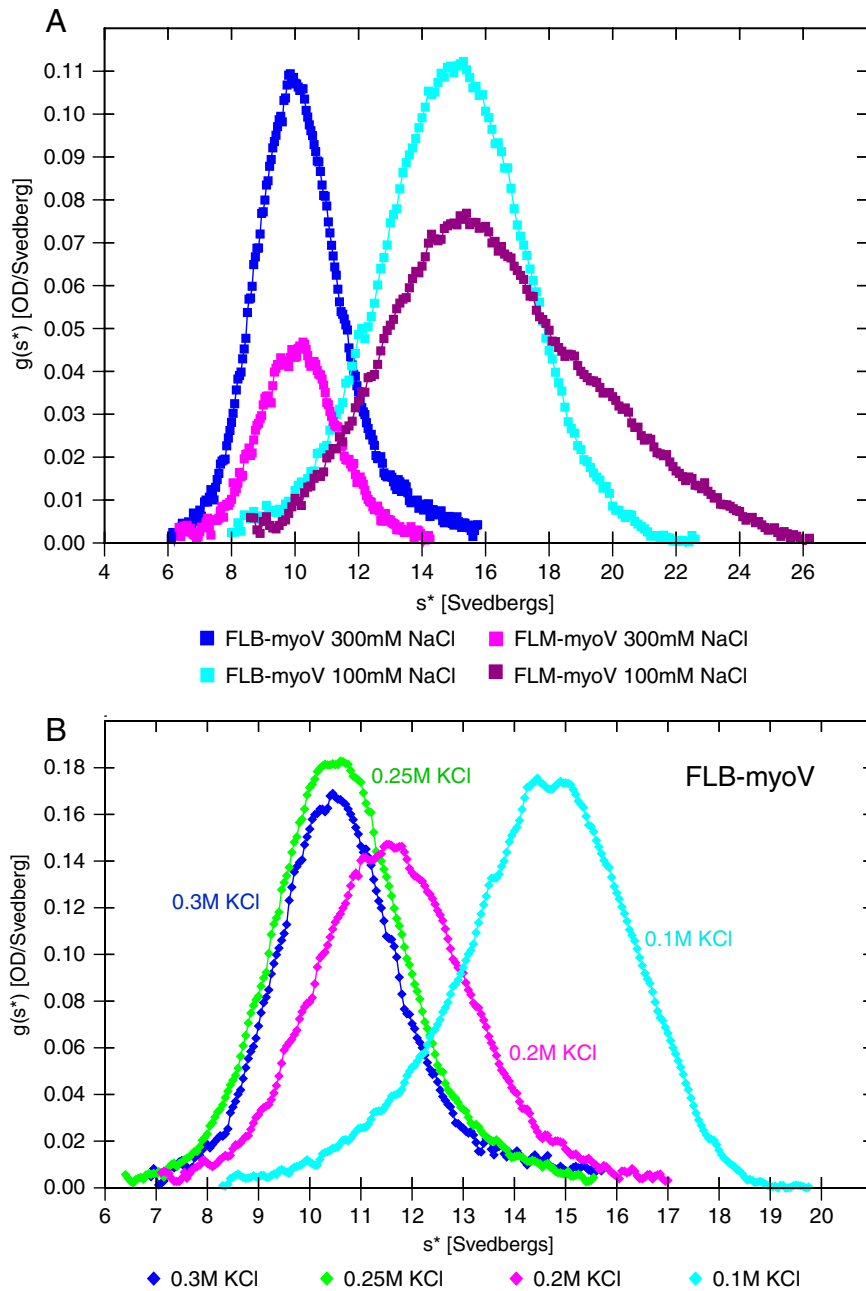
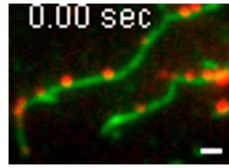


Fig. S2. Characterization of full-length constructs by analytical ultracentrifugation. (A) At 100 mM NaCl both FLB-myov (cyan) and FLM-myov (burgundy) adopt the folded conformation which sediments at approximately 15 S. At 300 mM NaCl, both isoforms form an extended conformation that sediments at approximately 10 S (FLB-myov, blue; FLM-myov, magenta). Buffer: 10 mM HEPES pH 7.4, 1 mM EGTA and DTT, 0.1 M, or 0.3 M NaCl. (B) Sedimentation of FLB-myov as a function of KCl concentration shows that the molecule is primarily extended at 0.2 M KCl. Sedimentation values are: 14.8 S (0.1 M KCl); 11.5 S (0.2 M KCl); 10.5 S (0.25 M KCl); 10.5 S (0.3 M KCl). The buffer used for these experiments is identical to that used for the single-molecule studies (25 mM Imidazole pH 7.4, 4 mM $MgCl_2$, 1 mM EGTA and DTT, KCl at 0.1 M, 0.2 M, 0.25 M, or 0.3 M).



Movie S2. HMM-myosin V moves processively along actin filaments at low ionic strength (25 mM KCl) and 1 mM ATP. Qdot-labeled HMM-myosin V (red) are seen moving along actin filaments (green) at 25 mM KCl and 1 mM MgATP. In contrast to the full-length motors (see Movie S1), nearly all of the actin-associated motors are processive. The scale bar represents 1 μm . The original video was captured for 29.4 s (video playback speed is 2 \times).

[Movie S2 \(AVI\)](#)



Movie S3. FLB-myosin V moves processively along actin at low ionic strength (25 mM KCl) and 1 mM ATP. A single Qdot-labeled FLB-myosin V (red) is seen moving along an actin filament (green). As described in the text, this processive motion can be broken up in to periods of fast and slow movement. The scale bar represents 1 μm . The original video was captured for 49.5 s (video playback speed is 4 \times).

[Movie S3 \(AVI\)](#)



Movie S4. HMM-myosin V moves processively along actin at low ionic strength (25 mM KCl) and 1 mM ATP. Two Qdot-labeled HMM-myosin V (red) are seen moving along an actin filament (green). In contrast to FLB-myosin V, HMM-myosin V moves at a constant velocity throughout the entire trajectory. The scale bar represents 1 μm . The original video was captured for 9.5 s (video playback speed is 4 \times).

[Movie S4 \(AVI\)](#)