Figure 1. Increased body weight and impaired muscle mass maintenance in mice with persistent GSK-3 activation. Body (A, B) or muscle (C, D, E) weights were determined at baseline, or following 14 days of hind limb suspension (HS) of 12 wks old WT or GSK-3a/b S21/9A KI mice (n>7).
Figure 2. GSK-3β is required for glucocorticoid-driven muscle atrophy.

WT or MLC-Cre/GSK-3βfl/fl (muscle-specific GSK-3β KO) mice (n>8) were subjected to 48h starvation (A-D) or daily s.c. dexamethasone injections for 14 days (E-F). Plasma corticosterone (A), muscle weight (B) or mRNA transcript levels of Atrogin-1 or MuRF1 (C), or LC3b or Bnip3 (D) were assessed as indices of ubiquitin 26S-proteasome-, or autophagy-mediated muscle proteolysis, respectively following starvation. Alternatively, muscle weights (E) or myofiber cross sectional area (CSA: F) were determined to assess muscle atrophy following dexamethasone injections.
**Figure 3.** A GSK-3β-GR signaling axis is required for pulmonary inflammation-induced muscle atrophy.

WT or MLC-Cre/GSK-3βfl/fl (muscle-specific GSK-3β KO: A-D) or MLC-Cre/GRfl/fl (muscle-specific GR KO: E-F) mice (n>8) received an intra-tracheal instillation with LPS (single bolus) to induce pulmonary inflammation, and skeletal muscles were collected 48h later. Plasma corticosteron (A), muscle weight or myofiber cross sectional area (CSA) were determined to assess muscle atrophy (B, E). mRNA transcript levels of Atrogin-1 or MuRF1 (C, E), or FoXO1 or KLF15 (D, F) were assessed as indices of ubiquitin 26S-proteasome-mediated muscle proteolysis, or glucorticoid receptor-controlled regulators therefore, respectively.
Figure 4. Accelerated muscle mass recovery and regeneration of disuse-atrophied muscle in absence of GSK-3b.

WT or MLC-Cre/GSK-3bfl/fl (muscle-specific GSK-3b KO) mice (n>8) were subjected to 14 days of hind limb suspension followed by reloading (RL). Muscle weight (A) or myofiber cross sectional area (CSA: B) were determined to assess muscle mass recovery. RNA was extracted and various mRNA transcript levels were assessed: FoxO1 and MuRF1 (C) as regulators and effectors of muscle proteolysis, Pax7 and PCNA (D) to evaluate satellite cell activation and proliferation, or MyoD and myogenin (E) to assess myogenesis.